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(54) Title: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE RELATED DISEASES

(57) Abstract: The present invention relates to compositions containing novel proteins and methods of using those compositions for the diagnosis and treatment of immune related diseases.

COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE RELATED DISEASES

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Field of the Invention

The present invention relates to compositions and methods useful for the diagnosis and treatment of immune related diseases.

Background of the Invention

10 Immune related and inflammatory diseases are the manifestation or consequence of fairly complex, often multiple interconnected biological pathways which in normal physiology are critical to respond to insult or injury, initiate repair from insult or injury, and mount innate and acquired defense against foreign organisms. Disease or pathology occurs when these normal physiological pathways cause additional insult or injury either as directly related to the intensity of the response, as a consequence of abnormal regulation or excessive stimulation, as a reaction to self, or as a combination of these.

Though the genesis of these diseases often involves multistep pathways and often multiple different biological systems/pathways, intervention at critical points in one or more of these pathways can have an ameliorative or therapeutic effect. Therapeutic intervention can occur by either antagonism of a detrimental process/pathway or stimulation of a beneficial process/pathway.

20 Many immune related diseases are known and have been extensively studied. Such diseases include immune-mediated inflammatory diseases, non-immune-mediated inflammatory diseases, infectious diseases, immunodeficiency diseases, neoplasia, *etc.*

T lymphocytes (T cells) are an important component of a mammalian immune response. T cells recognize antigens which are associated with a self-molecule encoded by genes within the major histocompatibility complex (MHC). The antigen may be displayed together with MHC molecules on the surface of antigen presenting cells, virus infected cells, cancer cells, grafts, *etc.* The T cell system eliminates these altered cells which pose a health threat to the host mammal. T cells include helper T cells and cytotoxic T cells. Helper T cells proliferate extensively following recognition of an antigen-MHC complex on an antigen-presenting cell. Helper T cells also secrete a variety of cytokines, *i.e.*, lymphokines, which play a central role in the activation of B cells, cytotoxic T cells and a variety of other cells which participate in the immune response.

30 Immune related diseases could be treated by suppressing the immune response. Using neutralizing antibodies that inhibit molecules having immune stimulatory activity would be beneficial in the treatment of immune-mediated and inflammatory diseases. Molecules which inhibit the immune response can be utilized (proteins directly or via the use of antibody agonists) to inhibit the immune response and thus ameliorate immune related disease.

CD4+ T cells are known to be important regulators of inflammation. Herein, CD4+ T cells were activated and the profile of genes differentially expressed upon activation was analyzed. As such, the activation specific genes may be potential therapeutic targets. *In vivo* co-stimulation is necessary for a productive immune proliferative response. The list of costimulatory molecules is quite extensive and it is

still unclear just which co-stimulatory molecules play critical roles in different types and stages of inflammation. In this application the focus is on genes which are specifically upregulated by stimulation with ICAM, anti-CD28 or ICAM/anti-CD28 in combination and may be useful in targeting inflammatory processes which are associated with these different molecules.

5

Summary of the Invention

A. Embodiments

The present invention concerns compositions and methods useful for the diagnosis and treatment of immune related disease in mammals, including humans. The present invention is based on the identification of proteins (including agonist and antagonist antibodies) which are a result of stimulation of the immune response in mammals. Immune related diseases can be treated by suppressing or enhancing the immune response. Molecules that enhance the immune response stimulate or potentiate the immune response to an antigen. Molecules which stimulate the immune response can be used therapeutically where enhancement of the immune response would be beneficial. Alternatively, molecules that suppress the immune response attenuate or reduce the immune response to an antigen (*e.g.*, neutralizing antibodies) can be used therapeutically where attenuation of the immune response would be beneficial (*e.g.*, inflammation). Accordingly, the PRO polypeptides, agonists and antagonists thereof are also useful to prepare medicines and medicaments for the treatment of immune-related and inflammatory diseases. In a specific aspect, such medicines and medicaments comprise a therapeutically effective amount of a PRO polypeptide, agonist or antagonist thereof with a pharmaceutically acceptable carrier. Preferably, the admixture is sterile.

In a further embodiment, the invention concerns a method of identifying agonists or antagonists to a PRO polypeptide which comprises contacting the PRO polypeptide with a candidate molecule and monitoring a biological activity mediated by said PRO polypeptide. Preferably, the PRO polypeptide is a native sequence PRO polypeptide. In a specific aspect, the PRO agonist or antagonist is an anti-PRO antibody.

In another embodiment, the invention concerns a composition of matter comprising a PRO polypeptide or an agonist or antagonist antibody which binds the polypeptide in admixture with a carrier or excipient. In one aspect, the composition comprises a therapeutically effective amount of the polypeptide or antibody. In another aspect, when the composition comprises an immune stimulating molecule, the composition is useful for: (a) increasing infiltration of inflammatory cells into a tissue of a mammal in need thereof, (b) stimulating or enhancing an immune response in a mammal in need thereof, (c) increasing the proliferation of T-lymphocytes in a mammal in need thereof in response to an antigen, (d) stimulating the activity of T-lymphocytes or (e) increasing the vascular permeability. In a further aspect, when the composition comprises an immune inhibiting molecule, the composition is useful for: (a) decreasing infiltration of inflammatory cells into a tissue of a mammal in need thereof, (b) inhibiting or reducing an immune response in a mammal in need thereof, (c) decreasing the activity of T-lymphocytes or (d) decreasing the proliferation of T-lymphocytes in a mammal in need thereof in response to an antigen. In another aspect, the composition comprises a further active ingredient, which may, for example, be a further antibody or a cytotoxic or chemotherapeutic agent. Preferably, the composition is sterile.

In another embodiment, the invention concerns a method of treating an immune related disorder in

a mammal in need thereof, comprising administering to the mammal an effective amount of a PRO polypeptide, an agonist thereof, or an antagonist thereto. In a preferred aspect, the immune related disorder is selected from the group consisting of: systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjögren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic anemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems such as multiple sclerosis, idiopathic demyelinating polyneuropathy or Guillain-Barré syndrome, and chronic inflammatory demyelinating polyneuropathy, hepatobiliary diseases such as infectious, autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, and sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, and Whipple's disease, autoimmune or immune-mediated skin diseases including bullous skin diseases, erythema multiforme and contact dermatitis, psoriasis, allergic diseases such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria, immunologic diseases of the lung such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonitis, transplantation associated diseases including graft rejection and graft -versus-host-disease.

In another embodiment, the invention provides an antibody which specifically binds to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, humanized antibody, antibody fragment or single-chain antibody. In one aspect, the present invention concerns an isolated antibody which binds a PRO polypeptide. In another aspect, the antibody mimics the activity of a PRO polypeptide (an agonist antibody) or conversely the antibody inhibits or neutralizes the activity of a PRO polypeptide (an antagonist antibody). In another aspect, the antibody is a monoclonal antibody, which preferably has nonhuman complementarity determining region (CDR) residues and human framework region (FR) residues. The antibody may be labeled and may be immobilized on a solid support. In a further aspect, the antibody is an antibody fragment, a monoclonal antibody, a single-chain antibody, or an anti-idiotypic antibody.

In yet another embodiment, the present invention provides a composition comprising an anti-PRO antibody in admixture with a pharmaceutically acceptable carrier. In one aspect, the composition comprises a therapeutically effective amount of the antibody. Preferably, the composition is sterile. The composition may be administered in the form of a liquid pharmaceutical formulation, which may be preserved to achieve extended storage stability. Alternatively, the antibody is a monoclonal antibody, an antibody fragment, a humanized antibody, or a single-chain antibody.

In a further embodiment, the invention concerns an article of manufacture, comprising:

- (a) a composition of matter comprising a PRO polypeptide or agonist or antagonist thereof;
- (b) a container containing said composition; and
- (c) a label affixed to said container, or a package insert included in said container referring to the use of said PRO polypeptide or agonist or antagonist thereof in the treatment of an immune related disease. The composition may comprise a therapeutically effective amount of the PRO polypeptide or the agonist or antagonist thereof.

In yet another embodiment, the present invention concerns a method of diagnosing an immune related disease in a mammal, comprising detecting the level of expression of a gene encoding a PRO

polypeptide (a) in a test sample of tissue cells obtained from the mammal, and (b) in a control sample of known normal tissue cells of the same cell type, wherein a higher or lower expression level in the test sample as compared to the control sample indicates the presence of immune related disease in the mammal from which the test tissue cells were obtained.

5 In another embodiment, the present invention concerns a method of diagnosing an immune disease in a mammal, comprising (a) contacting an anti-PRO antibody with a test sample of tissue cells obtained from the mammal, and (b) detecting the formation of a complex between the antibody and a PRO polypeptide, in the test sample; wherein the formation of said complex is indicative of the presence or absence of said disease. The detection may be qualitative or quantitative, and may be performed in
10 comparison with monitoring the complex formation in a control sample of known normal tissue cells of the same cell type. A larger quantity of complexes formed in the test sample indicates the presence or absence of an immune disease in the mammal from which the test tissue cells were obtained. The antibody preferably carries a detectable label. Complex formation can be monitored, for example, by light microscopy, flow cytometry, fluorimetry, or other techniques known in the art. The test sample is usually
15 obtained from an individual suspected of having a deficiency or abnormality of the immune system.

In another embodiment, the invention provides a method for determining the presence of a PRO polypeptide in a sample comprising exposing a test sample of cells suspected of containing the PRO polypeptide to an anti-PRO antibody and determining the binding of said antibody to said cell sample. In a specific aspect, the sample comprises a cell suspected of containing the PRO polypeptide and the antibody
20 binds to the cell. The antibody is preferably detectably labeled and/or bound to a solid support.

In another embodiment, the present invention concerns an immune-related disease diagnostic kit, comprising an anti-PRO antibody and a carrier in suitable packaging. The kit preferably contains instructions for using the antibody to detect the presence of the PRO polypeptide. Preferably the carrier is pharmaceutically acceptable.

25 In another embodiment, the present invention concerns a diagnostic kit, containing an anti-PRO antibody in suitable packaging. The kit preferably contains instructions for using the antibody to detect the PRO polypeptide.

In another embodiment, the invention provides a method of diagnosing an immune-related disease in a mammal which comprises detecting the presence or absence of a PRO polypeptide in a test sample of
30 tissue cells obtained from said mammal, wherein the presence or absence of the PRO polypeptide in said test sample is indicative of the presence of an immune-related disease in said mammal.

In another embodiment, the present invention concerns a method for identifying an agonist of a PRO polypeptide comprising:

(a) contacting cells and a test compound to be screened under conditions suitable for the induction
35 of a cellular response normally induced by a PRO polypeptide; and

(b) determining the induction of said cellular response to determine if the test compound is an effective agonist, wherein the induction of said cellular response is indicative of said test compound being an effective agonist.

In another embodiment, the invention concerns a method for identifying a compound capable of
40 inhibiting the activity of a PRO polypeptide comprising contacting a candidate compound with a PRO

polypeptide under conditions and for a time sufficient to allow these two components to interact and determining whether the activity of the PRO polypeptide is inhibited. In a specific aspect, either the candidate compound or the PRO polypeptide is immobilized on a solid support. In another aspect, the non-immobilized component carries a detectable label. In a preferred aspect, this method comprises the steps of:

- 5 (a) contacting cells and a test compound to be screened in the presence of a PRO polypeptide under conditions suitable for the induction of a cellular response normally induced by a PRO polypeptide; and
- (b) determining the induction of said cellular response to determine if the test compound is an effective antagonist.

In another embodiment, the invention provides a method for identifying a compound that inhibits the expression of a PRO polypeptide in cells that normally express the polypeptide, wherein the method comprises contacting the cells with a test compound and determining whether the expression of the PRO polypeptide is inhibited. In a preferred aspect, this method comprises the steps of:

- (a) contacting cells and a test compound to be screened under conditions suitable for allowing expression of the PRO polypeptide; and
- 15 (b) determining the inhibition of expression of said polypeptide.

In yet another embodiment, the present invention concerns a method for treating an immune-related disorder in a mammal that suffers therefrom comprising administering to the mammal a nucleic acid molecule that codes for either (a) a PRO polypeptide, (b) an agonist of a PRO polypeptide or (c) an antagonist of a PRO polypeptide, wherein said agonist or antagonist may be an anti-PRO antibody. In a preferred embodiment, the mammal is human. In another preferred embodiment, the nucleic acid is administered via *ex vivo* gene therapy. In a further preferred embodiment, the nucleic acid is comprised within a vector, more preferably an adenoviral, adeno-associated viral, lentiviral or retroviral vector.

In yet another aspect, the invention provides a recombinant viral particle comprising a viral vector consisting essentially of a promoter, nucleic acid encoding (a) a PRO polypeptide, (b) an agonist polypeptide of a PRO polypeptide, or (c) an antagonist polypeptide of a PRO polypeptide, and a signal sequence for cellular secretion of the polypeptide, wherein the viral vector is in association with viral structural proteins. Preferably, the signal sequence is from a mammal, such as from a native PRO polypeptide.

In a still further embodiment, the invention concerns an *ex vivo* producer cell comprising a nucleic acid construct that expresses retroviral structural proteins and also comprises a retroviral vector consisting essentially of a promoter, nucleic acid encoding (a) a PRO polypeptide, (b) an agonist polypeptide of a PRO polypeptide or (c) an antagonist polypeptide of a PRO polypeptide, and a signal sequence for cellular secretion of the polypeptide, wherein said producer cell packages the retroviral vector in association with the structural proteins to produce recombinant retroviral particles.

In a still further embodiment, the invention provides a method of increasing the activity of T-lymphocytes in a mammal comprising administering to said mammal (a) a PRO polypeptide, (b) an agonist of a PRO polypeptide, or (c) an antagonist of a PRO polypeptide, wherein the activity of T-lymphocytes in the mammal is increased.

In a still further embodiment, the invention provides a method of decreasing the activity of T-lymphocytes in a mammal comprising administering to said mammal (a) a PRO polypeptide, (b) an agonist of a PRO polypeptide, or (c) an antagonist of a PRO polypeptide, wherein the activity of T-lymphocytes in

the mammal is decreased.

In a still further embodiment, the invention provides a method of increasing the proliferation of T-lymphocytes in a mammal comprising administering to said mammal (a) a PRO polypeptide, (b) an agonist of a PRO polypeptide, or (c) an antagonist of a PRO polypeptide, wherein the proliferation of T-lymphocytes in the mammal is increased.

In a still further embodiment, the invention provides a method of decreasing the proliferation of T-lymphocytes in a mammal comprising administering to said mammal (a) a PRO polypeptide, (b) an agonist of a PRO polypeptide, or (c) an antagonist of a PRO polypeptide, wherein the proliferation of T-lymphocytes in the mammal is decreased.

10 B. Additional Embodiments

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described polypeptides. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli*, or yeast. A process for producing any of the herein described polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

In other embodiments, the invention provides chimeric molecules comprising any of the herein described polypeptides fused to a heterologous polypeptide or amino acid sequence. Example of such chimeric molecules comprise any of the herein described polypeptides fused to an epitope tag sequence or a Fc region of an immunoglobulin.

In another embodiment, the invention provides an antibody which specifically binds to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, humanized antibody, antibody fragment or single-chain antibody.

In yet other embodiments, the invention provides oligonucleotide probes useful for isolating genomic and cDNA nucleotide sequences or as antisense probes, wherein those probes may be derived from any of the above or below described nucleotide sequences.

In other embodiments, the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a PRO polypeptide.

In one aspect, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid

sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule encoding a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In other aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule comprising the coding sequence of a full-length PRO polypeptide cDNA as disclosed herein, the coding sequence of a PRO polypeptide lacking the signal peptide as disclosed herein, the coding sequence of an extracellular domain of a transmembrane PRO polypeptide, with or without the signal peptide, as disclosed herein or the coding sequence of any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In a further aspect, the invention concerns an isolated nucleic acid molecule comprising a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule that encodes the same mature polypeptide encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein, or (b) the complement of the DNA molecule of (a).

Another aspect the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated, or is complementary to such encoding nucleotide sequence, wherein the transmembrane domain(s) of such polypeptide are disclosed herein. Therefore, soluble extracellular domains of the herein described PRO polypeptides are contemplated.

Another embodiment is directed to fragments of a PRO polypeptide coding sequence, or the complement thereof, that may find use as, for example, hybridization probes, for encoding fragments of a PRO polypeptide that may optionally encode a polypeptide comprising a binding site for an anti-PRO antibody or as antisense oligonucleotide probes. Such nucleic acid fragments are usually at least about 20 nucleotides in length, alternatively at least about 30 nucleotides in length, alternatively at least about 40 nucleotides in length, alternatively at least about 50 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 70 nucleotides in length, alternatively at least about 80 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 100 nucleotides in length, alternatively at least about 110 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 130 nucleotides in length, alternatively at least about 140 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 160 nucleotides in length, alternatively at least about 170 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 190 nucleotides in length, alternatively at least about 200 nucleotides in length, alternatively at least about 250 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 350 nucleotides in length, alternatively at least about 400 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 500 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 700 nucleotides in length, alternatively at least about 800 nucleotides in length, alternatively at least about 900 nucleotides in length and alternatively at least about 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length. It is noted that novel fragments of a PRO polypeptide-encoding nucleotide sequence may be determined in a routine manner by aligning the PRO polypeptide-encoding nucleotide sequence with other known nucleotide sequences using any of a number of well known sequence alignment programs and determining which PRO polypeptide-encoding nucleotide sequence fragment(s) are novel. All of such PRO polypeptide-encoding nucleotide sequences are contemplated herein. Also contemplated are the PRO polypeptide fragments encoded by these nucleotide molecule fragments, preferably those PRO polypeptide fragments that comprise a binding site for an anti-PRO antibody.

In another embodiment, the invention provides isolated PRO polypeptide encoded by any of the isolated nucleic acid sequences herein above identified.

In a certain aspect, the invention concerns an isolated PRO polypeptide, comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about

88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein.

In a further aspect, the invention concerns an isolated PRO polypeptide comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to an amino acid sequence encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein.

In a specific aspect, the invention provides an isolated PRO polypeptide without the N-terminal signal sequence and/or the initiating methionine and is encoded by a nucleotide sequence that encodes such an amino acid sequence as herein before described. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

Another aspect the invention provides an isolated PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

In yet another embodiment, the invention concerns agonists and antagonists of a native PRO polypeptide as defined herein. In a particular embodiment, the agonist or antagonist is an anti-PRO antibody or a small molecule.

In a further embodiment, the invention concerns a method of identifying agonists or antagonists to a PRO polypeptide which comprise contacting the PRO polypeptide with a candidate molecule and monitoring a biological activity mediated by said PRO polypeptide. Preferably, the PRO polypeptide is a native PRO polypeptide.

5 In a still further embodiment, the invention concerns a composition of matter comprising a PRO polypeptide, or an agonist or antagonist of a PRO polypeptide as herein described, or an anti-PRO antibody, in combination with a carrier. Optionally, the carrier is a pharmaceutically acceptable carrier.

Another embodiment of the present invention is directed to the use of a PRO polypeptide, or an agonist or antagonist thereof as herein before described, or an anti-PRO antibody, for the preparation of a medicament useful in the treatment of a condition which is responsive to the PRO polypeptide, an agonist or
10 antagonist thereof or an anti-PRO antibody.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a nucleotide sequence (SEQ ID NO:1) of a native sequence PRO69457 cDNA, wherein SEQ ID NO:1 is a clone designated herein as "DNA287163".
15

Figure 2 shows the amino acid sequence (SEQ ID NO:2) derived from the coding sequence of SEQ ID NO:1 shown in Figure 1.

Figure 3 shows a nucleotide sequence (SEQ ID NO:3) of a native sequence PRO69458 cDNA, wherein SEQ ID NO:3 is a clone designated herein as "DNA287164".

20 Figure 4 shows the amino acid sequence (SEQ ID NO:4) derived from the coding sequence of SEQ ID NO:3 shown in Figure 3.

Figure 5 shows a nucleotide sequence (SEQ ID NO:5) of a native sequence PRO52268 cDNA, wherein SEQ ID NO:5 is a clone designated herein as "DNA287165".

25 Figure 6 shows the amino acid sequence (SEQ ID NO:6) derived from the coding sequence of SEQ ID NO:5 shown in Figure 5.

Figure 7 shows a nucleotide sequence (SEQ ID NO:7) of a native sequence PRO69459 cDNA, wherein SEQ ID NO:7 is a clone designated herein as "DNA287166".

Figure 8 shows the amino acid sequence (SEQ ID NO:8) derived from the coding sequence of SEQ ID NO:7 shown in Figure 7.

30 Figure 9 shows a nucleotide sequence (SEQ ID NO:9) of a native sequence PRO62927 cDNA, wherein SEQ ID NO:9 is a clone designated herein as "DNA275240".

Figure 10 shows the amino acid sequence (SEQ ID NO:10) derived from the coding sequence of SEQ ID NO:9 shown in Figure 9.

35 Figure 11 shows a nucleotide sequence (SEQ ID NO:11) of a native sequence PRO59136 cDNA, wherein SEQ ID NO:11 is a clone designated herein as "DNA287167".

Figure 12 shows the amino acid sequence (SEQ ID NO:12) derived from the coding sequence of SEQ ID NO:11 shown in Figure 11.

Figure 13 shows a nucleotide sequence (SEQ ID NO:13) of a native sequence PRO37121 cDNA, wherein SEQ ID NO:13 is a clone designated herein as "DNA226658".

Figure 14 shows the amino acid sequence (SEQ ID NO:14) derived from the coding sequence of SEQ ID NO:14 shown in Figure 14.

Figure 15 shows a nucleotide sequence (SEQ ID NO:15) of a native sequence PRO69460 cDNA, wherein SEQ ID NO:15 is a clone designated herein as "DNA287168".

5 Figure 16 shows the amino acid sequence (SEQ ID NO:16) derived from the coding sequence of SEQ ID NO:15 shown in Figure 15.

Figure 17 shows a nucleotide sequence (SEQ ID NO:17) of a native sequence PRO60475 cDNA, wherein SEQ ID NO:17 is a clone designated herein as "DNA272213".

10 Figure 18 shows the amino acid sequence (SEQ ID NO:18) derived from the coding sequence of SEQ ID NO:17 shown in Figure 17.

Figure 19 shows a nucleotide sequence (SEQ ID NO:19) of a native sequence PRO34451 cDNA, wherein SEQ ID NO:19 is a clone designated herein as "DNA218655".

Figure 20 shows the amino acid sequence (SEQ ID NO:20) derived from the coding sequence of SEQ ID NO:19 shown in Figure 19.

15 Figure 21 shows a nucleotide sequence (SEQ ID NO:21) of a native sequence PRO38070 cDNA, wherein SEQ ID NO:21 is a clone designated herein as "DNA227607".

Figure 22 shows the amino acid sequence (SEQ ID NO:22) derived from the coding sequence of SEQ ID NO:21 shown in Figure 21.

20 Figure 23 shows a nucleotide sequence (SEQ ID NO:23) of a native sequence PRO23756 cDNA, wherein SEQ ID NO:23 is a clone designated herein as "DNA194378".

Figure 24 shows the amino acid sequence (SEQ ID NO:24) derived from the coding sequence of SEQ ID NO:23 shown in Figure 23.

Figure 25 shows a nucleotide sequence (SEQ ID NO:25) of a native sequence PRO10404 cDNA, wherein SEQ ID NO:25 is a clone designated herein as "DNA287169".

25 Figure 26 shows the amino acid sequence (SEQ ID NO:26) derived from the coding sequence of SEQ ID NO:25 shown in Figure 25.

Figure 27 shows a nucleotide sequence (SEQ ID NO:27) of a native sequence PRO69461 cDNA, wherein SEQ ID NO:27 is a clone designated herein as "DNA288240".

30 Figure 28 shows the amino acid sequence (SEQ ID NO:28) derived from the coding sequence of SEQ ID NO:27 shown in Figure 27.

Figure 29 shows a nucleotide sequence (SEQ ID NO:29) of a native sequence PRO70006 cDNA, wherein SEQ ID NO:29 is a clone designated herein as "DNA288241".

Figure 30 shows the amino acid sequence (SEQ ID NO:30) derived from the coding sequence of SEQ ID NO:29 shown in Figure 29.

35 Figure 31 shows a nucleotide sequence (SEQ ID NO:31) of a native sequence PRO69462 cDNA, wherein SEQ ID NO:31 is a clone designated herein as "DNA287171".

Figure 32 shows the amino acid sequence (SEQ ID NO:32) derived from the coding sequence of SEQ ID NO:31 shown in Figure 31.

40 Figure 33 shows a nucleotide sequence (SEQ ID NO:33) of a native sequence PRO2081 cDNA, wherein SEQ ID NO:33 is a clone designated herein as "DNA287620".

Figure 34 shows the amino acid sequence (SEQ ID NO:34) derived from the coding sequence of SEQ ID NO:33 shown in Figure 33.

Figure 35A-B shows a nucleotide sequence (SEQ ID NO:35A-B) of a native sequence PRO70007 cDNA, wherein SEQ ID NO:35A-B is a clone designated herein as "DNA288242".

5 Figure 36 shows the amino acid sequence (SEQ ID NO:36) derived from the coding sequence of SEQ ID NO:35A-B shown in Figure 35A-B.

Figure 37 shows a nucleotide sequence (SEQ ID NO:37) of a native sequence PRO69463 cDNA, wherein SEQ ID NO:37 is a clone designated herein as "DNA287173".

10 Figure 38 shows the amino acid sequence (SEQ ID NO:38) derived from the coding sequence of SEQ ID NO:37 shown in Figure 37.

Figure 39 shows a nucleotide sequence (SEQ ID NO:39) of a native sequence PRO62908 cDNA, wherein SEQ ID NO:39 is a clone designated herein as "DNA275214".

Figure 40 shows the amino acid sequence (SEQ ID NO:40) derived from the coding sequence of SEQ ID NO:39 shown in Figure 39.

15 Figure 41 shows a nucleotide sequence (SEQ ID NO:41) of a native sequence PRO69464 cDNA, wherein SEQ ID NO:41 is a clone designated herein as "DNA287174".

Figure 42 shows the amino acid sequence (SEQ ID NO:42) derived from the coding sequence of SEQ ID NO:41 shown in Figure 41

20 Figure 43 shows a nucleotide sequence (SEQ ID NO:43) of a native sequence PRO52804 cDNA, wherein SEQ ID NO:43 is a clone designated herein as "DNA287175".

Figure 44 shows the amino acid sequence (SEQ ID NO:44) derived from the coding sequence of SEQ ID NO:43 shown in Figure 43.

Figure 45 shows a nucleotide sequence (SEQ ID NO:45) of a native sequence PRO60438 cDNA, wherein SEQ ID NO:45 is a clone designated herein as "DNA272171".

25 Figure 46 shows the amino acid sequence (SEQ ID NO:46) derived from the coding sequence of SEQ ID NO:45 shown in Figure 45.

Figure 47 shows a nucleotide sequence (SEQ ID NO:47) of a native sequence PRO69465 cDNA, wherein SEQ ID NO:47 is a clone designated herein as "DNA287176".

30 Figure 48 shows the amino acid sequence (SEQ ID NO:48) derived from the coding sequence of SEQ ID NO:47 shown in Figure 47.

Figure 49 shows a nucleotide sequence (SEQ ID NO:49) of a native sequence PRO37421 cDNA, wherein SEQ ID NO:49 is a clone designated herein as "DNA226958".

Figure 50 shows the amino acid sequence (SEQ ID NO:50) derived from the coding sequence of SEQ ID NO:49 shown in Figure 49.

35 Figure 51 shows a nucleotide sequence (SEQ ID NO:51) of a native sequence PRO37596 cDNA, wherein SEQ ID NO:51 is a clone designated herein as "DNA227133".

Figure 52 shows the amino acid sequence (SEQ ID NO:52) derived from the coding sequence of SEQ ID NO:51 shown in Figure 51.

40 Figure 53 shows a nucleotide sequence (SEQ ID NO:53) of a native sequence PRO36124 cDNA, wherein SEQ ID NO:53 is a clone designated herein as "DNA225661".

Figure 54 shows the amino acid sequence (SEQ ID NO:54) derived from the coding sequence of SEQ ID NO:53 shown in Figure 53.

Figure 55 shows a nucleotide sequence (SEQ ID NO:55) of a native sequence PRO69466 cDNA, wherein SEQ ID NO:55 is a clone designated herein as "DNA287177".

5 Figure 56 shows the amino acid sequence (SEQ ID NO:56) derived from the coding sequence of SEQ ID NO:55 shown in Figure 55.

Figure 57 shows a nucleotide sequence (SEQ ID NO:57) of a native sequence PRO60499 cDNA, wherein SEQ ID NO:57 is a clone designated herein as "DNA272237".

10 Figure 58 shows the amino acid sequence (SEQ ID NO:58) derived from the coding sequence of SEQ ID NO:57 shown in Figure 57.

Figure 59 shows a nucleotide sequence (SEQ ID NO:59) of a native sequence PRO69467 cDNA, wherein SEQ ID NO:59 is a clone designated herein as "DNA287178".

Figure 60 shows the amino acid sequence (SEQ ID NO:60) derived from the coding sequence of SEQ ID NO:59 shown in Figure 59.

15 Figure 61 shows a nucleotide sequence (SEQ ID NO:61) of a native sequence PRO61824 cDNA, wherein SEQ ID NO:61 is a clone designated herein as "DNA273865".

Figure 62 shows the amino acid sequence (SEQ ID NO:62) derived from the coding sequence of SEQ ID NO:61 shown in Figure 61.

20 Figure 63 shows a nucleotide sequence (SEQ ID NO:63) of a native sequence PRO69468 cDNA, wherein SEQ ID NO:63 is a clone designated herein as "DNA287179".

Figure 64 shows the amino acid sequence (SEQ ID NO:64) derived from the coding sequence of SEQ ID NO:63 shown in Figure 63.

Figure 65 shows a nucleotide sequence (SEQ ID NO:65) of a native sequence PRO21341 cDNA, wherein SEQ ID NO:65 is a clone designated herein as "DNA287180".

25 Figure 66 shows the amino acid sequence (SEQ ID NO:66) derived from the coding sequence of SEQ ID NO:65 shown in Figure 65.

Figure 67A-B shows a nucleotide sequence (SEQ ID NO:67A-B) of a native sequence PRO38213 cDNA, wherein SEQ ID NO:67A-B is a clone designated herein as "DNA227750".

30 Figure 68 shows the amino acid sequence (SEQ ID NO:68) derived from the coding sequence of SEQ ID NO:67A-B shown in Figure 67A-B.

Figure 69 shows a nucleotide sequence (SEQ ID NO:69) of a native sequence PRO69469 cDNA, wherein SEQ ID NO:69 is a clone designated herein as "DNA287181".

Figure 70 shows the amino acid sequence (SEQ ID NO:70) derived from the coding sequence of SEQ ID NO:69 shown in Figure 69.

35 Figure 71 shows a nucleotide sequence (SEQ ID NO:71) of a native sequence PRO37172 cDNA, wherein SEQ ID NO:71 is a clone designated herein as "DNA226709".

Figure 72 shows the amino acid sequence (SEQ ID NO:72) derived from the coding sequence of SEQ ID NO:71 shown in Figure 71.

40 Figure 73 shows a nucleotide sequence (SEQ ID NO:73) of a native sequence PRO35991 cDNA, wherein SEQ ID NO:73 is a clone designated herein as "DNA225528".

Figure 74 shows the amino acid sequence (SEQ ID NO:74) derived from the coding sequence of SEQ ID NO:73 shown in Figure 73.

Figure 75A-B shows a nucleotide sequence (SEQ ID NO:75A-B) of a native sequence PRO36905 cDNA, wherein SEQ ID NO:75A-B is a clone designated herein as "DNA226442".

5 Figure 76 shows the amino acid sequence (SEQ ID NO:76) derived from the coding sequence of SEQ ID NO:75A-B shown in Figure 75A-B.

Figure 77 shows a nucleotide sequence (SEQ ID NO:77) of a native sequence PRO69470 cDNA, wherein SEQ ID NO:77 is a clone designated herein as "DNA287182".

10 Figure 78 shows the amino acid sequence (SEQ ID NO:78) derived from the coding sequence of SEQ ID NO:77 shown in Figure 77.

Figure 79 shows a nucleotide sequence (SEQ ID NO:79) of a native sequence PRO36451 cDNA, wherein SEQ ID NO:79 is a clone designated herein as "DNA288243".

Figure 80 shows the amino acid sequence (SEQ ID NO:80) derived from the coding sequence of SEQ ID NO:79 shown in Figure 79.

15 Figure 81 shows a nucleotide sequence (SEQ ID NO:81) of a native sequence PRO69471 cDNA, wherein SEQ ID NO:81 is a clone designated herein as "DNA287184".

Figure 82 shows the amino acid sequence (SEQ ID NO:82) derived from the coding sequence of SEQ ID NO:81 shown in Figure 81.

20 Figure 83 shows a nucleotide sequence (SEQ ID NO:83) of a native sequence PRO37492 cDNA, wherein SEQ ID NO:83 is a clone designated herein as "DNA227029".

Figure 84 shows the amino acid sequence (SEQ ID NO:84) derived from the coding sequence of SEQ ID NO:83 shown in Figure 83.

Figure 85A-B shows a nucleotide sequence (SEQ ID NO:85A-B) of a native sequence PRO70008 cDNA, wherein SEQ ID NO:85A-B is a clone designated herein as "DNA288244".

25 Figure 86 shows the amino acid sequence (SEQ ID NO:86) derived from the coding sequence of SEQ ID NO:85A-B shown in Figure 85A-B.

Figure 87 shows a nucleotide sequence (SEQ ID NO:87) of a native sequence PRO69472 cDNA, wherein SEQ ID NO:87 is a clone designated herein as "DNA287186".

30 Figure 88 shows the amino acid sequence (SEQ ID NO:88) derived from the coding sequence of SEQ ID NO:87 shown in Figure 87.

Figure 89 shows a nucleotide sequence (SEQ ID NO:89) of a native sequence PRO69473 cDNA, wherein SEQ ID NO:89 is a clone designated herein as "DNA287187".

Figure 90 shows the amino acid sequence (SEQ ID NO:90) derived from the coding sequence of SEQ ID NO:89 shown in Figure 89.

35 Figure 91 shows a nucleotide sequence (SEQ ID NO:91) of a native sequence PRO36996 cDNA, wherein SEQ ID NO:91 is a clone designated herein as "DNA226533".

Figure 92 shows the amino acid sequence (SEQ ID NO:92) derived from the coding sequence of SEQ ID NO:91 shown in Figure 91.

40 Figure 93 shows a nucleotide sequence (SEQ ID NO:93) of a native sequence PRO22613 cDNA, wherein SEQ ID NO:93 is a clone designated herein as "DNA189698".

Figure 94 shows the amino acid sequence (SEQ ID NO:94) derived from the coding sequence of SEQ ID NO:93 shown in Figure 93.

Figure 95 shows a nucleotide sequence (SEQ ID NO:95) of a native sequence PRO69475 cDNA, wherein SEQ ID NO:95 is a clone designated herein as "DNA287189".

5 Figure 96 shows the amino acid sequence (SEQ ID NO:96) derived from the coding sequence of SEQ ID NO:95 shown in Figure 95.

Figure 97 shows a nucleotide sequence (SEQ ID NO:97) of a native sequence PRO61755 cDNA, wherein SEQ ID NO:97 is a clone designated herein as "DNA273794".

10 Figure 98 shows the amino acid sequence (SEQ ID NO:98) derived from the coding sequence of SEQ ID NO:97 shown in Figure 97.

Figure 99 shows a nucleotide sequence (SEQ ID NO:99) of a native sequence PRO70009 cDNA, wherein SEQ ID NO:99 is a clone designated herein as "DNA288245".

Figure 100 shows the amino acid sequence (SEQ ID NO:100) derived from the coding sequence of SEQ ID NO:99 shown in Figure 99.

15 Figure 101 shows a nucleotide sequence (SEQ ID NO:101) of a native sequence PRO69476 cDNA, wherein SEQ ID NO:101 is a clone designated herein as "DNA287190".

Figure 102 shows the amino acid sequence (SEQ ID NO:102) derived from the coding sequence of SEQ ID NO:101 shown in Figure 101.

20 Figure 103 shows a nucleotide sequence (SEQ ID NO:103) of a native sequence PRO4881 cDNA, wherein SEQ ID NO:103 is a clone designated herein as "DNA103554".

Figure 104 shows the amino acid sequence (SEQ ID NO:104) derived from the coding sequence of SEQ ID NO:103 shown in Figure 103.

Figure 105A-B shows a nucleotide sequence (SEQ ID NO:105A-B) of a native sequence PRO12876 cDNA, wherein SEQ ID NO:105A-B is a clone designated herein as "DNA151420".

25 Figure 106 shows the amino acid sequence (SEQ ID NO:106) derived from the coding sequence of SEQ ID NO:105A-B shown in Figure 105A-B.

Figure 107 shows a nucleotide sequence (SEQ ID NO:107) of a native sequence PRO70010 cDNA, wherein SEQ ID NO:107 is a clone designated herein as "DNA288246".

30 Figure 108 shows the amino acid sequence (SEQ ID NO:108) derived from the coding sequence of SEQ ID NO:107 shown in Figure 107.

Figure 109 shows a nucleotide sequence (SEQ ID NO:109) of a native sequence PRO37534 cDNA, wherein SEQ ID NO:109 is a clone designated herein as "DNA227071".

Figure 110 shows the amino acid sequence (SEQ ID NO:110) derived from the coding sequence of SEQ ID NO:109 shown in Figure 109.

35 Figure 111A-B shows a nucleotide sequence (SEQ ID NO:111A-B) of a native sequence PRO21928 cDNA, wherein SEQ ID NO:111A-B is a clone designated herein as "DNA188400".

Figure 112 shows the amino acid sequence (SEQ ID NO:112) derived from the coding sequence of SEQ ID NO:111A-B shown in Figure 111A-B.

40 Figure 113A-B shows a nucleotide sequence (SEQ ID NO:113A-B) of a native sequence PRO69478 cDNA, wherein SEQ ID NO:113A-B is a clone designated herein as "DNA287192".

Figure 114 shows the amino acid sequence (SEQ ID NO:114) derived from the coding sequence of SEQ ID NO:113A-B shown in Figure 113A-B.

Figure 115A-B shows a nucleotide sequence (SEQ ID NO:115A-B) of a native sequence PRO69479 cDNA, wherein SEQ ID NO:115A-B is a clone designated herein as "DNA287193".

5 Figure 116 shows the amino acid sequence (SEQ ID NO:116) derived from the coding sequence of SEQ ID NO:115A-B shown in Figure 115A-B.

Figure 117 shows a nucleotide sequence (SEQ ID NO:117) of a native sequence PRO69480 cDNA, wherein SEQ ID NO:117 is a clone designated herein as "DNA287194".

10 Figure 118 shows the amino acid sequence (SEQ ID NO:118) derived from the coding sequence of SEQ ID NO:117 shown in Figure 117.

Figure 119 shows a nucleotide sequence (SEQ ID NO:119) of a native sequence PRO69481 cDNA, wherein SEQ ID NO:119 is a clone designated herein as "DNA287195".

Figure 120 shows the amino acid sequence (SEQ ID NO:120) derived from the coding sequence of SEQ ID NO:119 shown in Figure 119.

15 Figure 121 shows a nucleotide sequence (SEQ ID NO:121) of a native sequence PRO69482 cDNA, wherein SEQ ID NO:121 is a clone designated herein as "DNA287196".

Figure 122 shows the amino acid sequence (SEQ ID NO:122) derived from the coding sequence of SEQ ID NO:121 shown in Figure 121.

20 Figure 123 shows a nucleotide sequence (SEQ ID NO:123) of a native sequence PRO69483 cDNA, wherein SEQ ID NO:123 is a clone designated herein as "DNA287197".

Figure 124 shows the amino acid sequence (SEQ ID NO:124) derived from the coding sequence of SEQ ID NO:123 shown in Figure 123.

Figure 125 shows a nucleotide sequence (SEQ ID NO:125) of a native sequence PRO38642 cDNA, wherein SEQ ID NO:125 is a clone designated herein as "DNA228179".

25 Figure 126 shows the amino acid sequence (SEQ ID NO:126) derived from the coding sequence of SEQ ID NO:125 shown in Figure 125.

Figure 127 shows a nucleotide sequence (SEQ ID NO:127) of a native sequence PRO69484 cDNA, wherein SEQ ID NO:127 is a clone designated herein as "DNA287198".

30 Figure 128 shows the amino acid sequence (SEQ ID NO:128) derived from the coding sequence of SEQ ID NO:127 shown in Figure 127.

Figure 129 shows a nucleotide sequence (SEQ ID NO:129) of a native sequence PRO66269 cDNA, wherein SEQ ID NO:129 is a clone designated herein as "DNA287199".

Figure 130 shows the amino acid sequence (SEQ ID NO:130) derived from the coding sequence of SEQ ID NO:129 shown in Figure 129.

35 Figure 131 shows a nucleotide sequence (SEQ ID NO:131) of a native sequence PRO1723 cDNA, wherein SEQ ID NO:131 is a clone designated herein as "DNA82376".

Figure 132 shows the amino acid sequence (SEQ ID NO:132) derived from the coding sequence of SEQ ID NO:131 shown in Figure 131.

40 Figure 133 shows a nucleotide sequence (SEQ ID NO:133) of a native sequence PRO22297 cDNA, wherein SEQ ID NO:133 is a clone designated herein as "DNA287623".

Figure 134 shows the amino acid sequence (SEQ ID NO:134) derived from the coding sequence of SEQ ID NO:133 shown in Figure 133.

Figure 135 shows a nucleotide sequence (SEQ ID NO:135) of a native sequence PRO61349 cDNA, wherein SEQ ID NO:135 is a clone designated herein as "DNA273346".

5 Figure 136 shows the amino acid sequence (SEQ ID NO:136) derived from the coding sequence of SEQ ID NO:135 shown in Figure 135.

Figure 137 shows a nucleotide sequence (SEQ ID NO:137) of a native sequence PRO69485 cDNA, wherein SEQ ID NO:137 is a clone designated herein as "DNA287201".

10 Figure 138 shows the amino acid sequence (SEQ ID NO:138) derived from the coding sequence of SEQ ID NO:137 shown in Figure 137.

Figure 139 shows a nucleotide sequence (SEQ ID NO:139) of a native sequence PRO69486 cDNA, wherein SEQ ID NO:139 is a clone designated herein as "DNA287202".

Figure 140 shows the amino acid sequence (SEQ ID NO:140) derived from the coding sequence of SEQ ID NO:139 shown in Figure 139.

15 Figure 141 shows a nucleotide sequence (SEQ ID NO:141) of a native sequence PRO69487 cDNA, wherein SEQ ID NO:141 is a clone designated herein as "DNA287203".

Figure 142 shows the amino acid sequence (SEQ ID NO:142) derived from the coding sequence of SEQ ID NO:141 shown in Figure 141.

20 Figure 143 shows a nucleotide sequence (SEQ ID NO:143) of a native sequence PRO36963 cDNA, wherein SEQ ID NO:143 is a clone designated herein as "DNA226500".

Figure 144 shows the amino acid sequence (SEQ ID NO:144) derived from the coding sequence of SEQ ID NO:143 shown in Figure 143.

Figure 145 shows a nucleotide sequence (SEQ ID NO:145) of a native sequence PRO23814 cDNA, wherein SEQ ID NO:145 is a clone designated herein as "DNA287204".

25 Figure 146 shows the amino acid sequence (SEQ ID NO:146) derived from the coding sequence of SEQ ID NO:145 shown in Figure 145.

Figure 147 shows a nucleotide sequence (SEQ ID NO:147) of a native sequence PRO57980 cDNA, wherein SEQ ID NO:147 is a clone designated herein as "DNA287205".

30 Figure 148 shows the amino acid sequence (SEQ ID NO:148) derived from the coding sequence of SEQ ID NO:147 shown in Figure 147.

Figure 149 shows a nucleotide sequence (SEQ ID NO:149) of a native sequence PRO20128 cDNA, wherein SEQ ID NO:149 is a clone designated herein as "DNA171400".

Figure 150 shows the amino acid sequence (SEQ ID NO:150) derived from the coding sequence of SEQ ID NO:149 shown in Figure 149.

35 Figure 151 shows a nucleotide sequence (SEQ ID NO:151) of a native sequence PRO4551 cDNA, wherein SEQ ID NO:151 is a clone designated herein as "DNA103221".

Figure 152 shows the amino acid sequence (SEQ ID NO:152) derived from the coding sequence of SEQ ID NO:151 shown in Figure 151.

40 Figure 153 shows a nucleotide sequence (SEQ ID NO:153) of a native sequence PRO69488 cDNA, wherein SEQ ID NO:153 is a clone designated herein as "DNA287206".

Figure 154 shows the amino acid sequence (SEQ ID NO:154) derived from the coding sequence of SEQ ID NO:153 shown in Figure 153.

Figure 155 shows a nucleotide sequence (SEQ ID NO:155) of a native sequence PRO39268 cDNA, wherein SEQ ID NO:155 is a clone designated herein as "DNA287207".

5 Figure 156 shows the amino acid sequence (SEQ ID NO:156) derived from the coding sequence of SEQ ID NO:155 shown in Figure 155.

Figure 157 shows a nucleotide sequence (SEQ ID NO:157) of a native sequence PRO69489 cDNA, wherein SEQ ID NO:157 is a clone designated herein as "DNA287208".

10 Figure 158 shows the amino acid sequence (SEQ ID NO:158) derived from the coding sequence of SEQ ID NO:157 shown in Figure 157.

Figure 159 shows a nucleotide sequence (SEQ ID NO:159) of a native sequence PRO69490 cDNA, wherein SEQ ID NO:159 is a clone designated herein as "DNA287209".

Figure 160 shows the amino acid sequence (SEQ ID NO:160) derived from the coding sequence of SEQ ID NO:159 shown in Figure 159.

15 Figure 161 shows a nucleotide sequence (SEQ ID NO:161) of a native sequence PRO69491 cDNA, wherein SEQ ID NO:161 is a clone designated herein as "DNA287625".

Figure 162 shows the amino acid sequence (SEQ ID NO:162) derived from the coding sequence of SEQ ID NO:161 shown in Figure 161.

20 Figure 163 shows a nucleotide sequence (SEQ ID NO:163) of a native sequence PRO69492 cDNA, wherein SEQ ID NO:163 is a clone designated herein as "DNA287211".

Figure 164 shows the amino acid sequence (SEQ ID NO:164) derived from the coding sequence of SEQ ID NO:163 shown in Figure 163.

Figure 165 shows a nucleotide sequence (SEQ ID NO:165) of a native sequence PRO37713 cDNA, wherein SEQ ID NO:165 is a clone designated herein as "DNA227250".

25 Figure 166 shows the amino acid sequence (SEQ ID NO:166) derived from the coding sequence of SEQ ID NO:165 shown in Figure 165.

Figure 167 shows a nucleotide sequence (SEQ ID NO:167) of a native sequence PRO58993cDNA, wherein SEQ ID NO:167 is a clone designated herein as "DNA287212".

30 Figure 168 shows the amino acid sequence (SEQ ID NO:168) derived from the coding sequence of SEQ ID NO:167 shown in Figure 167.

Figure 169 shows a nucleotide sequence (SEQ ID NO:169) of a native sequence PRO69493 cDNA, wherein SEQ ID NO:169 is a clone designated herein as "DNA287213".

Figure 170 shows the amino acid sequence (SEQ ID NO:170) derived from the coding sequence of SEQ ID NO:169 shown in Figure 169.

35 Figure 171 shows a nucleotide sequence (SEQ ID NO:171) of a native sequence PRO69494 cDNA, wherein SEQ ID NO:171 is a clone designated herein as "DNA287214".

Figure 172 shows the amino acid sequence (SEQ ID NO:172) derived from the coding sequence of SEQ ID NO:171 shown in Figure 171.

40 Figure 173 shows a nucleotide sequence (SEQ ID NO:173) of a native sequence PRO69495 cDNA, wherein SEQ ID NO:173 is a clone designated herein as "DNA287215".

Figure 174 shows the amino acid sequence (SEQ ID NO:174) derived from the coding sequence of SEQ ID NO:173 shown in Figure 173.

Figure 175 shows a nucleotide sequence (SEQ ID NO:175) of a native sequence PRO70011 cDNA, wherein SEQ ID NO:175 is a clone designated herein as "DNA288247".

5 Figure 176 shows the amino acid sequence (SEQ ID NO:176) derived from the coding sequence of SEQ ID NO:175 shown in Figure 175.

Figure 177 shows a nucleotide sequence (SEQ ID NO:177) of a native sequence PRO62861 cDNA, wherein SEQ ID NO:177 is a clone designated herein as "DNA275157".

10 Figure 178 shows the amino acid sequence (SEQ ID NO:178) derived from the coding sequence of SEQ ID NO:177 shown in Figure 177.

Figure 179 shows a nucleotide sequence (SEQ ID NO:179) of a native sequence PRO36640 cDNA, wherein SEQ ID NO:179 is a clone designated herein as "DNA226177".

Figure 180 shows the amino acid sequence (SEQ ID NO:180) derived from the coding sequence of SEQ ID NO:179 shown in Figure 179.

15 Figure 181A-B shows a nucleotide sequence (SEQ ID NO:181A-B) of a native sequence PRO36766 cDNA, wherein SEQ ID NO:181A-B is a clone designated herein as "DNA287217".

Figure 182 shows the amino acid sequence (SEQ ID NO:182) derived from the coding sequence of SEQ ID NO:181A-B shown in Figure 181A-B.

20 Figure 183 shows a nucleotide sequence (SEQ ID NO:183) of a native sequence PRO69497 cDNA, wherein SEQ ID NO:183 is a clone designated herein as "DNA287218".

Figure 184 shows the amino acid sequence (SEQ ID NO:184) derived from the coding sequence of SEQ ID NO:183 shown in Figure 183.

Figure 185 shows a nucleotide sequence (SEQ ID NO:185) of a native sequence PRO69498 cDNA, wherein SEQ ID NO:185 is a clone designated herein as "DNA287219".

25 Figure 186 shows the amino acid sequence (SEQ ID NO:186) derived from the coding sequence of SEQ ID NO:185 shown in Figure 185.

Figure 187 shows a nucleotide sequence (SEQ ID NO:187) of a native sequence PRO69499 cDNA, wherein SEQ ID NO:187 is a clone designated herein as "DNA287220".

30 Figure 188 shows the amino acid sequence (SEQ ID NO:188) derived from the coding sequence of SEQ ID NO:187 shown in Figure 187.

Figure 189 shows a nucleotide sequence (SEQ ID NO:189) of a native sequence PRO69500 cDNA, wherein SEQ ID NO:189 is a clone designated herein as "DNA287221".

Figure 190 shows the amino acid sequence (SEQ ID NO:190) derived from the coding sequence of SEQ ID NO:189 shown in Figure 189.

35 Figure 191 shows a nucleotide sequence (SEQ ID NO:191) of a native sequence PRO69501 cDNA, wherein SEQ ID NO:191 is a clone designated herein as "DNA287222".

Figure 192 shows the amino acid sequence (SEQ ID NO:192) derived from the coding sequence of SEQ ID NO:191 shown in Figure 191.

40 Figure 193 shows a nucleotide sequence (SEQ ID NO:193) of a native sequence PRO70012 cDNA, wherein SEQ ID NO:193 is a clone designated herein as "DNA288248".

Figure 194 shows the amino acid sequence (SEQ ID NO:194) derived from the coding sequence of SEQ ID NO:193 shown in Figure 193.

Figure 195 shows a nucleotide sequence (SEQ ID NO:195) of a native sequence PRO69503 cDNA, wherein SEQ ID NO:195 is a clone designated herein as "DNA287224".

5 Figure 196 shows the amino acid sequence (SEQ ID NO:196) derived from the coding sequence of SEQ ID NO:195 shown in Figure 195.

Figure 197 shows a nucleotide sequence (SEQ ID NO:197) of a native sequence PRO69474 cDNA, wherein SEQ ID NO:197 is a clone designated herein as "DNA287188".

10 Figure 198 shows the amino acid sequence (SEQ ID NO:198) derived from the coding sequence of SEQ ID NO:197 shown in Figure 197.

Figure 199 shows a nucleotide sequence (SEQ ID NO:199) of a native sequence PRO69505 cDNA, wherein SEQ ID NO:199 is a clone designated herein as "DNA287226".

Figure 200 shows the amino acid sequence (SEQ ID NO:200) derived from the coding sequence of SEQ ID NO:199 shown in Figure 199.

15 Figure 201 shows a nucleotide sequence (SEQ ID NO:201) of a native sequence PRO69506 cDNA, wherein SEQ ID NO:201 is a clone designated herein as "DNA287227".

Figure 202 shows the amino acid sequence (SEQ ID NO:202) derived from the coding sequence of SEQ ID NO:201 shown in Figure 201.

20 Figure 203 shows a nucleotide sequence (SEQ ID NO:203) of a native sequence PRO69507 cDNA, wherein SEQ ID NO:203 is a clone designated herein as "DNA288249".

Figure 204 shows the amino acid sequence (SEQ ID NO:204) derived from the coding sequence of SEQ ID NO:203 shown in Figure 203.

Figure 205 shows a nucleotide sequence (SEQ ID NO:205) of a native sequence PRO51301 cDNA, wherein SEQ ID NO:205 is a clone designated herein as "DNA256257".

25 Figure 206 shows the amino acid sequence (SEQ ID NO:206) derived from the coding sequence of SEQ ID NO:205 shown in Figure 205.

Figure 207 shows a nucleotide sequence (SEQ ID NO:207) of a native sequence PRO69508 cDNA, wherein SEQ ID NO:207 is a clone designated herein as "DNA287229".

30 Figure 208 shows the amino acid sequence (SEQ ID NO:208) derived from the coding sequence of SEQ ID NO:207 shown in Figure 207.

Figure 209 shows a nucleotide sequence (SEQ ID NO:209) of a native sequence PRO69509 cDNA, wherein SEQ ID NO:209 is a clone designated herein as "DNA287230".

Figure 210 shows the amino acid sequence (SEQ ID NO:210) derived from the coding sequence of SEQ ID NO:209 shown in Figure 209.

35 Figure 211 shows a nucleotide sequence (SEQ ID NO:211) of a native sequence PRO69510 cDNA, wherein SEQ ID NO:211 is a clone designated herein as "DNA287231".

Figure 212 shows the amino acid sequence (SEQ ID NO:212) derived from the coding sequence of SEQ ID NO:211 shown in Figure 211.

40 Figure 213 shows a nucleotide sequence (SEQ ID NO:213) of a native sequence PRO69511 cDNA, wherein SEQ ID NO:213 is a clone designated herein as "DNA287232".

Figure 214 shows the amino acid sequence (SEQ ID NO:214) derived from the coding sequence of SEQ ID NO:213 shown in Figure 213.

Figure 215 shows a nucleotide sequence (SEQ ID NO:215) of a native sequence PRO51309 cDNA, wherein SEQ ID NO:215 is a clone designated herein as "DNA256265".

5 Figure 216 shows the amino acid sequence (SEQ ID NO:216) derived from the coding sequence of SEQ ID NO:215 shown in Figure 215.

Figure 217A-B shows a nucleotide sequence (SEQ ID NO:217A-B) of a native sequence PRO50578 cDNA, wherein SEQ ID NO:217A-B is a clone designated herein as "DNA255513".

10 Figure 218 shows the amino acid sequence (SEQ ID NO:218) derived from the coding sequence of SEQ ID NO:217A-B shown in Figure 217A-B.

Figure 219A-B shows a nucleotide sequence (SEQ ID NO:219A-B) of a native sequence PRO69512 cDNA, wherein SEQ ID NO:219A-B is a clone designated herein as "DNA287233".

Figure 220 shows the amino acid sequence (SEQ ID NO:220) derived from the coding sequence of SEQ ID NO:219A-B shown in Figure 219A-B.

15 Figure 221 shows a nucleotide sequence (SEQ ID NO:221) of a native sequence PRO69513 cDNA, wherein SEQ ID NO:221 is a clone designated herein as "DNA287234".

Figure 222 shows the amino acid sequence (SEQ ID NO:222) derived from the coding sequence of SEQ ID NO:221 shown in Figure 221.

20 Figure 223 shows a nucleotide sequence (SEQ ID NO:223) of a native sequence PRO69514 cDNA, wherein SEQ ID NO:223 is a clone designated herein as "DNA287235".

Figure 224 shows the amino acid sequence (SEQ ID NO:224) derived from the coding sequence of SEQ ID NO:223 shown in Figure 223.

Figure 225A-B shows a nucleotide sequence (SEQ ID NO:225A-B) of a native sequence PRO10607 cDNA, wherein SEQ ID NO:225A-B is a clone designated herein as "DNA287236".

25 Figure 226 shows the amino acid sequence (SEQ ID NO:226) derived from the coding sequence of SEQ ID NO:225A-B shown in Figure 225A-B.

Figure 227A-B shows a nucleotide sequence (SEQ ID NO:227A-B) of a native sequence PRO61705 cDNA, wherein SEQ ID NO:227A-B is a clone designated herein as "DNA273742".

30 Figure 228 shows the amino acid sequence (SEQ ID NO:228) derived from the coding sequence of SEQ ID NO:227A-B shown in Figure 227A-B.

Figure 229 shows a nucleotide sequence (SEQ ID NO:229) of a native sequence PRO49214 cDNA, wherein SEQ ID NO:229 is a clone designated herein as "DNA253811".

Figure 230 shows the amino acid sequence (SEQ ID NO:230) derived from the coding sequence of SEQ ID NO:229 shown in Figure 229.

35 Figure 231 shows a nucleotide sequence (SEQ ID NO:231) of a native sequence PRO39648 cDNA, wherein SEQ ID NO:231 is a clone designated herein as "DNA287237".

Figure 232 shows the amino acid sequence (SEQ ID NO:232) derived from the coding sequence of SEQ ID NO:231 shown in Figure 231.

40 Figure 233 shows a nucleotide sequence (SEQ ID NO:233) of a native sequence PRO69515 cDNA, wherein SEQ ID NO:233 is a clone designated herein as "DNA287238".

Figure 234 shows the amino acid sequence (SEQ ID NO:234) derived from the coding sequence of SEQ ID NO:233 shown in Figure 233.

Figure 235 shows a nucleotide sequence (SEQ ID NO:235) of a native sequence PRO38497 cDNA, wherein SEQ ID NO:235 is a clone designated herein as "DNA287239".

5 Figure 236 shows the amino acid sequence (SEQ ID NO:236) derived from the coding sequence of SEQ ID NO:235 shown in Figure 235.

Figure 237 shows a nucleotide sequence (SEQ ID NO:237) of a native sequence PRO29371 cDNA, wherein SEQ ID NO:237 is a clone designated herein as "DNA287240".

10 Figure 238 shows the amino acid sequence (SEQ ID NO:238) derived from the coding sequence of SEQ ID NO:237 shown in Figure 237.

Figure 239 shows a nucleotide sequence (SEQ ID NO:239) of a native sequence PRO70013 cDNA, wherein SEQ ID NO:239 is a clone designated herein as "DNA288250".

Figure 240 shows the amino acid sequence (SEQ ID NO:240) derived from the coding sequence of SEQ ID NO:239 shown in Figure 239.

15 Figure 241 shows a nucleotide sequence (SEQ ID NO:241) of a native sequence PRO69516 cDNA, wherein SEQ ID NO:241 is a clone designated herein as "DNA287241".

Figure 242 shows the amino acid sequence (SEQ ID NO:242) derived from the coding sequence of SEQ ID NO:241 shown in Figure 241.

20 Figure 243 shows a nucleotide sequence (SEQ ID NO:243) of a native sequence PRO69517 cDNA, wherein SEQ ID NO:243 is a clone designated herein as "DNA287242".

Figure 244 shows the amino acid sequence (SEQ ID NO:244) derived from the coding sequence of SEQ ID NO:243 shown in Figure 243.

Figure 245 shows a nucleotide sequence (SEQ ID NO:245) of a native sequence PRO69518 cDNA, wherein SEQ ID NO:245 is a clone designated herein as "DNA287243".

25 Figure 246 shows the amino acid sequence (SEQ ID NO:246) derived from the coding sequence of SEQ ID NO:245 shown in Figure 245.

Figure 247 shows a nucleotide sequence (SEQ ID NO:247) of a native sequence PRO70014 cDNA, wherein SEQ ID NO:247 is a clone designated herein as "DNA288251".

30 Figure 248 shows the amino acid sequence (SEQ ID NO:248) derived from the coding sequence of SEQ ID NO:247 shown in Figure 247.

Figure 249 shows a nucleotide sequence (SEQ ID NO:249) of a native sequence PRO69520 cDNA, wherein SEQ ID NO:249 is a clone designated herein as "DNA287245".

Figure 250 shows the amino acid sequence (SEQ ID NO:250) derived from the coding sequence of SEQ ID NO:249 shown in Figure 249.

35 Figure 251 shows a nucleotide sequence (SEQ ID NO:251) of a native sequence PRO69521 cDNA, wherein SEQ ID NO:251 is a clone designated herein as "DNA287246".

Figure 252 shows the amino acid sequence (SEQ ID NO:252) derived from the coding sequence of SEQ ID NO:251 shown in Figure 251.

40 Figure 253 shows a nucleotide sequence (SEQ ID NO:253) of a native sequence PRO69522 cDNA, wherein SEQ ID NO:253 is a clone designated herein as "DNA287247".

Figure 254 shows the amino acid sequence (SEQ ID NO:254) derived from the coding sequence of SEQ ID NO:253 shown in Figure 253.

Figure 255 shows a nucleotide sequence (SEQ ID NO:255) of a native sequence PRO69523 cDNA, wherein SEQ ID NO:255 is a clone designated herein as "DNA287628".

5 Figure 256 shows the amino acid sequence (SEQ ID NO:256) derived from the coding sequence of SEQ ID NO:255 shown in Figure 255.

Figure 257 shows a nucleotide sequence (SEQ ID NO:257) of a native sequence PRO60513 cDNA, wherein SEQ ID NO:257 is a clone designated herein as "DNA272251".

10 Figure 258 shows the amino acid sequence (SEQ ID NO:258) derived from the coding sequence of SEQ ID NO:257 shown in Figure 257.

Figure 259 shows a nucleotide sequence (SEQ ID NO:259) of a native sequence PRO2512 cDNA, wherein SEQ ID NO:259 is a clone designated herein as "DNA288252".

Figure 260 shows the amino acid sequence (SEQ ID NO:260) derived from the coding sequence of SEQ ID NO:259 shown in Figure 259.

15 Figure 261 shows a nucleotide sequence (SEQ ID NO:261) of a native sequence PRO69524 cDNA, wherein SEQ ID NO:261 is a clone designated herein as "DNA287250".

Figure 262 shows the amino acid sequence (SEQ ID NO:262) derived from the coding sequence of SEQ ID NO:261 shown in Figure 261.

20 Figure 263 shows a nucleotide sequence (SEQ ID NO:263) of a native sequence PRO12569 cDNA, wherein SEQ ID NO:263 is a clone designated herein as "DNA150989".

Figure 264 shows the amino acid sequence (SEQ ID NO:264) derived from the coding sequence of SEQ ID NO:263 shown in Figure 263.

Figure 265 shows a nucleotide sequence (SEQ ID NO:265) of a native sequence PRO69525 cDNA, wherein SEQ ID NO:265 is a clone designated herein as "DNA287251".

25 Figure 266 shows the amino acid sequence (SEQ ID NO:266) derived from the coding sequence of SEQ ID NO:265 shown in Figure 265.

Figure 267 shows a nucleotide sequence (SEQ ID NO:267) of a native sequence PRO69526 cDNA, wherein SEQ ID NO:267 is a clone designated herein as "DNA287252".

30 Figure 268 shows the amino acid sequence (SEQ ID NO:268) derived from the coding sequence of SEQ ID NO:267 shown in Figure 267.

Figure 269 shows a nucleotide sequence (SEQ ID NO:269) of a native sequence PRO69527 cDNA, wherein SEQ ID NO:269 is a clone designated herein as "DNA287253".

Figure 270 shows the amino acid sequence (SEQ ID NO:270) derived from the coding sequence of SEQ ID NO:269 shown in Figure 269.

35 Figure 271 shows a nucleotide sequence (SEQ ID NO:271) of a native sequence PRO69528 cDNA, wherein SEQ ID NO:271 is a clone designated herein as "DNA287254".

Figure 272 shows the amino acid sequence (SEQ ID NO:272) derived from the coding sequence of SEQ ID NO:271 shown in Figure 271.

40 Figure 273 shows a nucleotide sequence (SEQ ID NO:273) of a native sequence PRO69529 cDNA, wherein SEQ ID NO:273 is a clone designated herein as "DNA287255".

Figure 274 shows the amino acid sequence (SEQ ID NO:274) derived from the coding sequence of - SEQ ID NO:273 shown in Figure 273.

Figure 275 shows a nucleotide sequence (SEQ ID NO:275) of a native sequence PRO12166 cDNA, wherein SEQ ID NO:275 is a clone designated herein as "DNA151021".

5 Figure 276 shows the amino acid sequence (SEQ ID NO:276) derived from the coding sequence of SEQ ID NO:275 shown in Figure 275.

Figure 277 shows a nucleotide sequence (SEQ ID NO:277) of a native sequence PRO2154 cDNA, wherein SEQ ID NO:277 is a clone designated herein as "DNA287630".

10 Figure 278 shows the amino acid sequence (SEQ ID NO:278) derived from the coding sequence of SEQ ID NO:277 shown in Figure 277.

Figure 279 shows a nucleotide sequence (SEQ ID NO:279) of a native sequence PRO69530 cDNA, wherein SEQ ID NO:279 is a clone designated herein as "DNA287257".

Figure 280 shows the amino acid sequence (SEQ ID NO:280) derived from the coding sequence of SEQ ID NO:279 shown in Figure 279.

15 Figure 281 shows a nucleotide sequence (SEQ ID NO:281) of a native sequence PRO51916 cDNA, wherein SEQ ID NO:281 is a clone designated herein as "DNA257326".

Figure 282 shows the amino acid sequence (SEQ ID NO:282) derived from the coding sequence of SEQ ID NO:281 shown in Figure 281.

20 Figure 283 shows a nucleotide sequence (SEQ ID NO:283) of a native sequence PRO52174 cDNA, wherein SEQ ID NO:283 is a clone designated herein as "DNA287258".

Figure 284 shows the amino acid sequence (SEQ ID NO:284) derived from the coding sequence of SEQ ID NO:283 shown in Figure 283.

Figure 285 shows a nucleotide sequence (SEQ ID NO:285) of a native sequence PRO69531 cDNA, wherein SEQ ID NO:285 is a clone designated herein as "DNA287259".

25 Figure 286 shows the amino acid sequence (SEQ ID NO:286) derived from the coding sequence of SEQ ID NO:285 shown in Figure 285.

Figure 287 shows a nucleotide sequence (SEQ ID NO:287) of a native sequence PRO69532 cDNA, wherein SEQ ID NO:287 is a clone designated herein as "DNA287260".

30 Figure 288 shows the amino acid sequence (SEQ ID NO:288) derived from the coding sequence of SEQ ID NO:287 shown in Figure 287.

Figure 289 shows a nucleotide sequence (SEQ ID NO:289) of a native sequence PRO69533 cDNA, wherein SEQ ID NO:289 is a clone designated herein as "DNA287261".

Figure 290 shows the amino acid sequence (SEQ ID NO:290) derived from the coding sequence of SEQ ID NO:289 shown in Figure 289.

35 Figure 291 shows a nucleotide sequence (SEQ ID NO:291) of a native sequence PRO69534 cDNA, wherein SEQ ID NO:291 is a clone designated herein as "DNA287262".

Figure 292 shows the amino acid sequence (SEQ ID NO:292) derived from the coding sequence of SEQ ID NO:291 shown in Figure 291.

40 Figure 293 shows a nucleotide sequence (SEQ ID NO:293) of a native sequence PRO54728 cDNA, wherein SEQ ID NO:293 is a clone designated herein as "DNA260982".

Figure 294 shows the amino acid sequence (SEQ ID NO:294) derived from the coding sequence of SEQ ID NO:293 shown in Figure 293.

Figure 295 shows a nucleotide sequence (SEQ ID NO:295) of a native sequence PRO70015 cDNA, wherein SEQ ID NO:295 is a clone designated herein as "DNA288253".

5 Figure 296 shows the amino acid sequence (SEQ ID NO:296) derived from the coding sequence of SEQ ID NO:295 shown in Figure 295.

Figure 297 shows a nucleotide sequence (SEQ ID NO:297) of a native sequence PRO69536 cDNA, wherein SEQ ID NO:297 is a clone designated herein as "DNA288254".

10 Figure 298 shows the amino acid sequence (SEQ ID NO:298) derived from the coding sequence of SEQ ID NO:297 shown in Figure 297.

Figure 299 shows a nucleotide sequence (SEQ ID NO:299) of a native sequence PRO69537 cDNA, wherein SEQ ID NO:299 is a clone designated herein as "DNA287265".

Figure 300 shows the amino acid sequence (SEQ ID NO:300) derived from the coding sequence of SEQ ID NO:299 shown in Figure 299.

15 Figure 301 shows a nucleotide sequence (SEQ ID NO:301) of a native sequence PRO37498 cDNA, wherein SEQ ID NO:301 is a clone designated herein as "DNA227035".

Figure 302 shows the amino acid sequence (SEQ ID NO:302) derived from the coding sequence of SEQ ID NO:301 shown in Figure 301.

20 Figure 303A-B shows a nucleotide sequence (SEQ ID NO:303A-B) of a native sequence PRO22175 cDNA, wherein SEQ ID NO:303A-B is a clone designated herein as "DNA189214".

Figure 304 shows the amino acid sequence (SEQ ID NO:304) derived from the coding sequence of SEQ ID NO:303A-B shown in Figure 303A-B.

Figure 305 shows a nucleotide sequence (SEQ ID NO:305) of a native sequence PRO69538 cDNA, wherein SEQ ID NO:305 is a clone designated herein as "DNA287266".

25 Figure 306 shows the amino acid sequence (SEQ ID NO:306) derived from the coding sequence of SEQ ID NO:305 shown in Figure 305.

Figure 307 shows a nucleotide sequence (SEQ ID NO:307) of a native sequence PRO37015 cDNA, wherein SEQ ID NO:307 is a clone designated herein as "DNA287267".

30 Figure 308 shows the amino acid sequence (SEQ ID NO:308) derived from the coding sequence of SEQ ID NO:307 shown in Figure 307.

Figure 309 shows a nucleotide sequence (SEQ ID NO:309) of a native sequence PRO12187 cDNA, wherein SEQ ID NO:309 is a clone designated herein as "DNA151799".

Figure 310 shows the amino acid sequence (SEQ ID NO:310) derived from the coding sequence of SEQ ID NO:309 shown in Figure 309.

35 Figure 311 shows a nucleotide sequence (SEQ ID NO:311) of a native sequence PRO69539 cDNA, wherein SEQ ID NO:311 is a clone designated herein as "DNA287268".

Figure 312 shows the amino acid sequence (SEQ ID NO:312) derived from the coding sequence of SEQ ID NO:311 shown in Figure 311.

40 Figure 313 shows a nucleotide sequence (SEQ ID NO:313) of a native sequence PRO69880 cDNA, wherein SEQ ID NO:313 is a clone designated herein as "DNA287632".

Figure 314 shows the amino acid sequence (SEQ ID NO:314) derived from the coding sequence of SEQ ID NO:313 shown in Figure 313.

Figure 315 shows a nucleotide sequence (SEQ ID NO:315) of a native sequence PRO69541 cDNA, wherein SEQ ID NO:315 is a clone designated herein as "DNA287270".

5 Figure 316 shows the amino acid sequence (SEQ ID NO:316) derived from the coding sequence of SEQ ID NO:315 shown in Figure 315.

Figure 317 shows a nucleotide sequence (SEQ ID NO:317) of a native sequence PRO69542 cDNA, wherein SEQ ID NO:317 is a clone designated herein as "DNA287271".

10 Figure 318 shows the amino acid sequence (SEQ ID NO:318) derived from the coding sequence of SEQ ID NO:317 shown in Figure 317.

Figure 319 shows a nucleotide sequence (SEQ ID NO:319) of a native sequence PRO69543 cDNA, wherein SEQ ID NO:319 is a clone designated herein as "DNA287272".

Figure 320 shows the amino acid sequence (SEQ ID NO:320) derived from the coding sequence of SEQ ID NO:319 shown in Figure 319.

15 Figure 321 shows a nucleotide sequence (SEQ ID NO:321) of a native sequence PRO70016 cDNA, wherein SEQ ID NO:321 is a clone designated herein as "DNA288255".

Figure 322 shows the amino acid sequence (SEQ ID NO:322) derived from the coding sequence of SEQ ID NO:321 shown in Figure 321.

20 Figure 323A-B shows a nucleotide sequence (SEQ ID NO:323A-B) of a native sequence PRO69545 cDNA, wherein SEQ ID NO:323A-B is a clone designated herein as "DNA287273".

Figure 324 shows the amino acid sequence (SEQ ID NO:324) derived from the coding sequence of SEQ ID NO:323A-B shown in Figure 323A-B.

Figure 325 shows a nucleotide sequence (SEQ ID NO:325) of a native sequence PRO50197 cDNA, wherein SEQ ID NO:325 is a clone designated herein as "DNA255115".

25 Figure 326 shows the amino acid sequence (SEQ ID NO:326) derived from the coding sequence of SEQ ID NO:325 shown in Figure 325.

Figure 327 shows a nucleotide sequence (SEQ ID NO:327) of a native sequence PRO69546 cDNA, wherein SEQ ID NO:327 is a clone designated herein as "DNA287274".

30 Figure 328 shows the amino acid sequence (SEQ ID NO:328) derived from the coding sequence of SEQ ID NO:327 shown in Figure 327.

Figure 329 shows a nucleotide sequence (SEQ ID NO:329) of a native sequence PRO69547 cDNA, wherein SEQ ID NO:329 is a clone designated herein as "DNA287275".

Figure 330 shows the amino acid sequence (SEQ ID NO:330) derived from the coding sequence of SEQ ID NO:329 shown in Figure 329.

35 Figure 331 shows a nucleotide sequence (SEQ ID NO:331) of a native sequence PRO69548 cDNA, wherein SEQ ID NO:331 is a clone designated herein as "DNA287276".

Figure 332 shows the amino acid sequence (SEQ ID NO:332) derived from the coding sequence of SEQ ID NO:331 shown in Figure 331.

40 Figure 333 shows a nucleotide sequence (SEQ ID NO:333) of a native sequence PRO69549 cDNA, wherein SEQ ID NO:333 is a clone designated herein as "DNA287277".

Figure 334 shows the amino acid sequence (SEQ ID NO:334) derived from the coding sequence of SEQ ID NO:333 shown in Figure 333.

Figure 335 shows a nucleotide sequence (SEQ ID NO:335) of a native sequence PRO69550 cDNA, wherein SEQ ID NO:335 is a clone designated herein as "DNA287278".

5 Figure 336 shows the amino acid sequence (SEQ ID NO:336) derived from the coding sequence of SEQ ID NO:335 shown in Figure 335.

Figure 337 shows a nucleotide sequence (SEQ ID NO:337) of a native sequence PRO69551 cDNA, wherein SEQ ID NO:337 is a clone designated herein as "DNA287279".

10 Figure 338 shows the amino acid sequence (SEQ ID NO:338) derived from the coding sequence of SEQ ID NO:337 shown in Figure 337.

Figure 339 shows a nucleotide sequence (SEQ ID NO:339) of a native sequence PRO69552 cDNA, wherein SEQ ID NO:339 is a clone designated herein as "DNA287280".

Figure 340 shows the amino acid sequence (SEQ ID NO:340) derived from the coding sequence of SEQ ID NO:339 shown in Figure 339.

15 Figure 341 shows a nucleotide sequence (SEQ ID NO:341) of a native sequence PRO37460 cDNA, wherein SEQ ID NO:341 is a clone designated herein as "DNA226997".

Figure 342 shows the amino acid sequence (SEQ ID NO:342) derived from the coding sequence of SEQ ID NO:341 shown in Figure 341.

20 Figure 343 shows a nucleotide sequence (SEQ ID NO:343) of a native sequence PRO42223 cDNA, wherein SEQ ID NO:343 is a clone designated herein as "DNA242927".

Figure 344 shows the amino acid sequence (SEQ ID NO:344) derived from the coding sequence of SEQ ID NO:343 shown in Figure 343.

Figure 345A-B shows a nucleotide sequence (SEQ ID NO:345A-B) of a native sequence PRO69553 cDNA, wherein SEQ ID NO:345A-B is a clone designated herein as "DNA287281".

25 Figure 346 shows the amino acid sequence (SEQ ID NO:346) derived from the coding sequence of SEQ ID NO:345A-B shown in Figure 345A-B.

Figure 347 shows a nucleotide sequence (SEQ ID NO:347) of a native sequence PRO69554 cDNA, wherein SEQ ID NO:347 is a clone designated herein as "DNA287282".

30 Figure 348 shows the amino acid sequence (SEQ ID NO:348) derived from the coding sequence of SEQ ID NO:347 shown in Figure 347.

Figure 349 shows a nucleotide sequence (SEQ ID NO:349) of a native sequence PRO69555 cDNA, wherein SEQ ID NO:349 is a clone designated herein as "DNA287283".

Figure 350 shows the amino acid sequence (SEQ ID NO:350) derived from the coding sequence of SEQ ID NO:349 shown in Figure 349.

35 Figure 351 shows a nucleotide sequence (SEQ ID NO:351) of a native sequence PRO61014 cDNA, wherein SEQ ID NO:351 is a clone designated herein as "DNA272930".

Figure 352 shows the amino acid sequence (SEQ ID NO:352) derived from the coding sequence of SEQ ID NO:351 shown in Figure 351.

40 Figure 353 shows a nucleotide sequence (SEQ ID NO:353) of a native sequence PRO59915 cDNA, wherein SEQ ID NO:353 is a clone designated herein as "DNA287284".

Figure 354 shows the amino acid sequence (SEQ ID NO:354) derived from the coding sequence of SEQ ID NO:353 shown in Figure 353.

Figure 355A-B shows a nucleotide sequence (SEQ ID NO:355A-B) of a native sequence PRO37891 cDNA, wherein SEQ ID NO:355A-B is a clone designated herein as "DNA227428".

5 Figure 356 shows the amino acid sequence (SEQ ID NO:356) derived from the coding sequence of SEQ ID NO:355A-B shown in Figure 355A-B.

Figure 357 shows a nucleotide sequence (SEQ ID NO:357) of a native sequence PRO69556 cDNA, wherein SEQ ID NO:357 is a clone designated herein as "DNA287285".

10 Figure 358 shows the amino acid sequence (SEQ ID NO:358) derived from the coding sequence of SEQ ID NO:357 shown in Figure 357.

Figure 359 shows a nucleotide sequence (SEQ ID NO:359) of a native sequence PRO12875 cDNA, wherein SEQ ID NO:359 is a clone designated herein as "DNA151237".

Figure 360 shows the amino acid sequence (SEQ ID NO:360) derived from the coding sequence of SEQ ID NO:359 shown in Figure 359.

15 Figure 361 shows a nucleotide sequence (SEQ ID NO:361) of a native sequence PRO70017 cDNA, wherein SEQ ID NO:361 is a clone designated herein as "DNA288256".

Figure 362 shows the amino acid sequence (SEQ ID NO:362) derived from the coding sequence of SEQ ID NO:361 shown in Figure 361.

20 Figure 363 shows a nucleotide sequence (SEQ ID NO:363) of a native sequence PRO70018 cDNA, wherein SEQ ID NO:363 is a clone designated herein as "DNA288257".

Figure 364 shows the amino acid sequence (SEQ ID NO:364) derived from the coding sequence of SEQ ID NO:363 shown in Figure 363.

Figure 365 shows a nucleotide sequence (SEQ ID NO:365) of a native sequence PRO4426 cDNA, wherein SEQ ID NO:365 is a clone designated herein as "DNA287287".

25 Figure 366 shows the amino acid sequence (SEQ ID NO:366) derived from the coding sequence of SEQ ID NO:365 shown in Figure 365.

Figure 367 shows a nucleotide sequence (SEQ ID NO:367) of a native sequence PRO69558 cDNA, wherein SEQ ID NO:367 is a clone designated herein as "DNA287288".

30 Figure 368 shows the amino acid sequence (SEQ ID NO:368) derived from the coding sequence of SEQ ID NO:367 shown in Figure 367.

Figure 369 shows a nucleotide sequence (SEQ ID NO:369) of a native sequence PRO69559 cDNA, wherein SEQ ID NO:369 is a clone designated herein as "DNA287289".

Figure 370 shows the amino acid sequence (SEQ ID NO:370) derived from the coding sequence of SEQ ID NO:369 shown in Figure 369.

35 Figure 371 shows a nucleotide sequence (SEQ ID NO:371) of a native sequence PRO37676 cDNA, wherein SEQ ID NO:371 is a clone designated herein as "DNA227213".

Figure 372 shows the amino acid sequence (SEQ ID NO:372) derived from the coding sequence of SEQ ID NO:371 shown in Figure 371.

40 Figure 373 shows a nucleotide sequence (SEQ ID NO:373) of a native sequence PRO69560 cDNA, wherein SEQ ID NO:373 is a clone designated herein as "DNA287290".

Figure 374 shows the amino acid sequence (SEQ ID NO:374) derived from the coding sequence of SEQ ID NO:373 shown in Figure 373.

Figure 375 shows a nucleotide sequence (SEQ ID NO:375) of a native sequence PRO69561 cDNA, wherein SEQ ID NO:375 is a clone designated herein as "DNA287291".

5 Figure 376 shows the amino acid sequence (SEQ ID NO:376) derived from the coding sequence of SEQ ID NO:375 shown in Figure 375.

Figure 377 shows a nucleotide sequence (SEQ ID NO:377) of a native sequence PRO69562 cDNA, wherein SEQ ID NO:377 is a clone designated herein as "DNA287292".

10 Figure 378 shows the amino acid sequence (SEQ ID NO:378) derived from the coding sequence of SEQ ID NO:377 shown in Figure 377.

Figure 379 shows a nucleotide sequence (SEQ ID NO:379) of a native sequence PRO63204 cDNA, wherein SEQ ID NO:379 is a clone designated herein as "DNA287293".

Figure 380 shows the amino acid sequence (SEQ ID NO:380) derived from the coding sequence of SEQ ID NO:379 shown in Figure 379.

15 Figure 381 shows a nucleotide sequence (SEQ ID NO:381) of a native sequence PRO70019 cDNA, wherein SEQ ID NO:381 is a clone designated herein as "DNA288258".

Figure 382 shows the amino acid sequence (SEQ ID NO:382) derived from the coding sequence of SEQ ID NO:381 shown in Figure 381.

20 Figure 383 shows a nucleotide sequence (SEQ ID NO:383) of a native sequence PRO69564 cDNA, wherein SEQ ID NO:383 is a clone designated herein as "DNA287295".

Figure 384 shows the amino acid sequence (SEQ ID NO:384) derived from the coding sequence of SEQ ID NO:383 shown in Figure 383.

Figure 385 shows a nucleotide sequence (SEQ ID NO:385) of a native sequence PRO62830 cDNA, wherein SEQ ID NO:385 is a clone designated herein as "DNA287296".

25 Figure 386 shows the amino acid sequence (SEQ ID NO:386) derived from the coding sequence of SEQ ID NO:385 shown in Figure 385.

Figure 387 shows a nucleotide sequence (SEQ ID NO:387) of a native sequence PRO69565 cDNA, wherein SEQ ID NO:387 is a clone designated herein as "DNA287297".

30 Figure 388 shows the amino acid sequence (SEQ ID NO:388) derived from the coding sequence of SEQ ID NO:387 shown in Figure 387.

Figure 389 shows a nucleotide sequence (SEQ ID NO:389) of a native sequence PRO69566 cDNA, wherein SEQ ID NO:389 is a clone designated herein as "DNA287298".

Figure 390 shows the amino acid sequence (SEQ ID NO:390) derived from the coding sequence of SEQ ID NO:389 shown in Figure 389.

35 Figure 391 shows a nucleotide sequence (SEQ ID NO:391) of a native sequence PRO69567 cDNA, wherein SEQ ID NO:391 is a clone designated herein as "DNA287299".

Figure 392 shows the amino acid sequence (SEQ ID NO:392) derived from the coding sequence of SEQ ID NO:391 shown in Figure 391.

40 Figure 393 shows a nucleotide sequence (SEQ ID NO:393) of a native sequence PRO49675 cDNA, wherein SEQ ID NO:393 is a clone designated herein as "DNA254572".

Figure 394 shows the amino acid sequence (SEQ ID NO:394) derived from the coding sequence of SEQ ID NO:393 shown in Figure 393.

Figure 395 shows a nucleotide sequence (SEQ ID NO:395) of a native sequence PRO69568 cDNA, wherein SEQ ID NO:395 is a clone designated herein as "DNA287300".

5 Figure 396 shows the amino acid sequence (SEQ ID NO:396) derived from the coding sequence of SEQ ID NO:395 shown in Figure 395.

Figure 397 shows a nucleotide sequence (SEQ ID NO:397) of a native sequence PRO2013 cDNA, wherein SEQ ID NO:397 is a clone designated herein as "DNA75526".

10 Figure 398 shows the amino acid sequence (SEQ ID NO:398) derived from the coding sequence of SEQ ID NO:397 shown in Figure 397.

Figure 399 shows a nucleotide sequence (SEQ ID NO:399) of a native sequence PRO69569 cDNA, wherein SEQ ID NO:399 is a clone designated herein as "DNA287302".

Figure 400 shows the amino acid sequence (SEQ ID NO:400) derived from the coding sequence of SEQ ID NO:399 shown in Figure 399.

15 Figure 401 shows a nucleotide sequence (SEQ ID NO:401) of a native sequence PRO69570 cDNA, wherein SEQ ID NO:401 is a clone designated herein as "DNA287303".

Figure 402 shows the amino acid sequence (SEQ ID NO:402) derived from the coding sequence of SEQ ID NO:401 shown in Figure 401.

20 Figure 403 shows a nucleotide sequence (SEQ ID NO:403) of a native sequence PRO69571 cDNA, wherein SEQ ID NO:403 is a clone designated herein as "DNA287304".

Figure 404 shows the amino acid sequence (SEQ ID NO:404) derived from the coding sequence of SEQ ID NO:403 shown in Figure 403.

Figure 405A-B shows a nucleotide sequence (SEQ ID NO:405A-B) of a native sequence PRO36403 cDNA, wherein SEQ ID NO:405A-B is a clone designated herein as "DNA225940".

25 Figure 406 shows the amino acid sequence (SEQ ID NO:406) derived from the coding sequence of SEQ ID NO:405A-B shown in Figure 405A-B.

Figure 407 shows a nucleotide sequence (SEQ ID NO:407) of a native sequence PRO4676 cDNA, wherein SEQ ID NO:407 is a clone designated herein as "DNA288259".

30 Figure 408 shows the amino acid sequence (SEQ ID NO:408) derived from the coding sequence of SEQ ID NO:407 shown in Figure 407.

Figure 409 shows a nucleotide sequence (SEQ ID NO:409) of a native sequence PRO37657 cDNA, wherein SEQ ID NO:409 is a clone designated herein as "DNA227194".

Figure 410 shows the amino acid sequence (SEQ ID NO:410) derived from the coding sequence of SEQ ID NO:409 shown in Figure 409.

35 Figure 411 shows a nucleotide sequence (SEQ ID NO:411) of a native sequence PRO62097 cDNA, wherein SEQ ID NO:411 is a clone designated herein as "DNA274167".

Figure 412 shows the amino acid sequence (SEQ ID NO:412) derived from the coding sequence of SEQ ID NO:411 shown in Figure 411.

40 Figure 413 shows a nucleotide sequence (SEQ ID NO:413) of a native sequence PRO38081 cDNA, wherein SEQ ID NO:413 is a clone designated herein as "DNA227618".

Figure 414 shows the amino acid sequence (SEQ ID NO:414) derived from the coding sequence of SEQ ID NO:413 shown in Figure 413.

Figure 415 shows a nucleotide sequence (SEQ ID NO:415) of a native sequence PRO69572 cDNA, wherein SEQ ID NO:415 is a clone designated herein as "DNA287306".

5 Figure 416 shows the amino acid sequence (SEQ ID NO:416) derived from the coding sequence of SEQ ID NO:415 shown in Figure 415.

Figure 417 shows a nucleotide sequence (SEQ ID NO:417) of a native sequence PRO69573 cDNA, wherein SEQ ID NO:417 is a clone designated herein as "DNA287307".

10 Figure 418 shows the amino acid sequence (SEQ ID NO:418) derived from the coding sequence of SEQ ID NO:417 shown in Figure 417.

Figure 419 shows a nucleotide sequence (SEQ ID NO:419) of a native sequence PRO69574 cDNA, wherein SEQ ID NO:419 is a clone designated herein as "DNA287308".

Figure 420 shows the amino acid sequence (SEQ ID NO:420) derived from the coding sequence of SEQ ID NO:419 shown in Figure 419.

15 Figure 421 shows a nucleotide sequence (SEQ ID NO:421) of a native sequence PRO69883 cDNA, wherein SEQ ID NO:421 is a clone designated herein as "DNA287635".

Figure 422 shows the amino acid sequence (SEQ ID NO:422) derived from the coding sequence of SEQ ID NO:421 shown in Figure 421.

20 Figure 423 shows a nucleotide sequence (SEQ ID NO:423) of a native sequence PRO69576 cDNA, wherein SEQ ID NO:423 is a clone designated herein as "DNA287310".

Figure 424 shows the amino acid sequence (SEQ ID NO:424) derived from the coding sequence of SEQ ID NO:423 shown in Figure 423.

Figure 425 shows a nucleotide sequence (SEQ ID NO:425) of a native sequence PRO37584 cDNA, wherein SEQ ID NO:425 is a clone designated herein as "DNA227121".

25 Figure 426 shows the amino acid sequence (SEQ ID NO:426) derived from the coding sequence of SEQ ID NO:425 shown in Figure 425.

Figure 427 shows a nucleotide sequence (SEQ ID NO:427) of a native sequence PRO11603 cDNA, wherein SEQ ID NO:427 is a clone designated herein as "DNA151007".

30 Figure 428 shows the amino acid sequence (SEQ ID NO:428) derived from the coding sequence of SEQ ID NO:427 shown in Figure 427.

Figure 429 shows a nucleotide sequence (SEQ ID NO:429) of a native sequence PRO70020 cDNA, wherein SEQ ID NO:429 is a clone designated herein as "DNA288260".

Figure 430 shows the amino acid sequence (SEQ ID NO:430) derived from the coding sequence of SEQ ID NO:429 shown in Figure 429.

35 Figure 431 shows a nucleotide sequence (SEQ ID NO:431) of a native sequence PRO51695 cDNA, wherein SEQ ID NO:431 is a clone designated herein as "DNA256762".

Figure 432 shows the amino acid sequence (SEQ ID NO:432) derived from the coding sequence of SEQ ID NO:431 shown in Figure 431.

40 Figure 433 shows a nucleotide sequence (SEQ ID NO:433) of a native sequence PRO69579 cDNA, wherein SEQ ID NO:433 is a clone designated herein as "DNA287314".

Figure 434 shows the amino acid sequence (SEQ ID NO:434) derived from the coding sequence of SEQ ID NO:433 shown in Figure 433.

Figure 435 shows a nucleotide sequence (SEQ ID NO:435) of a native sequence PRO69580 cDNA, wherein SEQ ID NO:435 is a clone designated herein as "DNA287315".

5 Figure 436 shows the amino acid sequence (SEQ ID NO:436) derived from the coding sequence of SEQ ID NO:435 shown in Figure 435.

Figure 437 shows a nucleotide sequence (SEQ ID NO:437) of a native sequence PRO69581 cDNA, wherein SEQ ID NO:437 is a clone designated herein as "DNA287316".

10 Figure 438 shows the amino acid sequence (SEQ ID NO:438) derived from the coding sequence of SEQ ID NO:437 shown in Figure 437.

Figure 439 shows a nucleotide sequence (SEQ ID NO:439) of a native sequence PRO69582 cDNA, wherein SEQ ID NO:439 is a clone designated herein as "DNA287317".

Figure 440 shows the amino acid sequence (SEQ ID NO:440) derived from the coding sequence of SEQ ID NO:439 shown in Figure 439.

15 Figure 441 shows a nucleotide sequence (SEQ ID NO:441) of a native sequence PRO69583 cDNA, wherein SEQ ID NO:441 is a clone designated herein as "DNA287318".

Figure 442 shows the amino acid sequence (SEQ ID NO:442) derived from the coding sequence of SEQ ID NO:441 shown in Figure 441.

20 Figure 443 shows a nucleotide sequence (SEQ ID NO:443) of a native sequence PRO69584 cDNA, wherein SEQ ID NO:443 is a clone designated herein as "DNA287319".

Figure 444 shows the amino acid sequence (SEQ ID NO:444) derived from the coding sequence of SEQ ID NO:443 shown in Figure 443.

Figure 445 shows a nucleotide sequence (SEQ ID NO:445) of a native sequence PRO69585 cDNA, wherein SEQ ID NO:445 is a clone designated herein as "DNA287320".

25 Figure 446 shows the amino acid sequence (SEQ ID NO:446) derived from the coding sequence of SEQ ID NO:445 shown in Figure 445.

Figure 447 shows a nucleotide sequence (SEQ ID NO:447) of a native sequence PRO69586 cDNA, wherein SEQ ID NO:447 is a clone designated herein as "DNA287321".

30 Figure 448 shows the amino acid sequence (SEQ ID NO:448) derived from the coding sequence of SEQ ID NO:447 shown in Figure 447.

Figure 449 shows a nucleotide sequence (SEQ ID NO:449) of a native sequence PRO69587 cDNA, wherein SEQ ID NO:449 is a clone designated herein as "DNA287322".

Figure 450 shows the amino acid sequence (SEQ ID NO:450) derived from the coding sequence of SEQ ID NO:449 shown in Figure 449.

35 Figure 451 shows a nucleotide sequence (SEQ ID NO:451) of a native sequence PRO69588 cDNA, wherein SEQ ID NO:451 is a clone designated herein as "DNA287323".

Figure 452 shows the amino acid sequence (SEQ ID NO:452) derived from the coding sequence of SEQ ID NO:451 shown in Figure 451.

40 Figure 453 shows a nucleotide sequence (SEQ ID NO:453) of a native sequence PRO69589 cDNA, wherein SEQ ID NO:453 is a clone designated herein as "DNA287637".

Figure 454 shows the amino acid sequence (SEQ ID NO:454) derived from the coding sequence of SEQ ID NO:453 shown in Figure 453.

Figure 455A-B shows a nucleotide sequence (SEQ ID NO:455A-B) of a native sequence PRO70021 cDNA, wherein SEQ ID NO:455A-B is a clone designated herein as "DNA288261".

5 Figure 456 shows the amino acid sequence (SEQ ID NO:456) derived from the coding sequence of SEQ ID NO:455A-B shown in Figure 455A-B.

Figure 457 shows a nucleotide sequence (SEQ ID NO:457) of a native sequence PRO69590 cDNA, wherein SEQ ID NO:457 is a clone designated herein as "DNA288262".

10 Figure 458 shows the amino acid sequence (SEQ ID NO:458) derived from the coding sequence of SEQ ID NO:457 shown in Figure 457.

Figure 459 shows a nucleotide sequence (SEQ ID NO:459) of a native sequence PRO70022 cDNA, wherein SEQ ID NO:459 is a clone designated herein as "DNA288263".

Figure 460 shows the amino acid sequence (SEQ ID NO:460) derived from the coding sequence of SEQ ID NO:459 shown in Figure 459.

15 Figure 461A-B shows a nucleotide sequence (SEQ ID NO:461A-B) of a native sequence PRO69592 cDNA, wherein SEQ ID NO:461A-B is a clone designated herein as "DNA287327".

Figure 462 shows the amino acid sequence (SEQ ID NO:462) derived from the coding sequence of SEQ ID NO:461A-B shown in Figure 461A-B.

20 Figure 463 shows a nucleotide sequence (SEQ ID NO:463) of a native sequence PRO37029 cDNA, wherein SEQ ID NO:463 is a clone designated herein as "DNA287328".

Figure 464 shows the amino acid sequence (SEQ ID NO:464) derived from the coding sequence of SEQ ID NO:463 shown in Figure 463.

Figure 465 shows a nucleotide sequence (SEQ ID NO:465) of a native sequence PRO69593 cDNA, wherein SEQ ID NO:465 is a clone designated herein as "DNA287329".

25 Figure 466 shows the amino acid sequence (SEQ ID NO:466) derived from the coding sequence of SEQ ID NO:465 shown in Figure 465.

Figure 467A-B shows a nucleotide sequence (SEQ ID NO:467A-B) of a native sequence PRO69594 cDNA, wherein SEQ ID NO:467A-B is a clone designated herein as "DNA287330".

30 Figure 468 shows the amino acid sequence (SEQ ID NO:468) derived from the coding sequence of SEQ ID NO:467A-B shown in Figure 467A-B.

Figure 469 shows a nucleotide sequence (SEQ ID NO:469) of a native sequence PRO69595 cDNA, wherein SEQ ID NO:469 is a clone designated herein as "DNA287331".

Figure 470 shows the amino acid sequence (SEQ ID NO:470) derived from the coding sequence of SEQ ID NO:469 shown in Figure 469.

35 Figure 471 shows a nucleotide sequence (SEQ ID NO:471) of a native sequence PRO1207 cDNA, wherein SEQ ID NO:471 is a clone designated herein as "DNA66480".

Figure 472 shows the amino acid sequence (SEQ ID NO:472) derived from the coding sequence of SEQ ID NO:471 shown in Figure 471.

40 Figure 473 shows a nucleotide sequence (SEQ ID NO:473) of a native sequence PRO69596 cDNA, wherein SEQ ID NO:473 is a clone designated herein as "DNA287332".

Figure 474 shows the amino acid sequence (SEQ ID NO:474) derived from the coding sequence of SEQ ID NO:473 shown in Figure 473.

Figure 475 shows a nucleotide sequence (SEQ ID NO:475) of a native sequence PRO69597 cDNA, wherein SEQ ID NO:475 is a clone designated herein as "DNA287333".

5 Figure 476 shows the amino acid sequence (SEQ ID NO:476) derived from the coding sequence of SEQ ID NO:475 shown in Figure 475.

Figure 477 shows a nucleotide sequence (SEQ ID NO:477) of a native sequence PRO51139 cDNA, wherein SEQ ID NO:477 is a clone designated herein as "DNA256089".

10 Figure 478 shows the amino acid sequence (SEQ ID NO:478) derived from the coding sequence of SEQ ID NO:477 shown in Figure 477.

Figure 479 shows a nucleotide sequence (SEQ ID NO:479) of a native sequence PRO62545 cDNA, wherein SEQ ID NO: 479 is a clone designated herein as "DNA274778".

Figure 480 shows the amino acid sequence (SEQ ID NO:480) derived from the coding sequence of SEQ ID NO:479 shown in Figure 479.

15 Figure 481 shows a nucleotide sequence (SEQ ID NO:481) of a native sequence PRO3615 cDNA, wherein SEQ ID NO:481 is a clone designated herein as "DNA287334".

Figure 482 shows the amino acid sequence (SEQ ID NO:482) derived from the coding sequence of SEQ ID NO:481 shown in Figure 481.

20 Figure 483 shows a nucleotide sequence (SEQ ID NO:483) of a native sequence PRO38036 cDNA, wherein SEQ ID NO:483 is a clone designated herein as "DNA227573".

Figure 484 shows the amino acid sequence (SEQ ID NO:484) derived from the coding sequence of SEQ ID NO:483 shown in Figure 483.

Figure 485 shows a nucleotide sequence (SEQ ID NO:485) of a native sequence PRO69598 cDNA, wherein SEQ ID NO:485 is a clone designated herein as "DNA287335".

25 Figure 486 shows the amino acid sequence (SEQ ID NO:486) derived from the coding sequence of SEQ ID NO:485 shown in Figure 485.

Figure 487 shows a nucleotide sequence (SEQ ID NO:487) of a native sequence PRO4701 cDNA, wherein SEQ ID NO:487 is a clone designated herein as "DNA103371".

30 Figure 488 shows the amino acid sequence (SEQ ID NO:488) derived from the coding sequence of SEQ ID NO:487 shown in Figure 487.

Figure 489 shows a nucleotide sequence (SEQ ID NO:489) of a native sequence PRO69599 cDNA, wherein SEQ ID NO:489 is a clone designated herein as "DNA287336".

Figure 490 shows the amino acid sequence (SEQ ID NO:490) derived from the coding sequence of SEQ ID NO:489 shown in Figure 489.

35 Figure 491 shows a nucleotide sequence (SEQ ID NO:491) of a native sequence PRO69600 cDNA, wherein SEQ ID NO:491 is a clone designated herein as "DNA287337".

Figure 492 shows the amino acid sequence (SEQ ID NO:492) derived from the coding sequence of SEQ ID NO:491 shown in Figure 491.

40 Figure 493 shows a nucleotide sequence (SEQ ID NO:493) of a native sequence PRO69601 cDNA, wherein SEQ ID NO:493 is a clone designated herein as "DNA287338".

Figure 494 shows the amino acid sequence (SEQ ID NO:494) derived from the coding sequence of SEQ ID NO:493 shown in Figure 493.

Figure 495 shows a nucleotide sequence (SEQ ID NO:495) of a native sequence PRO69887 cDNA, wherein SEQ ID NO:495 is a clone designated herein as "DNA287640".

5 Figure 496 shows the amino acid sequence (SEQ ID NO:496) derived from the coding sequence of SEQ ID NO:495 shown in Figure 495.

Figure 497 shows a nucleotide sequence (SEQ ID NO:497) of a native sequence PRO69603 cDNA, wherein SEQ ID NO:497 is a clone designated herein as "DNA287340".

10 Figure 498 shows the amino acid sequence (SEQ ID NO:498) derived from the coding sequence of SEQ ID NO:497 shown in Figure 497.

Figure 499 shows a nucleotide sequence (SEQ ID NO:499) of a native sequence PRO69604 cDNA, wherein SEQ ID NO:499 is a clone designated herein as "DNA287341".

Figure 500 shows the amino acid sequence (SEQ ID NO:500) derived from the coding sequence of SEQ ID NO:499 shown in Figure 499.

15 Figure 501 shows a nucleotide sequence (SEQ ID NO:501) of a native sequence PRO70023 cDNA, wherein SEQ ID NO:501 is a clone designated herein as "DNA288264".

Figure 502 shows the amino acid sequence (SEQ ID NO:502) derived from the coding sequence of SEQ ID NO:501 shown in Figure 501.

20 Figure 503 shows a nucleotide sequence (SEQ ID NO:503) of a native sequence PRO69606 cDNA, wherein SEQ ID NO:503 is a clone designated herein as "DNA287343".

Figure 504 shows the amino acid sequence (SEQ ID NO:504) derived from the coding sequence of SEQ ID NO:503 shown in Figure 503.

Figure 505 shows a nucleotide sequence (SEQ ID NO:505) of a native sequence PRO69607 cDNA, wherein SEQ ID NO:505 is a clone designated herein as "DNA287344".

25 Figure 506 shows the amino acid sequence (SEQ ID NO:506) derived from the coding sequence of SEQ ID NO:505 shown in Figure 505.

Figure 507 shows a nucleotide sequence (SEQ ID NO:507) of a native sequence PRO69608 cDNA, wherein SEQ ID NO:507 is a clone designated herein as "DNA287345".

30 Figure 508 shows the amino acid sequence (SEQ ID NO:508) derived from the coding sequence of SEQ ID NO:507 shown in Figure 507.

Figure 509 shows a nucleotide sequence (SEQ ID NO:509) of a native sequence PRO69609 cDNA, wherein SEQ ID NO:509 is a clone designated herein as "DNA287346".

Figure 510 shows the amino acid sequence (SEQ ID NO:510) derived from the coding sequence of SEQ ID NO:509 shown in Figure 509.

35 Figure 511 shows a nucleotide sequence (SEQ ID NO:511) of a native sequence PRO69610 cDNA, wherein SEQ ID NO:511 is a clone designated herein as "DNA287347".

Figure 512 shows the amino acid sequence (SEQ ID NO:512) derived from the coding sequence of SEQ ID NO:511 shown in Figure 511.

40 Figure 513 shows a nucleotide sequence (SEQ ID NO:513) of a native sequence PRO9902 cDNA, wherein SEQ ID NO:513 is a clone designated herein as "DNA287642".

Figure 514 shows the amino acid sequence (SEQ ID NO:514) derived from the coding sequence of SEQ ID NO:513 shown in Figure 513.

Figure 515 shows a nucleotide sequence (SEQ ID NO:515) of a native sequence PRO69611 cDNA, wherein SEQ ID NO:515 is a clone designated herein as "DNA287349".

5 Figure 516 shows the amino acid sequence (SEQ ID NO:516) derived from the coding sequence of SEQ ID NO:515 shown in Figure 515.

Figure 517 shows a nucleotide sequence (SEQ ID NO:517) of a native sequence PRO69612 cDNA, wherein SEQ ID NO:517 is a clone designated herein as "DNA287350".

10 Figure 518 shows the amino acid sequence (SEQ ID NO:518) derived from the coding sequence of SEQ ID NO:517 shown in Figure 517.

Figure 519 shows a nucleotide sequence (SEQ ID NO:519) of a native sequence PRO69613 cDNA, wherein SEQ ID NO:519 is a clone designated herein as "DNA287351".

Figure 520 shows the amino acid sequence (SEQ ID NO:520) derived from the coding sequence of SEQ ID NO:519 shown in Figure 519.

15 Figure 521 shows a nucleotide sequence (SEQ ID NO:521) of a native sequence PRO69614 cDNA, wherein SEQ ID NO:521 is a clone designated herein as "DNA287352".

Figure 522 shows the amino acid sequence (SEQ ID NO:522) derived from the coding sequence of SEQ ID NO:521 shown in Figure 521.

20 Figure 523 shows a nucleotide sequence (SEQ ID NO:523) of a native sequence PRO69615 cDNA, wherein SEQ ID NO:523 is a clone designated herein as "DNA287643".

Figure 524 shows the amino acid sequence (SEQ ID NO:524) derived from the coding sequence of SEQ ID NO:523 shown in Figure 523.

Figure 525 shows a nucleotide sequence (SEQ ID NO:525) of a native sequence PRO70024 cDNA, wherein SEQ ID NO:525 is a clone designated herein as "DNA288265".

25 Figure 526 shows the amino acid sequence (SEQ ID NO:526) derived from the coding sequence of SEQ ID NO:525 shown in Figure 525.

Figure 527 shows a nucleotide sequence (SEQ ID NO:527) of a native sequence PRO69616 cDNA, wherein SEQ ID NO:527 is a clone designated herein as "DNA287354".

30 Figure 528 shows the amino acid sequence (SEQ ID NO:528) derived from the coding sequence of SEQ ID NO:527 shown in Figure 527.

Figure 529 shows a nucleotide sequence (SEQ ID NO:529) of a native sequence PRO49619 cDNA, wherein SEQ ID NO:529 is a clone designated herein as "DNA254512".

Figure 530 shows the amino acid sequence (SEQ ID NO:530) derived from the coding sequence of SEQ ID NO:529 shown in Figure 529.

35 Figure 531 shows a nucleotide sequence (SEQ ID NO:531) of a native sequence PRO69617 cDNA, wherein SEQ ID NO:531 is a clone designated herein as "DNA287355".

Figure 532 shows the amino acid sequence (SEQ ID NO:532) derived from the coding sequence of SEQ ID NO:531 shown in Figure 531.

40 Figure 533 shows a nucleotide sequence (SEQ ID NO:533) of a native sequence PRO69618 cDNA, wherein SEQ ID NO:533 is a clone designated herein as "DNA287356".

Figure 534 shows the amino acid sequence (SEQ ID NO:534) derived from the coding sequence of SEQ ID NO:533 shown in Figure 533.

Figure 535 shows a nucleotide sequence (SEQ ID NO:535) of a native sequence PRO38040 cDNA, wherein SEQ ID NO:535 is a clone designated herein as "DNA227577".

5 Figure 536 shows the amino acid sequence (SEQ ID NO:536) derived from the coding sequence of SEQ ID NO:535 shown in Figure 535.

Figure 537 shows a nucleotide sequence (SEQ ID NO:537) of a native sequence PRO69619 cDNA, wherein SEQ ID NO:537 is a clone designated herein as "DNA287357".

10 Figure 538 shows the amino acid sequence (SEQ ID NO:538) derived from the coding sequence of SEQ ID NO:537 shown in Figure 537.

Figure 539 shows a nucleotide sequence (SEQ ID NO:539) of a native sequence PRO69620 cDNA, wherein SEQ ID NO:539 is a clone designated herein as "DNA287358".

Figure 540 shows the amino acid sequence (SEQ ID NO:540) derived from the coding sequence of SEQ ID NO:539 shown in Figure 539.

15 Figure 541 shows a nucleotide sequence (SEQ ID NO:541) of a native sequence PRO69621 cDNA, wherein SEQ ID NO:541 is a clone designated herein as "DNA287359".

Figure 542 shows the amino acid sequence (SEQ ID NO:542) derived from the coding sequence of SEQ ID NO:541 shown in Figure 541.

20 Figure 543A-B shows a nucleotide sequence (SEQ ID NO:543A-B) of a native sequence PRO69622 cDNA, wherein SEQ ID NO:543A-B is a clone designated herein as "DNA287360".

Figure 544 shows the amino acid sequence (SEQ ID NO:544) derived from the coding sequence of SEQ ID NO:543A-B shown in Figure 543A-B.

Figure 545 shows a nucleotide sequence (SEQ ID NO:545) of a native sequence PRO4401 cDNA, wherein SEQ ID NO:545 is a clone designated herein as "DNA287362".

25 Figure 546 shows the amino acid sequence (SEQ ID NO:546) derived from the coding sequence of SEQ ID NO:545 shown in Figure 545.

Figure 547 shows a nucleotide sequence (SEQ ID NO:547) of a native sequence PRO70025 cDNA, wherein SEQ ID NO:547 is a clone designated herein as "DNA288266".

30 Figure 548 shows the amino acid sequence (SEQ ID NO:548) derived from the coding sequence of SEQ ID NO:547 shown in Figure 547.

Figure 549 shows a nucleotide sequence (SEQ ID NO:549) of a native sequence PRO69625 cDNA, wherein SEQ ID NO:549 is a clone designated herein as "DNA287364".

Figure 550 shows the amino acid sequence (SEQ ID NO:550) derived from the coding sequence of SEQ ID NO:549 shown in Figure 549.

35 Figure 551 shows a nucleotide sequence (SEQ ID NO:551) of a native sequence PRO12025 cDNA, wherein SEQ ID NO:551 is a clone designated herein as "DNA288267".

Figure 552 shows the amino acid sequence (SEQ ID NO:552) derived from the coding sequence of SEQ ID NO:551 shown in Figure 551.

40 Figure 553 shows a nucleotide sequence (SEQ ID NO:553) of a native sequence PRO70026 cDNA, wherein SEQ ID NO:553 is a clone designated herein as "DNA288268".

Figure 554 shows the amino acid sequence (SEQ ID NO:554) derived from the coding sequence of SEQ ID NO:553 shown in Figure 553.

Figure 555 shows a nucleotide sequence (SEQ ID NO:555) of a native sequence PRO69627 cDNA, wherein SEQ ID NO:555 is a clone designated herein as "DNA287367".

5 Figure 556 shows the amino acid sequence (SEQ ID NO:556) derived from the coding sequence of SEQ ID NO:555 shown in Figure 555.

Figure 557 shows a nucleotide sequence (SEQ ID NO:557) of a native sequence PRO69628 cDNA, wherein SEQ ID NO:557 is a clone designated herein as "DNA287368".

10 Figure 558 shows the amino acid sequence (SEQ ID NO:558) derived from the coding sequence of SEQ ID NO:557 shown in Figure 557.

Figure 559 shows a nucleotide sequence (SEQ ID NO:559) of a native sequence PRO22637 cDNA, wherein SEQ ID NO:559 is a clone designated herein as "DNA189703".

Figure 560 shows the amino acid sequence (SEQ ID NO:560) derived from the coding sequence of SEQ ID NO:559 shown in Figure 559.

15 Figure 561A-B shows a nucleotide sequence (SEQ ID NO:561A-B) of a native sequence PRO69629 cDNA, wherein SEQ ID NO:561A-B is a clone designated herein as "DNA287369".

Figure 562 shows the amino acid sequence (SEQ ID NO:562) derived from the coding sequence of SEQ ID NO:561A-B shown in Figure 561A-B.

20 Figure 563 shows a nucleotide sequence (SEQ ID NO:563) of a native sequence PRO70027 cDNA, wherein SEQ ID NO:563 is a clone designated herein as "DNA288269".

Figure 564 shows the amino acid sequence (SEQ ID NO:564) derived from the coding sequence of SEQ ID NO:563 shown in Figure 563.

Figure 565 shows a nucleotide sequence (SEQ ID NO:565) of a native sequence PRO70028 cDNA, wherein SEQ ID NO:565 is a clone designated herein as "DNA288270".

25 Figure 566 shows the amino acid sequence (SEQ ID NO:566) derived from the coding sequence of SEQ ID NO:565 shown in Figure 565.

Figure 567 shows a nucleotide sequence (SEQ ID NO:567) of a native sequence PRO69632 cDNA, wherein SEQ ID NO:567 is a clone designated herein as "DNA287372".

30 Figure 568 shows the amino acid sequence (SEQ ID NO:568) derived from the coding sequence of SEQ ID NO:567 shown in Figure 567.

Figure 569 shows a nucleotide sequence (SEQ ID NO:569) of a native sequence PRO69634 cDNA, wherein SEQ ID NO:569 is a clone designated herein as "DNA287374".

Figure 570 shows the amino acid sequence (SEQ ID NO:570) derived from the coding sequence of SEQ ID NO:569 shown in Figure 569.

35 Figure 571 shows a nucleotide sequence (SEQ ID NO:571) of a native sequence PRO36857 cDNA, wherein SEQ ID NO:571 is a clone designated herein as "DNA226394".

Figure 572 shows the amino acid sequence (SEQ ID NO:572) derived from the coding sequence of SEQ ID NO:571 shown in Figure 571.

40 Figure 573 shows a nucleotide sequence (SEQ ID NO:573) of a native sequence PRO69893 cDNA, wherein SEQ ID NO:573 is a clone designated herein as "DNA287648".

Figure 574 shows the amino acid sequence (SEQ ID NO:574) derived from the coding sequence of SEQ ID NO:573 shown in Figure 573.

Figure 575 shows a nucleotide sequence (SEQ ID NO:575) of a native sequence PRO69635 cDNA, wherein SEQ ID NO:575 is a clone designated herein as "DNA287375".

5 Figure 576 shows the amino acid sequence (SEQ ID NO:576) derived from the coding sequence of SEQ ID NO:575 shown in Figure 575.

Figure 577 shows a nucleotide sequence (SEQ ID NO:577) of a native sequence PRO6180 cDNA, wherein SEQ ID NO:577 is a clone designated herein as "DNA287376".

10 Figure 578 shows the amino acid sequence (SEQ ID NO:578) derived from the coding sequence of SEQ ID NO:577 shown in Figure 577.

Figure 579 shows a nucleotide sequence (SEQ ID NO:579) of a native sequence PRO69637 cDNA, wherein SEQ ID NO:579 is a clone designated herein as "DNA287378".

Figure 580 shows the amino acid sequence (SEQ ID NO:580) derived from the coding sequence of SEQ ID NO:579 shown in Figure 579.

15 Figure 581 shows a nucleotide sequence (SEQ ID NO:581) of a native sequence PRO69638 cDNA, wherein SEQ ID NO:581 is a clone designated herein as "DNA287379".

Figure 582 shows the amino acid sequence (SEQ ID NO:582) derived from the coding sequence of SEQ ID NO:581 shown in Figure 581.

20 Figure 583 shows a nucleotide sequence (SEQ ID NO:583) of a native sequence PRO69639 cDNA, wherein SEQ ID NO:583 is a clone designated herein as "DNA287380".

Figure 584 shows the amino acid sequence (SEQ ID NO:584) derived from the coding sequence of SEQ ID NO:583 shown in Figure 583.

Figure 585 shows a nucleotide sequence (SEQ ID NO:585) of a native sequence PRO69640 cDNA, wherein SEQ ID NO:585 is a clone designated herein as "DNA287381".

25 Figure 586 shows the amino acid sequence (SEQ ID NO:586) derived from the coding sequence of SEQ ID NO:585 shown in Figure 585.

Figure 587 shows a nucleotide sequence (SEQ ID NO:587) of a native sequence PRO69641 cDNA, wherein SEQ ID NO:587 is a clone designated herein as "DNA287382".

30 Figure 588 shows the amino acid sequence (SEQ ID NO:588) derived from the coding sequence of SEQ ID NO:587 shown in Figure 587.

Figure 589 shows a nucleotide sequence (SEQ ID NO:589) of a native sequence PRO62766 cDNA, wherein SEQ ID NO:589 is a clone designated herein as "DNA275043".

Figure 590 shows the amino acid sequence (SEQ ID NO:590) derived from the coding sequence of SEQ ID NO:589 shown in Figure 589.

35 Figure 591 shows a nucleotide sequence (SEQ ID NO:591) of a native sequence PRO53782 cDNA, wherein SEQ ID NO:591 is a clone designated herein as "DNA287383".

Figure 592 shows the amino acid sequence (SEQ ID NO:592) derived from the coding sequence of SEQ ID NO:591 shown in Figure 591.

40 Figure 593 shows a nucleotide sequence (SEQ ID NO:593) of a native sequence PRO61472 cDNA, wherein SEQ ID NO:593 is a clone designated herein as "DNA273489".

Figure 594 shows the amino acid sequence (SEQ ID NO:594) derived from the coding sequence of SEQ ID NO:593 shown in Figure 593.

Figure 595 shows a nucleotide sequence (SEQ ID NO:595) of a native sequence PRO38179 cDNA, wherein SEQ ID NO:595 is a clone designated herein as "DNA227716".

5 Figure 596 shows the amino acid sequence (SEQ ID NO:596) derived from the coding sequence of SEQ ID NO:595 shown in Figure 595.

Figure 597 shows a nucleotide sequence (SEQ ID NO:597) of a native sequence PRO69642 cDNA, wherein SEQ ID NO:597 is a clone designated herein as "DNA287384".

10 Figure 598 shows the amino acid sequence (SEQ ID NO:598) derived from the coding sequence of SEQ ID NO:597 shown in Figure 597.

Figure 599 shows a nucleotide sequence (SEQ ID NO:599) of a native sequence PRO69643 cDNA, wherein SEQ ID NO:599 is a clone designated herein as "DNA287385".

Figure 600 shows the amino acid sequence (SEQ ID NO:600) derived from the coding sequence of SEQ ID NO:599 shown in Figure 599.

15 Figure 601 shows a nucleotide sequence (SEQ ID NO:601) of a native sequence PRO69644 cDNA, wherein SEQ ID NO:601 is a clone designated herein as "DNA287386".

Figure 602 shows the amino acid sequence (SEQ ID NO:602) derived from the coding sequence of SEQ ID NO:601 shown in Figure 601.

20 Figure 603 shows a nucleotide sequence (SEQ ID NO:603) of a native sequence PRO69645 cDNA, wherein SEQ ID NO:603 is a clone designated herein as "DNA287387".

Figure 604 shows the amino acid sequence (SEQ ID NO:604) derived from the coding sequence of SEQ ID NO:603 shown in Figure 603.

Figure 605 shows a nucleotide sequence (SEQ ID NO:605) of a native sequence PRO11608 cDNA, wherein SEQ ID NO:605 is a clone designated herein as "DNA151077".

25 Figure 606 shows the amino acid sequence (SEQ ID NO:606) derived from the coding sequence of SEQ ID NO:605 shown in Figure 605.

Figure 607 shows a nucleotide sequence (SEQ ID NO:607) of a native sequence PRO69646 cDNA, wherein SEQ ID NO:607 is a clone designated herein as "DNA287388".

30 Figure 608 shows the amino acid sequence (SEQ ID NO:608) derived from the coding sequence of SEQ ID NO:607 shown in Figure 607.

Figure 609 shows a nucleotide sequence (SEQ ID NO:609) of a native sequence PRO59825 cDNA, wherein SEQ ID NO:609 is a clone designated herein as "DNA271536".

Figure 610 shows the amino acid sequence (SEQ ID NO:610) derived from the coding sequence of SEQ ID NO:609 shown in Figure 609.

35 Figure 611 shows a nucleotide sequence (SEQ ID NO:611) of a native sequence PRO69647 cDNA, wherein SEQ ID NO:611 is a clone designated herein as "DNA287389".

Figure 612 shows the amino acid sequence (SEQ ID NO:612) derived from the coding sequence of SEQ ID NO:611 shown in Figure 611.

40 Figure 613 shows a nucleotide sequence (SEQ ID NO:613) of a native sequence PRO69648 cDNA, wherein SEQ ID NO:613 is a clone designated herein as "DNA287390".

Figure 614 shows the amino acid sequence (SEQ ID NO:614) derived from the coding sequence of SEQ ID NO:613 shown in Figure 613.

Figure 615 shows a nucleotide sequence (SEQ ID NO:615) of a native sequence PRO70029 cDNA, wherein SEQ ID NO:615 is a clone designated herein as "DNA288271".

5 Figure 616 shows the amino acid sequence (SEQ ID NO:616) derived from the coding sequence of SEQ ID NO:615 shown in Figure 615.

Figure 617 shows a nucleotide sequence (SEQ ID NO:617) of a native sequence PRO1213 cDNA, wherein SEQ ID NO:617 is a clone designated herein as "DNA66487".

10 Figure 618 shows the amino acid sequence (SEQ ID NO:618) derived from the coding sequence of SEQ ID NO:617 shown in Figure 617.

Figure 619 shows a nucleotide sequence (SEQ ID NO:619) of a native sequence PRO70030 cDNA, wherein SEQ ID NO:619 is a clone designated herein as "DNA288272".

Figure 620 shows the amino acid sequence (SEQ ID NO:620) derived from the coding sequence of SEQ ID NO:619 shown in Figure 619.

15 Figure 621 shows a nucleotide sequence (SEQ ID NO:621) of a native sequence PRO50195 cDNA, wherein SEQ ID NO:621 is a clone designated herein as "DNA255113".

Figure 622 shows the amino acid sequence (SEQ ID NO:622) derived from the coding sequence of SEQ ID NO:621 shown in Figure 621.

20 Figure 623 shows a nucleotide sequence (SEQ ID NO:623) of a native sequence PRO69651 cDNA, wherein SEQ ID NO:623 is a clone designated herein as "DNA287393".

Figure 624 shows the amino acid sequence (SEQ ID NO:624) derived from the coding sequence of SEQ ID NO:623 shown in Figure 623.

Figure 625A-B shows a nucleotide sequence (SEQ ID NO:625A-B) of a native sequence PRO37538 cDNA, wherein SEQ ID NO:625A-B is a clone designated herein as "DNA227075".

25 Figure 626 shows the amino acid sequence (SEQ ID NO:626) derived from the coding sequence of SEQ ID NO:625A-B shown in Figure 625A-B.

Figure 627 shows a nucleotide sequence (SEQ ID NO:627) of a native sequence PRO69652 cDNA, wherein SEQ ID NO:627 is a clone designated herein as "DNA287394".

30 Figure 628 shows the amino acid sequence (SEQ ID NO:628) derived from the coding sequence of SEQ ID NO:627 shown in Figure 627.

Figure 629 shows a nucleotide sequence (SEQ ID NO:629) of a native sequence PRO59210 cDNA, wherein SEQ ID NO:629 is a clone designated herein as "DNA270875".

Figure 630 shows the amino acid sequence (SEQ ID NO:630) derived from the coding sequence of SEQ ID NO:629 shown in Figure 629.

35 Figure 631 shows a nucleotide sequence (SEQ ID NO:631) of a native sequence PRO23374 cDNA, wherein SEQ ID NO:631 is a clone designated herein as "DNA193967".

Figure 632 shows the amino acid sequence (SEQ ID NO:632) derived from the coding sequence of SEQ ID NO:631 shown in Figure 631.

40 Figure 633 shows a nucleotide sequence (SEQ ID NO:633) of a native sequence PRO24844 cDNA, wherein SEQ ID NO:633 is a clone designated herein as "DNA288273".

Figure 634 shows the amino acid sequence (SEQ ID NO:634) derived from the coding sequence of SEQ ID NO:633 shown in Figure 633.

Figure 635 shows a nucleotide sequence (SEQ ID NO:635) of a native sequence PRO70031 cDNA, wherein SEQ ID NO:635 is a clone designated herein as "DNA288274".

5 Figure 636 shows the amino acid sequence (SEQ ID NO:636) derived from the coding sequence of SEQ ID NO:635 shown in Figure 635.

Figure 637 shows a nucleotide sequence (SEQ ID NO:637) of a native sequence PRO69653 cDNA, wherein SEQ ID NO:637 is a clone designated herein as "DNA287396".

10 Figure 638 shows the amino acid sequence (SEQ ID NO:638) derived from the coding sequence of SEQ ID NO:637 shown in Figure 637.

Figure 639 shows a nucleotide sequence (SEQ ID NO:639) of a native sequence PRO69654 cDNA, wherein SEQ ID NO:639 is a clone designated herein as "DNA287397".

Figure 640 shows the amino acid sequence (SEQ ID NO:640) derived from the coding sequence of SEQ ID NO:639 shown in Figure 639.

15 Figure 641 shows a nucleotide sequence (SEQ ID NO:641) of a native sequence PRO69655 cDNA, wherein SEQ ID NO:641 is a clone designated herein as "DNA287398".

Figure 642 shows the amino acid sequence (SEQ ID NO:642) derived from the coding sequence of SEQ ID NO:641 shown in Figure 641.

20 Figure 643 shows a nucleotide sequence (SEQ ID NO:643) of a native sequence PRO69656 cDNA, wherein SEQ ID NO:643 is a clone designated herein as "DNA287399".

Figure 644 shows the amino acid sequence (SEQ ID NO:644) derived from the coding sequence of SEQ ID NO:643 shown in Figure 643.

Figure 645 shows a nucleotide sequence (SEQ ID NO:645) of a native sequence PRO70032 cDNA, wherein SEQ ID NO:645 is a clone designated herein as "DNA288275".

25 Figure 646 shows the amino acid sequence (SEQ ID NO:646) derived from the coding sequence of SEQ ID NO:645 shown in Figure 645.

Figure 647 shows a nucleotide sequence (SEQ ID NO:647) of a native sequence PRO69659 cDNA, wherein SEQ ID NO:647 is a clone designated herein as "DNA287402".

30 Figure 648 shows the amino acid sequence (SEQ ID NO:648) derived from the coding sequence of SEQ ID NO:647 shown in Figure 647.

Figure 649 shows a nucleotide sequence (SEQ ID NO:649) of a native sequence PRO69660 cDNA, wherein SEQ ID NO:649 is a clone designated herein as "DNA287403".

Figure 650 shows the amino acid sequence (SEQ ID NO:650) derived from the coding sequence of SEQ ID NO:649 shown in Figure 649.

35 Figure 651A-B shows a nucleotide sequence (SEQ ID NO:651A-B) of a native sequence PRO58054 cDNA, wherein SEQ ID NO:651A-B is a clone designated herein as "DNA269642".

Figure 652 shows the amino acid sequence (SEQ ID NO:652) derived from the coding sequence of SEQ ID NO:651A-B shown in Figure 651A-B.

40 Figure 653 shows a nucleotide sequence (SEQ ID NO:653) of a native sequence PRO69661 cDNA, wherein SEQ ID NO:653 is a clone designated herein as "DNA287404".

Figure 654 shows the amino acid sequence (SEQ ID NO:654) derived from the coding sequence of SEQ ID NO:653 shown in Figure 653.

Figure 655 shows a nucleotide sequence (SEQ ID NO:655) of a native sequence PRO69662 cDNA, wherein SEQ ID NO:655 is a clone designated herein as "DNA287405".

5 Figure 656 shows the amino acid sequence (SEQ ID NO:656) derived from the coding sequence of SEQ ID NO:655 shown in Figure 655.

Figure 657 shows a nucleotide sequence (SEQ ID NO:657) of a native sequence PRO69898 cDNA, wherein SEQ ID NO:657 is a clone designated herein as "DNA287653".

10 Figure 658 shows the amino acid sequence (SEQ ID NO:658) derived from the coding sequence of SEQ ID NO:657 shown in Figure 657.

Figure 659 shows a nucleotide sequence (SEQ ID NO:659) of a native sequence PRO69664 cDNA, wherein SEQ ID NO:659 is a clone designated herein as "DNA287407".

Figure 660 shows the amino acid sequence (SEQ ID NO:660) derived from the coding sequence of SEQ ID NO:659 shown in Figure 659.

15 Figure 661 shows a nucleotide sequence (SEQ ID NO:661) of a native sequence PRO69665 cDNA, wherein SEQ ID NO:661 is a clone designated herein as "DNA287408".

Figure 662 shows the amino acid sequence (SEQ ID NO:662) derived from the coding sequence of SEQ ID NO:661 shown in Figure 661.

20 Figure 663 shows a nucleotide sequence (SEQ ID NO:663) of a native sequence PRO69666 cDNA, wherein SEQ ID NO:663 is a clone designated herein as "DNA287409".

Figure 664 shows the amino acid sequence (SEQ ID NO:664) derived from the coding sequence of SEQ ID NO:663 shown in Figure 663.

Figure 665 shows a nucleotide sequence (SEQ ID NO:665) of a native sequence PRO69667 cDNA, wherein SEQ ID NO:665 is a clone designated herein as "DNA287410".

25 Figure 666 shows the amino acid sequence (SEQ ID NO:666) derived from the coding sequence of SEQ ID NO:665 shown in Figure 665.

Figure 667 shows a nucleotide sequence (SEQ ID NO:667) of a native sequence PRO69669 cDNA, wherein SEQ ID NO:667 is a clone designated herein as "DNA287412".

30 Figure 668 shows the amino acid sequence (SEQ ID NO:668) derived from the coding sequence of SEQ ID NO:667 shown in Figure 667.

Figure 669 shows a nucleotide sequence (SEQ ID NO:669) of a native sequence PRO69671 cDNA, wherein SEQ ID NO:669 is a clone designated herein as "DNA287414".

Figure 670 shows the amino acid sequence (SEQ ID NO:670) derived from the coding sequence of SEQ ID NO:669 shown in Figure 669.

35 Figure 671 shows a nucleotide sequence (SEQ ID NO:671) of a native sequence PRO69672 cDNA, wherein SEQ ID NO:671 is a clone designated herein as "DNA287415".

Figure 672 shows the amino acid sequence (SEQ ID NO:672) derived from the coding sequence of SEQ ID NO:671 shown in Figure 671.

40 Figure 673A-B shows a nucleotide sequence (SEQ ID NO:673A-B) of a native sequence PRO58204 cDNA, wherein SEQ ID NO:673A-B is a clone designated herein as "DNA269799".

Figure 674 shows the amino acid sequence (SEQ ID NO:674) derived from the coding sequence of SEQ ID NO:673A-B shown in Figure 673A-B.

Figure 675 shows a nucleotide sequence (SEQ ID NO:675) of a native sequence PRO49419 cDNA, wherein SEQ ID NO:675 is a clone designated herein as "DNA254308".

5 Figure 676 shows the amino acid sequence (SEQ ID NO:676) derived from the coding sequence of SEQ ID NO:675 shown in Figure 675.

Figure 677 shows a nucleotide sequence (SEQ ID NO:677) of a native sequence PRO69673 cDNA, wherein SEQ ID NO:677 is a clone designated herein as "DNA287416".

10 Figure 678 shows the amino acid sequence (SEQ ID NO:678) derived from the coding sequence of SEQ ID NO:677 shown in Figure 677.

Figure 679 shows a nucleotide sequence (SEQ ID NO:679) of a native sequence PRO69674 cDNA, wherein SEQ ID NO:679 is a clone designated herein as "DNA287417".

Figure 680 shows the amino acid sequence (SEQ ID NO:680) derived from the coding sequence of SEQ ID NO:679 shown in Figure 679.

15 Figure 681 shows a nucleotide sequence (SEQ ID NO:681) of a native sequence PRO49810 cDNA, wherein SEQ ID NO:681 is a clone designated herein as "DNA254710".

Figure 682 shows the amino acid sequence (SEQ ID NO:682) derived from the coding sequence of SEQ ID NO:681 shown in Figure 681.

20 Figure 683 shows a nucleotide sequence (SEQ ID NO:683) of a native sequence PRO70033 cDNA, wherein SEQ ID NO:683 is a clone designated herein as "DNA288276".

Figure 684 shows the amino acid sequence (SEQ ID NO:684) derived from the coding sequence of SEQ ID NO:683 shown in Figure 683.

Figure 685 shows a nucleotide sequence (SEQ ID NO:685) of a native sequence PRO69676 cDNA, wherein SEQ ID NO:685 is a clone designated herein as "DNA287419".

25 Figure 686 shows the amino acid sequence (SEQ ID NO:686) derived from the coding sequence of SEQ ID NO:685 shown in Figure 685.

Figure 687 shows a nucleotide sequence (SEQ ID NO:687) of a native sequence PRO58076 cDNA, wherein SEQ ID NO:687 is a clone designated herein as "DNA269665".

30 Figure 688 shows the amino acid sequence (SEQ ID NO:688) derived from the coding sequence of SEQ ID NO:687 shown in Figure 687.

Figure 689 shows a nucleotide sequence (SEQ ID NO:689) of a native sequence PRO69677 cDNA, wherein SEQ ID NO:689 is a clone designated herein as "DNA287420".

Figure 690 shows the amino acid sequence (SEQ ID NO:690) derived from the coding sequence of SEQ ID NO:689 shown in Figure 689.

35 Figure 691 shows a nucleotide sequence (SEQ ID NO:691) of a native sequence PRO69678 cDNA, wherein SEQ ID NO:691 is a clone designated herein as "DNA287421".

Figure 692 shows the amino acid sequence (SEQ ID NO:692) derived from the coding sequence of SEQ ID NO:691 shown in Figure 691.

40 Figure 693 shows a nucleotide sequence (SEQ ID NO:693) of a native sequence PRO69679 cDNA, wherein SEQ ID NO:693 is a clone designated herein as "DNA287422".

Figure 694 shows the amino acid sequence (SEQ ID NO:694) derived from the coding sequence of SEQ ID NO:693 shown in Figure 693.

Figure 695 shows a nucleotide sequence (SEQ ID NO:695) of a native sequence PRO1718 cDNA, wherein SEQ ID NO:695 is a clone designated herein as "DNA82362".

5 Figure 696 shows the amino acid sequence (SEQ ID NO:696) derived from the coding sequence of SEQ ID NO:695 shown in Figure 695.

Figure 697 shows a nucleotide sequence (SEQ ID NO:697) of a native sequence PRO51161 cDNA, wherein SEQ ID NO:697 is a clone designated herein as "DNA256112".

10 Figure 698 shows the amino acid sequence (SEQ ID NO:698) derived from the coding sequence of SEQ ID NO:697 shown in Figure 697.

Figure 699 shows a nucleotide sequence (SEQ ID NO:699) of a native sequence PRO69680 cDNA, wherein SEQ ID NO:699 is a clone designated herein as "DNA287423".

Figure 700 shows the amino acid sequence (SEQ ID NO:700) derived from the coding sequence of SEQ ID NO:699 shown in Figure 699.

15 Figure 701 shows a nucleotide sequence (SEQ ID NO:701) of a native sequence PRO59281 cDNA, wherein SEQ ID NO:701 is a clone designated herein as "DNA270950".

Figure 702 shows the amino acid sequence (SEQ ID NO:702) derived from the coding sequence of SEQ ID NO:701 shown in Figure 701.

20 Figure 703 shows a nucleotide sequence (SEQ ID NO:703) of a native sequence PRO36102 cDNA, wherein SEQ ID NO:703 is a clone designated herein as "DNA225639".

Figure 704 shows the amino acid sequence (SEQ ID NO:704) derived from the coding sequence of SEQ ID NO:703 shown in Figure 703.

Figure 705 shows a nucleotide sequence (SEQ ID NO:705) of a native sequence PRO61799 cDNA, wherein SEQ ID NO:705 is a clone designated herein as "DNA273839".

25 Figure 706 shows the amino acid sequence (SEQ ID NO:706) derived from the coding sequence of SEQ ID NO:705 shown in Figure 705.

Figure 707 shows a nucleotide sequence (SEQ ID NO:707) of a native sequence PRO69681 cDNA, wherein SEQ ID NO:707 is a clone designated herein as "DNA287424".

30 Figure 708 shows the amino acid sequence (SEQ ID NO:708) derived from the coding sequence of SEQ ID NO:707 shown in Figure 707.

Figure 709 shows a nucleotide sequence (SEQ ID NO:709) of a native sequence PRO69682 cDNA, wherein SEQ ID NO:709 is a clone designated herein as "DNA287425".

Figure 710 shows the amino acid sequence (SEQ ID NO:710) derived from the coding sequence of SEQ ID NO:710 shown in Figure 710.

35 Figure 711 shows a nucleotide sequence (SEQ ID NO:711) of a native sequence PRO69901 cDNA, wherein SEQ ID NO:711 is a clone designated herein as "DNA287656".

Figure 712 shows the amino acid sequence (SEQ ID NO:712) derived from the coding sequence of SEQ ID NO:711 shown in Figure 711.

40 Figure 713 shows a nucleotide sequence (SEQ ID NO:713) of a native sequence PRO69684 cDNA, wherein SEQ ID NO:713 is a clone designated herein as "DNA287427".

Figure 714 shows the amino acid sequence (SEQ ID NO:714) derived from the coding sequence of SEQ ID NO:713 shown in Figure 713.

Figure 715 shows a nucleotide sequence (SEQ ID NO:715) of a native sequence PRO69685 cDNA, wherein SEQ ID NO:715 is a clone designated herein as "DNA287428".

5 Figure 716 shows the amino acid sequence (SEQ ID NO:716) derived from the coding sequence of SEQ ID NO:715 shown in Figure 715.

Figure 717 shows a nucleotide sequence (SEQ ID NO:717) of a native sequence PRO69686 cDNA, wherein SEQ ID NO:717 is a clone designated herein as "DNA287429".

10 Figure 718 shows the amino acid sequence (SEQ ID NO:718) derived from the coding sequence of SEQ ID NO:717 shown in Figure 717.

Figure 719 shows a nucleotide sequence (SEQ ID NO:719) of a native sequence PRO69687 cDNA, wherein SEQ ID NO:719 is a clone designated herein as "DNA287430".

Figure 720 shows the amino acid sequence (SEQ ID NO:720) derived from the coding sequence of SEQ ID NO:719 shown in Figure 719.

15 Figure 721 shows a nucleotide sequence (SEQ ID NO:721) of a native sequence PRO38469 cDNA, wherein SEQ ID NO:721 is a clone designated herein as "DNA228006".

Figure 722 shows the amino acid sequence (SEQ ID NO:722) derived from the coding sequence of SEQ ID NO:721 shown in Figure 721.

20 Figure 723 shows a nucleotide sequence (SEQ ID NO:723) of a native sequence PRO69688 cDNA, wherein SEQ ID NO:723 is a clone designated herein as "DNA287657".

Figure 724 shows the amino acid sequence (SEQ ID NO:724) derived from the coding sequence of SEQ ID NO:723 shown in Figure 723.

Figure 725 shows a nucleotide sequence (SEQ ID NO:725) of a native sequence PRO70034 cDNA, wherein SEQ ID NO:725 is a clone designated herein as "DNA288277".

25 Figure 726 shows the amino acid sequence (SEQ ID NO:726) derived from the coding sequence of SEQ ID NO:725 shown in Figure 725.

Figure 727 shows a nucleotide sequence (SEQ ID NO:727) of a native sequence PRO59354 cDNA, wherein SEQ ID NO:727 is a clone designated herein as "DNA271026".

30 Figure 728 shows the amino acid sequence (SEQ ID NO:728) derived from the coding sequence of SEQ ID NO:727 shown in Figure 727.

Figure 729 shows a nucleotide sequence (SEQ ID NO:729) of a native sequence PRO59189 cDNA, wherein SEQ ID NO:729 is a clone designated herein as "DNA270851".

Figure 730 shows the amino acid sequence (SEQ ID NO:730) derived from the coding sequence of SEQ ID NO:729 shown in Figure 729.

35 Figure 731 shows a nucleotide sequence (SEQ ID NO:731) of a native sequence PRO38197 cDNA, wherein SEQ ID NO:731 is a clone designated herein as "DNA227734".

Figure 732 shows the amino acid sequence (SEQ ID NO:732) derived from the coding sequence of SEQ ID NO:731 shown in Figure 731.

40 Figure 733 shows a nucleotide sequence (SEQ ID NO:733) of a native sequence PRO69902 cDNA, wherein SEQ ID NO:733 is a clone designated herein as "DNA287658".

Figure 734 shows the amino acid sequence (SEQ ID NO:734) derived from the coding sequence of SEQ ID NO:733 shown in Figure 733.

Figure 735 shows a nucleotide sequence (SEQ ID NO:735) of a native sequence PRO69690 cDNA, wherein SEQ ID NO:735 is a clone designated herein as "DNA287433".

5 Figure 736 shows the amino acid sequence (SEQ ID NO:736) derived from the coding sequence of SEQ ID NO:735 shown in Figure 735.

Figure 737A-B shows a nucleotide sequence (SEQ ID NO:737A-B) of a native sequence PRO61569 cDNA, wherein SEQ ID NO:737A-B is a clone designated herein as "DNA273593".

10 Figure 738 shows the amino acid sequence (SEQ ID NO:738) derived from the coding sequence of SEQ ID NO:737A-B shown in Figure 737A-B.

Figure 739 shows a nucleotide sequence (SEQ ID NO:739) of a native sequence PRO69903 cDNA, wherein SEQ ID NO:739 is a clone designated herein as "DNA287659".

Figure 740 shows the amino acid sequence (SEQ ID NO:740) derived from the coding sequence of SEQ ID NO:739 shown in Figure 739.

15 Figure 741 shows a nucleotide sequence (SEQ ID NO:741) of a native sequence PRO1970 cDNA, wherein SEQ ID NO:741 is a clone designated herein as "DNA287434".

Figure 742 shows the amino acid sequence (SEQ ID NO:742) derived from the coding sequence of SEQ ID NO:741 shown in Figure 741.

20 DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

I. Definitions

The terms "PRO polypeptide" and "PRO" as used herein and when immediately followed by a numerical designation refer to various polypeptides, wherein the complete designation (i.e., PRO/number) refers to specific polypeptide sequences as described herein. The terms "PRO/number polypeptide" and
25 "PRO/number" wherein the term "number" is provided as an actual numerical designation as used herein encompass native sequence polypeptides and polypeptide variants (which are further defined herein). The PRO polypeptides described herein may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods. The term "PRO polypeptide" refers to each individual PRO/number polypeptide disclosed herein. All disclosures in this
30 specification which refer to the "PRO polypeptide" refer to each of the polypeptides individually as well as jointly. For example, descriptions of the preparation of, purification of, derivation of, formation of antibodies to or against, administration of, compositions containing, treatment of a disease with, etc., pertain to each polypeptide of the invention individually. The term "PRO polypeptide" also includes variants of the PRO/number polypeptides disclosed herein.

35 A "native sequence PRO polypeptide" comprises a polypeptide having the same amino acid sequence as the corresponding PRO polypeptide derived from nature. Such native sequence PRO polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence PRO polypeptide" specifically encompasses naturally-occurring truncated or secreted forms of the specific PRO polypeptide (e.g., an extracellular domain sequence), naturally-occurring variant
40 forms (e.g., alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In

various embodiments of the invention, the native sequence PRO polypeptides disclosed herein are mature or full-length native sequence polypeptides comprising the full-length amino acids sequences shown in the accompanying figures. Start and stop codons are shown in bold font and underlined in the figures.

However, while the PRO polypeptide disclosed in the accompanying figures are shown to begin with methionine residues designated herein as amino acid position 1 in the figures, it is conceivable and possible that other methionine residues located either upstream or downstream from the amino acid position 1 in the figures may be employed as the starting amino acid residue for the PRO polypeptides.

The PRO polypeptide "extracellular domain" or "ECD" refers to a form of the PRO polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a PRO polypeptide ECD will have less than 1% of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5% of such domains. It will be understood that any transmembrane domains identified for the PRO polypeptides of the present invention are identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain as initially identified herein. Optionally, therefore, an extracellular domain of a PRO polypeptide may contain from about 5 or fewer amino acids on either side of the transmembrane domain/extracellular domain boundary as identified in the Examples or specification and such polypeptides, with or without the associated signal peptide, and nucleic acid encoding them, are contemplated by the present invention.

The approximate location of the "signal peptides" of the various PRO polypeptides disclosed herein are shown in the present specification and/or the accompanying figures. It is noted, however, that the C-terminal boundary of a signal peptide may vary, but most likely by no more than about 5 amino acids on either side of the signal peptide C-terminal boundary as initially identified herein, wherein the C-terminal boundary of the signal peptide may be identified pursuant to criteria routinely employed in the art for identifying that type of amino acid sequence element (e.g., Nielsen et al., Prot. Eng. 10:1-6 (1997) and von Heinje et al., Nucl. Acids. Res. 14:4683-4690 (1986)). Moreover, it is also recognized that, in some cases, cleavage of a signal sequence from a secreted polypeptide is not entirely uniform, resulting in more than one secreted species. These mature polypeptides, where the signal peptide is cleaved within no more than about 5 amino acids on either side of the C-terminal boundary of the signal peptide as identified herein, and the polynucleotides encoding them, are contemplated by the present invention.

"PRO polypeptide variant" means an active PRO polypeptide as defined above or below having at least about 80% amino acid sequence identity with a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Such PRO polypeptide variants include, for instance, PRO polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a PRO polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about

86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, PRO variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20 amino acids in length, alternatively at least about 30 amino acids in length, alternatively at least about 40 amino acids in length, alternatively at least about 50 amino acids in length, alternatively at least about 60 amino acids in length, alternatively at least about 70 amino acids in length, alternatively at least about 80 amino acids in length, alternatively at least about 90 amino acids in length, alternatively at least about 100 amino acids in length, alternatively at least about 150 amino acids in length, alternatively at least about 200 amino acids in length, alternatively at least about 300 amino acids in length, or more.

"Percent (%) amino acid sequence identity" with respect to the PRO polypeptide sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific PRO polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B

(which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

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where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. As examples of % amino acid sequence identity calculations using this method, Tables 2 and 3 demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated "Comparison Protein" to the amino acid sequence designated "PRO", wherein "PRO" represents the amino acid sequence of a hypothetical PRO polypeptide of interest, "Comparison Protein" represents the amino acid sequence of a polypeptide against which the "PRO" polypeptide of interest is being compared, and "X," "Y" and "Z" each represent different hypothetical amino acid residues.

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Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % amino acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % amino acid sequence identity value is determined by dividing (a) the number of matching identical amino acid residues between the amino acid sequence of the PRO polypeptide of interest having a sequence derived from the native PRO polypeptide and the comparison amino acid sequence of interest (i.e., the sequence against which the PRO polypeptide of interest is being compared which may be a PRO variant polypeptide) as determined by WU-BLAST-2 by (b) the total number of amino acid residues of the PRO polypeptide of interest. For example, in the statement "a polypeptide comprising an the amino acid sequence A which has or having at least 80% amino acid sequence identity to the amino acid sequence B", the amino acid sequence A is the comparison amino acid sequence of interest and the amino acid sequence B is the amino acid sequence of the PRO polypeptide of interest.

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Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

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In situations where NCBI-BLAST2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid

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sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

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100 times the fraction X/Y

where X is the number of amino acid residues scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

"PRO variant polynucleotide" or "PRO variant nucleic acid sequence" means a nucleic acid molecule which encodes an active PRO polypeptide as defined below and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, a PRO variant polynucleotide will have at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal sequence, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.

Ordinarily, PRO variant polynucleotides are at least about 30 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 210 nucleotides in length, alternatively at least about 240 nucleotides in length, alternatively at least about 270 nucleotides in length, alternatively at least

about 300 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 900 nucleotides in length, or more.

"Percent (%) nucleic acid sequence identity" with respect to PRO-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the PRO nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. For purposes herein, however, % nucleic acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for nucleic acid sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables 4 and 5, demonstrate how to calculate the % nucleic acid sequence identity of the nucleic acid sequence designated "Comparison DNA" to the nucleic acid sequence designated "PRO-DNA", wherein "PRO-DNA" represents a hypothetical PRO-encoding nucleic acid sequence of interest, "Comparison DNA" represents the nucleotide sequence of a nucleic acid molecule against which the "PRO-DNA" nucleic acid molecule of interest is being compared, and "N", "L" and "V" each represent different hypothetical nucleotides.

Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % nucleic acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word

threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % nucleic acid sequence identity value is determined by dividing (a) the number of matching identical nucleotides between the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest having a sequence derived from the native sequence PRO polypeptide-encoding nucleic acid and the comparison nucleic acid molecule of interest (i.e., the sequence against which the PRO polypeptide-encoding nucleic acid molecule of interest is being compared which may be a variant PRO polynucleotide) as determined by WU-BLAST-2 by (b) the total number of nucleotides of the PRO polypeptide-encoding nucleic acid molecule of interest. For example, in the statement "an isolated nucleic acid molecule comprising a nucleic acid sequence A which has or having at least 80% nucleic acid sequence identity to the nucleic acid sequence B", the nucleic acid sequence A is the comparison nucleic acid molecule of interest and the nucleic acid sequence B is the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest.

Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

In situations where NCBI-BLAST2 is employed for sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

where W is the number of nucleotides scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C.

In other embodiments, PRO variant polynucleotides are nucleic acid molecules that encode an active PRO polypeptide and which are capable of hybridizing, preferably under stringent hybridization and wash conditions, to nucleotide sequences encoding a full-length PRO polypeptide as disclosed herein. PRO variant polypeptides may be those that are encoded by a PRO variant polynucleotide.

"Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1)

to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one component of the PRO polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

An "isolated" PRO polypeptide-encoding nucleic acid or other polypeptide-encoding nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. An isolated polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the specific polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

The term "antibody" is used in the broadest sense and specifically covers, for example, single anti-PRO monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-PRO antibody compositions with polypeptidic specificity, single chain anti-PRO antibodies, and fragments of anti-PRO antibodies (see below). The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative

temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

5 "Stringent conditions" or "high stringency conditions", as defined herein, may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM
10 sodium chloride, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

15 "Moderately stringent conditions" may be identified as described by Sambrook et al., Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent than those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium
20 phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising a PRO
25 polypeptide fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10
30 and 20 amino acid residues).

As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (i.e., is
35 "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

"Active" or "activity" for the purposes herein refers to form(s) of a PRO polypeptide which retain a biological and/or an immunological activity of native or naturally-occurring PRO, wherein "biological" activity refers to a biological function (either inhibitory or stimulatory) caused by a native or naturally-occurring PRO other than the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO and an "immunological" activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO.

The term "antagonist" is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native PRO polypeptide disclosed herein. In a similar manner, the term "agonist" is used in the broadest sense and includes any molecule that mimics a biological activity of a native PRO polypeptide disclosed herein. Suitable agonist or antagonist molecules specifically include agonist or antagonist antibodies or antibody fragments, fragments or amino acid sequence variants of native PRO polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. Methods for identifying agonists or antagonists of a PRO polypeptide may comprise contacting a PRO polypeptide with a candidate agonist or antagonist molecule and measuring a detectable change in one or more biological activities normally associated with the PRO polypeptide.

"Treatment" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented.

"Chronic" administration refers to administration of the agent(s) in a continuous mode as opposed to an acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

"Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, etc. Preferably, the mammal is human.

Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

"Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are nontoxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, polyethylene glycol (PEG), and PLURONICS™.

"Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')₂, and Fv fragments; diabodies; linear antibodies (Zapata et al., Protein Eng. 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

5 Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. Pepsin treatment yields an F(ab')₂ fragment that has two antigen-combining sites and is still capable of cross-linking antigen.

10 "Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the V_H-V_L dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower
15 affinity than the entire binding site.

 The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab fragments differ from Fab' fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains
20 bear a free thiol group. F(ab')₂ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

 The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains.

25 Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA, and IgA2.

30 "Single-chain Fv" or "sFv" antibody fragments comprise the V_H and V_L domains of antibody, wherein these domains are present in a single polypeptide chain. Preferably, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenberg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

35 The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) in the same polypeptide chain (V_H-V_L). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993).

An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody
5 will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the
10 antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

An antibody that "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide is one that binds to that particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

15 The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody so as to generate a "labeled" antibody. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of a substrate compound or composition which is detectable.

20 By "solid phase" is meant a non-aqueous matrix to which the antibody of the present invention can adhere. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes a discontinuous solid phase of discrete particles, such as those described in U.S. Patent No.
25 4,275,149.

A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as a PRO polypeptide or antibody thereto) to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes.

30 A "small molecule" is defined herein to have a molecular weight below about 500 Daltons.

The term "immune related disease" means a disease in which a component of the immune system of a mammal causes, mediates or otherwise contributes to a morbidity in the mammal. Also included are diseases in which stimulation or intervention of the immune response has an ameliorative effect on progression of the disease. Included within this term are immune-mediated inflammatory diseases, non-immune-mediated inflammatory diseases, infectious diseases, immunodeficiency diseases, neoplasia, *etc.*
35

The term "T cell mediated disease" means a disease in which T cells directly or indirectly mediate or otherwise contribute to a morbidity in a mammal. The T cell mediated disease may be associated with cell mediated effects, lymphokine mediated effects, *etc.*, and even effects associated with B cells if the B cells are stimulated, for example, by the lymphokines secreted by T cells.

Examples of immune-related and inflammatory diseases, some of which are immune or T cell mediated, which can be treated according to the invention include systemic lupus erythematosus, rheumatoid arthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis (scleroderma), idiopathic inflammatory myopathies (dermatomyositis, polymyositis), Sjögren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic anemia (immune pancytopenia, paroxysmal nocturnal hemoglobinuria), autoimmune thrombocytopenia (idiopathic thrombocytopenic purpura, immune-mediated thrombocytopenia), thyroiditis (Grave's disease, Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, atrophic thyroiditis), diabetes mellitus, immune-mediated renal disease (glomerulonephritis, tubulointerstitial nephritis), demyelinating diseases of the central and peripheral nervous systems such as multiple sclerosis, idiopathic demyelinating polyneuropathy or Guillain-Barré syndrome, and chronic inflammatory demyelinating polyneuropathy, hepatobiliary diseases such as infectious hepatitis (hepatitis A, B, C, D, E and other non-hepatotropic viruses), autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, and sclerosing cholangitis, inflammatory bowel disease (ulcerative colitis: Crohn's disease), gluten-sensitive enteropathy, and Whipple's disease, autoimmune or immune-mediated skin diseases including bullous skin diseases, erythema multiforme and contact dermatitis, psoriasis, allergic diseases such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria, immunologic diseases of the lung such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonitis, transplantation associated diseases including graft rejection and graft -versus-host-disease. Infectious diseases including viral diseases such as AIDS (HIV infection), hepatitis A, B, C, D, and E, herpes, etc., bacterial infections, fungal infections, protozoal infections and parasitic infections.

The term "effective amount" is a concentration or amount of a PRO polypeptide and/or agonist/antagonist which results in achieving a particular stated purpose. An "effective amount" of a PRO polypeptide or agonist or antagonist thereof may be determined empirically. Furthermore, a "therapeutically effective amount" is a concentration or amount of a PRO polypeptide and/or agonist/antagonist which is effective for achieving a stated therapeutic effect. This amount may also be determined empirically.

The term "cytotoxic agent" as used herein refers to a substance that inhibits or prevents the function of cells and/or causes destruction of cells. The term is intended to include radioactive isotopes (e.g., I^{131} , I^{125} , Y^{90} and Re^{186}), chemotherapeutic agents, and toxins such as enzymatically active toxins of bacterial, fungal, plant or animal origin, or fragments thereof.

A "chemotherapeutic agent" is a chemical compound useful in the treatment of cancer. Examples of chemotherapeutic agents include adriamycin, doxorubicin, epirubicin, 5-fluorouracil, cytosine arabinoside ("Ara-C"), cyclophosphamide, thiotepa, busulfan, cytoxan, taxoids, e.g., paclitaxel (Taxol, Bristol-Myers Squibb Oncology, Princeton, NJ), and doxetaxel (Taxotere, Rhône-Poulenc Rorer, Antony, France), toxotere, methotrexate, cisplatin, melphalan, vinblastine, bleomycin, etoposide, ifosfamide, mitomycin C, mitoxantrone, vincristine, vinorelbine, carboplatin, teniposide, daunomycin, carminomycin, aminopterin, dactinomycin, mitomycins, esperamicins (see U.S. Pat. No. 4,675,187), melphalan and other related nitrogen mustards. Also included in this definition are hormonal agents that act to regulate or inhibit hormone action on tumors such as tamoxifen and onapristone.

A "growth inhibitory agent" when used herein refers to a compound or composition which inhibits growth of a cell, especially cancer cell overexpressing any of the genes identified herein, either *in vitro* or *in*

vivo. Thus, the growth inhibitory agent is one which significantly reduces the percentage of cells overexpressing such genes in S phase. Examples of growth inhibitory agents include agents that block cell cycle progression (at a place other than S phase), such as agents that induce G1 arrest and M-phase arrest. Classical M-phase blockers include the vincas (vincristine and vinblastine), taxol, and topo II inhibitors such as doxorubicin, epirubicin, daunorubicin, etoposide, and bleomycin. Those agents that arrest G1 also spill over into S-phase arrest, for example, DNA alkylating agents such as tamoxifen, prednisone, dacarbazine, mechlorethamine, cisplatin, methotrexate, 5-fluorouracil, and ara-C. Further information can be found in *The Molecular Basis of Cancer*, Mendelsohn and Israel, eds., Chapter 1, entitled "Cell cycle regulation, oncogens, and antineoplastic drugs" by Murakami *et al.* (WB Saunders: Philadelphia, 1995), especially p.

10 13.

The term "cytokine" is a generic term for proteins released by one cell population which act on another cell as intercellular mediators. Examples of such cytokines are lymphokines, monokines, and traditional polypeptide hormones. Included among the cytokines are growth hormone such as human growth hormone, N-methionyl human growth hormone, and bovine growth hormone; parathyroid hormone; thyroxine; insulin; proinsulin; relaxin; prorelaxin; glycoprotein hormones such as follicle stimulating hormone (FSH), thyroid stimulating hormone (TSH), and luteinizing hormone (LH); hepatic growth factor; fibroblast growth factor; prolactin; placental lactogen; tumor necrosis factor- α and - β ; mullerian-inhibiting substance; mouse gonadotropin-associated peptide; inhibin; activin; vascular endothelial growth factor; integrin; thrombopoietin (TPO); nerve growth factors such as NGF- β ; platelet-growth factor; transforming growth factors (TGFs) such as TGF- α and TGF- β ; insulin-like growth factor-I and -II; erythropoietin (EPO); osteoinductive factors; interferons such as interferon- α , - β , and - γ ; colony stimulating factors (CSFs) such as macrophage-CSF (M-CSF); granulocyte-macrophage-CSF (GM-CSF); and granulocyte-CSF (G-CSF); interleukins (ILs) such as IL-1, IL-1 α , IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-11, IL-12; a tumor necrosis factor such as TNF- α or TNF- β ; and other polypeptide factors including LIF and kit ligand (KL).

As used herein, the term cytokine includes proteins from natural sources or from recombinant cell culture and biologically active equivalents of the native sequence cytokines.

As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (*i.e.*, is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

As used herein, the term "inflammatory cells" designates cells that enhance the inflammatory response such as mononuclear cells, eosinophils, macrophages, and polymorphonuclear neutrophils (PMN).

Table 1

```

/*
5  *
  * C-C increased from 12 to 15
  * Z is average of EQ
  * B is average of ND
  * match with stop is _M; stop-stop = 0; J (joker) match = 0
10 */
#define _M      -8      /* value of a match with a stop */

int  _day[26][26] = {
/*  A B C D E F G H I J K L M N O P Q R S T U V W X Y Z */
15 /* A */ { 2, 0, -2, 0, 0, -4, 1, -1, -1, 0, -1, -2, -1, 0, _M, 1, 0, -2, 1, 1, 0, 0, -6, 0, -3, 0},
/* B */ { 0, 3, -4, 3, 2, -5, 0, 1, -2, 0, 0, -3, -2, 2, _M, -1, 1, 0, 0, 0, 0, -2, -5, 0, -3, 1},
/* C */ {-2, -4, 15, -5, -5, -4, -3, -3, -2, 0, -5, -6, -5, -4, _M, -3, -5, -4, 0, -2, 0, -2, -8, 0, 0, -5},
/* D */ { 0, 3, -5, 4, 3, -6, 1, 1, -2, 0, 0, -4, -3, 2, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 2},
/* E */ { 0, 2, -5, 3, 4, -5, 0, 1, -2, 0, 0, -3, -2, 1, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 3},
20 /* F */ {-4, -5, -4, -6, -5, 9, -5, -2, 1, 0, -5, 2, 0, -4, _M, -5, -5, -4, -3, -3, 0, -1, 0, 0, 7, -5},
/* G */ { 1, 0, -3, 1, 0, -5, 5, -2, -3, 0, -2, -4, -3, 0, _M, -1, -1, -3, 1, 0, 0, -1, -7, 0, -5, 0},
/* H */ {-1, 1, -3, 1, 1, -2, -2, 6, -2, 0, 0, -2, -2, 2, _M, 0, 3, 2, -1, -1, 0, -2, -3, 0, 0, 2},
/* I */ {-1, -2, -2, -2, -2, 1, -3, -2, 5, 0, -2, 2, 2, -2, _M, -2, -2, -2, -1, 0, 0, 4, -5, 0, -1, -2},
/* J */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
25 /* K */ {-1, 0, -5, 0, 0, -5, -2, 0, -2, 0, 5, -3, 0, 1, _M, -1, 1, 3, 0, 0, 0, -2, -3, 0, -4, 0},
/* L */ {-2, -3, -6, -4, -3, 2, -4, -2, 2, 0, -3, 6, 4, -3, _M, -3, -2, -3, -3, -1, 0, 2, -2, 0, -1, -2},
/* M */ {-1, -2, -5, -3, -2, 0, -3, -2, 2, 0, 0, 4, 6, -2, _M, -2, -1, 0, -2, -1, 0, 2, -4, 0, -2, -1},
/* N */ { 0, 2, -4, 2, 1, -4, 0, 2, -2, 0, 1, -3, -2, 2, _M, -1, 1, 0, 1, 0, 0, -2, -4, 0, -2, 1},
/* O */ { _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M},
30 /* P */ { 1, -1, -3, -1, -1, -5, -1, 0, -2, 0, -1, -3, -2, -1, _M, 6, 0, 0, 1, 0, 0, -1, -6, 0, -5, 0},
/* Q */ { 0, 1, -5, 2, 2, -5, -1, 3, -2, 0, 1, -2, -1, 1, _M, 0, 4, 1, -1, -1, 0, -2, -5, 0, -4, 3},
/* R */ {-2, 0, -4, -1, -1, -4, -3, 2, -2, 0, 3, -3, 0, 0, _M, 0, 1, 6, 0, -1, 0, -2, 2, 0, -4, 0},
/* S */ { 1, 0, 0, 0, 0, -3, 1, -1, -1, 0, 0, -3, -2, 1, _M, 1, -1, 0, 2, 1, 0, -1, -2, 0, -3, 0},
/* T */ { 1, 0, -2, 0, 0, -3, 0, -1, 0, 0, 0, -1, -1, 0, _M, 0, -1, -1, 1, 3, 0, 0, -5, 0, -3, 0},
35 /* U */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* V */ { 0, -2, -2, -2, -2, -1, -1, -2, 4, 0, -2, 2, 2, -2, _M, -1, -2, -2, -1, 0, 0, 4, -6, 0, -2, -2},
/* W */ {-6, -5, -8, -7, -7, 0, -7, -3, -5, 0, -3, -2, -4, -4, _M, -6, -5, 2, -2, -5, 0, -6, 17, 0, 0, -6},
/* X */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* Y */ {-3, -3, 0, -4, -4, 7, -5, 0, -1, 0, -4, -1, -2, -2, _M, -5, -4, -4, -3, -3, 0, -2, 0, 0, 10, -4},
40 /* Z */ { 0, 1, -5, 2, 3, -5, 0, 2, -2, 0, 0, -2, -1, 1, _M, 0, 3, 0, 0, 0, 0, -2, -6, 0, -4, 4}
};

```

45

50

55

Table 1 (cont')

```

/*
*/
#include <stdio.h>
5  #include <ctype.h>

#define MAXJMP      16      /* max jumps in a diag */
#define MAXGAP      24      /* don't continue to penalize gaps larger than this */
#define JMPS        1024    /* max jmps in an path */
10  #define MX        4      /* save if there's at least MX-1 bases since last jmp */

#define DMAT         3      /* value of matching bases */
#define DMIS         0      /* penalty for mismatched bases */
#define DINS0         8      /* penalty for a gap */
15  #define DINS1         1    /* penalty per base */
#define PINS0         8      /* penalty for a gap */
#define PINS1         4      /* penalty per residue */

struct jmp {
20      short          n[MAXJMP];    /* size of jmp (neg for dely) */
      unsigned short  x[MAXJMP];    /* base no. of jmp in seq x */
};
/* limits seq to 2^16 -1 */

struct diag {
25      int            score;         /* score at last jmp */
      long            offset;        /* offset of prev block */
      short           ijmp;          /* current jmp index */
      struct jmp      jp;            /* list of jmps */
};
30

struct path {
      int             spc;           /* number of leading spaces */
      short           n[JMPS];      /* size of jmp (gap) */
      int             x[JMPS];      /* loc of jmp (last elem before gap) */
35  };

char      *ofile;                  /* output file name */
char      *namex[2];               /* seq names: getseqs() */
char      *prog;                   /* prog name for err msgs */
40  char      *seqx[2];             /* seqs: getseqs() */
int        dmax;                   /* best diag: nw() */
int        dmax0;                  /* final diag */
int        dna;                    /* set if dna: main() */
int        endgaps;                /* set if penalizing end gaps */
45  int        gapx, gapy;           /* total gaps in seqs */
int        lcn0, len1;             /* seq lens */
int        ngapx, ngapy;           /* total size of gaps */
int        smax;                   /* max score: nw() */
int        *xbm;                   /* bitmap for matching */
50  long       offset;               /* current offset in jmp file */
struct     diag      *dx;           /* holds diagonals */
struct     path      pp[2];         /* holds path for seqs */

char      *calloc(), *malloc(), *index(), *strcpy();
55  char      *getseq(), *g_calloc();

```

60

Table 1 (cont')

```

/* Needleman-Wunsch alignment program
*
* usage: progs file1 file2
5 * where file1 and file2 are two dna or two protein sequences.
* The sequences can be in upper- or lower-case and may contain ambiguity
* Any lines beginning with ';', '>' or '<' are ignored
* Max file length is 65535 (limited by unsigned short x in the jmp struct)
* A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
10 * Output is in the file "align.out"
*
* The program may create a tmp file in /tmp to hold info about traceback.
* Original version developed under BSD 4.3 on a vax 8650
*/
15 #include "nw.h"
#include "day.h"

static _dbval[26] = {
20 1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
};

static _pbval[26] = {
25 1, 2|(1<<('D'-'A'))|(1<<('N'-'A')), 4, 8, 16, 32, 64,
128, 256, 0xFFFFFFF, 1<<10, 1<<11, 1<<12, 1<<13, 1<<14,
1<<15, 1<<16, 1<<17, 1<<18, 1<<19, 1<<20, 1<<21, 1<<22,
1<<23, 1<<24, 1<<25|(1<<('E'-'A'))|(1<<('Q'-'A'))
};

main(ac, av)
30 main
int ac;
char *av[ ];
{
35 prog = av[0];
if (ac != 3) {
fprintf(stderr, "usage: %s file1 file2\n", prog);
fprintf(stderr, "where file1 and file2 are two dna or two protein sequences.\n");
fprintf(stderr, "The sequences can be in upper- or lower-case\n");
40 fprintf(stderr, "Any lines beginning with ';', '>' or '<' are ignored\n");
fprintf(stderr, "Output is in the file \"align.out\"\n");
exit(1);
}
namex[0] = av[1];
namex[1] = av[2];
45 seqx[0] = getseq(namex[0], &len0);
seqx[1] = getseq(namex[1], &len1);
xbm = (dna)? _dbval : _pbval;

endgaps = 0; /* 1 to penalize endgaps */
50 ofile = "align.out"; /* output file */

nw(); /* fill in the matrix, get the possible jmps */
readjmps(); /* get the actual jmps */
print(); /* print stats, alignment */
55 cleanup(); /* unlink any tmp files */
}
60

```


Table 1 (cont')

```

/* do the alignment, return best score: main()
 * dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
 * pro: PAM 250 values
5  * When scores are equal, we prefer mismatches to any gap, prefer
 * a new gap to extending an ongoing gap, and prefer a gap in seqx
 * to a gap in seq y.
 */
nw()
10 {
    char      *px, *py;          /* seqs and ptrs */
    int        *ndely, *dely;    /* keep track of dely */
    int        ndelx, delx;      /* keep track of delx */
15    int        *tmp;           /* for swapping row0, row1 */
    int        mis;             /* score for each type */
    int        ins0, ins1;       /* insertion penalties */
    register   id;              /* diagonal index */
    register   ij;              /* jmp index */
20    register   *col0, *col1;    /* score for curr, last row */
    register   xx, yy;          /* index into seqs */

    dx = (struct diag *)g_calloc("to get diags", len0+len1+1, sizeof(struct diag));

25    ndely = (int *)g_calloc("to get ndely", len1+1, sizeof(int));
    dely = (int *)g_calloc("to get dely", len1+1, sizeof(int));
    col0 = (int *)g_calloc("to get col0", len1+1, sizeof(int));
    col1 = (int *)g_calloc("to get col1", len1+1, sizeof(int));
    ins0 = (dna)? DINS0 : PINS0;
30    ins1 = (dna)? DINS1 : PINS1;

    smax = -10000;
    if (endgaps) {
        for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
35            col0[yy] = dely[yy] = col0[yy-1] - ins1;
            ndely[yy] = yy;
        }
        col0[0] = 0;          /* Waterman Bull Math Biol 84 */
    }
40    else
        for (yy = 1; yy <= len1; yy++)
            dely[yy] = -ins0;

    /* fill in match matrix
    */
45    for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
        /* initialize first entry in col
        */
        if (endgaps) {
50            if (xx == 1)
                col1[0] = delx = -(ins0+ins1);
            else
                col1[0] = delx = col0[0] - ins1;
            ndelx = xx;
55        }
        else {
            col1[0] = 0;
            delx = -ins0;
            ndelx = 0;
60        }
    }

```

Table 1 (cont')

...nw

```

5      for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
        mis = col0[yy-1];
        if (dna)
            mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
        else
            mis += _day[*px-'A'][*py-'A'];

10      /* update penalty for del in x seq;
        * favor new del over ongoing del
        * ignore MAXGAP if weighting endgaps
        */
        if (endgaps || ndely[yy] < MAXGAP) {
15            if (col0[yy] - ins0 >= dely[yy]) {
                dely[yy] = col0[yy] - (ins0+ins1);
                ndely[yy] = 1;
            } else {
                dely[yy] -= ins1;
                ndely[yy]++;
            }
        } else {
20            if (col0[yy] - (ins0+ins1) >= dely[yy]) {
                dely[yy] = col0[yy] - (ins0+ins1);
                ndely[yy] = 1;
            } else
                ndely[yy]++;
        }

25      /* update penalty for del in y seq;
        * favor new del over ongoing del
        */
        if (endgaps || ndelx < MAXGAP) {
            if (col1[yy-1] - ins0 >= delx) {
35                delx = col1[yy-1] - (ins0+ins1);
                ndelx = 1;
            } else {
                delx -= ins1;
                ndelx++;
            }
        } else {
40            if (col1[yy-1] - (ins0+ins1) >= delx) {
                delx = col1[yy-1] - (ins0+ins1);
                ndelx = 1;
            } else
45                ndelx++;
        }

        /* pick the maximum score; we're favoring
50        * mis over any del and delx over dely
        */

```

55

60

Table 1 (cont')

...nw

```

5      id = xx - yy + len1 - 1;
      if (mis >= delx && mis >= dely[yy])
          coll[yy] = mis;
      else if (delx >= dely[yy]) {
          coll[yy] = delx;
          ij = dx[id].ijmp;
          if (dx[id].jp.n[0] && (!dna || (ndelx >= MAXJMP
10      && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
              dx[id].ijmp++;
              if (++ij >= MAXJMP) {
                  writejumps(id);
                  ij = dx[id].ijmp = 0;
15      dx[id].offset = offset;
                  offset += sizeof(struct jmp) + sizeof(offset);
              }
          }
          dx[id].jp.n[ij] = ndelx;
          dx[id].jp.x[ij] = xx;
          dx[id].score = delx;
      }
      else {
25      coll[yy] = dely[yy];
          ij = dx[id].ijmp;
          if (dx[id].jp.n[0] && (!dna || (ndely[yy] >= MAXJMP
              && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
              dx[id].ijmp++;
30      if (++ij >= MAXJMP) {
                  writejumps(id);
                  ij = dx[id].ijmp = 0;
                  dx[id].offset = offset;
                  offset += sizeof(struct jmp) + sizeof(offset);
              }
          }
          dx[id].jp.n[ij] = -ndely[yy];
          dx[id].jp.x[ij] = xx;
          dx[id].score = dely[yy];
      }
40      if (xx == len0 && yy < len1) {
          /* last col
             */
          if (endgaps)
              coll[yy] -= ins0+ins1*(len1-yy);
45      if (coll[yy] > smax) {
              smax = coll[yy];
              dmax = id;
          }
      }
50      if (endgaps && xx < len0)
          coll[yy-1] -= ins0+ins1*(len0-xx);
          if (coll[yy-1] > smax) {
              smax = coll[yy-1];
55      dmax = id;
          }
      tmp = col0; col0 = coll; coll = tmp;
  }
  (void) free((char *)ndely);
  (void) free((char *)dely);
  (void) free((char *)col0);
  (void) free((char *)col1);
  }

```

Table 1 (cont')

```

/*
 *
 * print() -- only routine visible outside this module
5  *
 * static:
 * getmat() -- trace back best path, count matches: print()
 * pr_align() -- print alignment of described in array p[ ]: print()
 * dumpblock() -- dump a block of lines with numbers, stars: pr_align()
10 * nums() -- put out a number line: dumpblock()
 * putline() -- put out a line (name, [num], seq, [num]): dumpblock()
 * stars() -- put a line of stars: dumpblock()
 * stripname() -- strip any path and prefix from a seqname
 */
15
#include "nw.h"

#define SPC      3
#define P_LINE   256 /* maximum output line */
20 #define P_SPC   3    /* space between name or num and seq */

extern _day[26][26];
int olen; /* set output line length */
FILE *fx; /* output file */
25

print()
{
    print
    {
        int lx, ly, firstgap, lastgap; /* overlap */
30
        if ((fx = fopen(ofile, "w")) == 0) {
            fprintf(stderr, "%s: can't write %s\n", prog, ofile);
            cleanup(1);
        }
35
        fprintf(fx, "<first sequence: %s (length = %d)\n", namex[0], len0);
        fprintf(fx, "<second sequence: %s (length = %d)\n", namex[1], len1);
        olen = 60;
        lx = len0;
        ly = len1;
40
        firstgap = lastgap = 0;
        if (dmax < len1 - 1) { /* leading gap in x */
            pp[0].spc = firstgap = len1 - dmax - 1;
            ly -= pp[0].spc;
        }
45
        else if (dmax > len1 - 1) { /* leading gap in y */
            pp[1].spc = firstgap = dmax - (len1 - 1);
            lx -= pp[1].spc;
        }
        if (dmax0 < len0 - 1) { /* trailing gap in x */
50
            lastgap = len0 - dmax0 - 1;
            lx -= lastgap;
        }
        else if (dmax0 > len0 - 1) { /* trailing gap in y */
55
            lastgap = dmax0 - (len0 - 1);
            ly -= lastgap;
        }
        getmat(lx, ly, firstgap, lastgap);
        pr_align();
    }
60

```

Table 1 (cont')

```

/*
 * trace back the best path, count matches
 */
5  static
   getmat(lx, ly, firstgap, lastgap)                                getmat
       int      lx, ly;
       int      firstgap, lastgap;
                               /* "core" (minus endgaps) */
                               /* leading trailing overlap */
{
10     int      nm, i0, i1, siz0, siz1;
       char     outx[32];
       double    pct;
       register  n0, n1;
       register char *p0, *p1;

15     /* get total matches, score
       */
       i0 = i1 = siz0 = siz1 = 0;
       p0 = seqx[0] + pp[1].spc;
20     p1 = seqx[1] + pp[0].spc;
       n0 = pp[1].spc + 1;
       n1 = pp[0].spc + 1;

       nm = 0;
25     while ( *p0 && *p1 ) {
         if (siz0) {
           p1++;
           n1++;
           siz0--;
30         }
         else if (siz1) {
           p0++;
           n0++;
           siz1--;
35         }
         else {
           if (xbm[*p0-'A'] & xbm[*p1-'A'])
             nm++;
           if (n0++ == pp[0].x[i0])
             siz0 = pp[0].n[i0++];
40           if (n1++ == pp[1].x[i1])
             siz1 = pp[1].n[i1++];
           p0++;
           p1++;
45         }
       }

       /* pct homology:
       * if penalizing endgaps, base is the shorter seq
50     * else, knock off overhangs and take shorter core
       */
       if (endgaps)
         lx = (len0 < len1)? len0 : len1;
       else
55         lx = (lx < ly)? lx : ly;
       pct = 100.*((double)nm/((double)lx);
       fprintf(fx, "\n");
       fprintf(fx, "<%d match%s in an overlap of %d: %.2f percent similarity\n",
60         nm, (nm == 1)? "" : "es", lx, pct);

```

Table 1 (cont')

```

5      fprintf(fx, "<gaps in first sequence: %d", gapx);
      if (gapx) {
          (void) sprintf(outx, " (%d %s%s)",
              ngapx, (dna)? "base": "residue", (ngapx == 1)? "" : "s");
          fprintf(fx, "%s", outx);

10     fprintf(fx, ", gaps in second sequence: %d", gapy);
      if (gapy) {
          (void) sprintf(outx, " (%d %s%s)",
              ngapy, (dna)? "base": "residue", (ngapy == 1)? "" : "s");
          fprintf(fx, "%s", outx);
      }
15     if (dna)
        fprintf(fx,
            "\n<score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
            smax, DMAT, DMIS, DINS0, DINS1);
      else
20         fprintf(fx,
            "\n<score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
            smax, PINS0, PINS1);
      if (endgaps)
25         fprintf(fx,
            "<endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
            firstgap, (dna)? "base" : "residue", (firstgap == 1)? "" : "s",
            lastgap, (dna)? "base" : "residue", (lastgap == 1)? "" : "s");
      else
30         fprintf(fx, "<endgaps not penalized\n");
    }
    static nm;          /* matches in core -- for checking */
    static lmax;        /* lengths of stripped file names */
    static ij[2];       /* jmp index for a path */
    static nc[2];       /* number at start of current line */
35    static ni[2];      /* current elem number -- for gapping */
    static siz[2];
    static char *ps[2]; /* ptr to current element */
    static char *po[2]; /* ptr to next output char slot */
    static char out[2][P_LINE]; /* output line */
40    static char star[P_LINE]; /* set by stars() */

    /*
     * print alignment of described in struct path pp[ ]
     */
45    static
    pr_align()
    {
        int nn;          /* char count */
        int more;
50        register i;

        for (i = 0, lmax = 0; i < 2; i++) {
            nn = stripname(nameex[i]);
            if (nn > lmax)
55                lmax = nn;

            nc[i] = 1;
            ni[i] = 1;
            siz[i] = ij[i] = 0;
60            ps[i] = seqx[i];
            po[i] = out[i];
        }

```

...getmat

pr_align

Table 1 (cont')

...pr_align

```

5      for (nn = nm = 0, more = 1; more;) {
          for (i = more = 0; i < 2; i++) {
              /*
              * do we have more of this sequence?
              */
              if (!*ps[i])
10                 continue;

                more++;

                if (pp[i].spc) { /* leading space */
                    *po[i]++ = ' ';
                    pp[i].spc--;
15                }
                else if (siz[i]) { /* in a gap */
                    *po[i]++ = '\0';
                    siz[i]--;
20                }
                else { /* we're putting a seq element
                    */
                    *po[i] = *ps[i];
                    if (islower(*ps[i]))
                        *ps[i] = toupper(*ps[i]);
25                    po[i]++;
                    ps[i]++;

                    /*
                    * are we at next gap for this seq?
                    */
                    if (ni[i] == pp[i].x[ij[i]]) {
                        /*
                        * we need to merge all gaps
                        * at this location
                        */
30                        siz[i] = pp[i].n[ij[i]++];
                        while (ni[i] == pp[i].x[ij[i]])
                            siz[i] += pp[i].n[ij[i]++];
35                        }
                        ni[i]++;
                    }
                }
            }
            if (++nn == olen || !more && nn) {
45                dumpblock();
                for (i = 0; i < 2; i++)
                    po[i] = out[i];
                nn = 0;
            }
50        }
    }

    /*
    * dump a block of lines, including numbers, stars: pr_align()
    */
55    static
    dumpblock()
        dumpblock
    {
60        register i;
        for (i = 0; i < 2; i++)
            *po[i]-- = '\0';

```

Table 1 (cont')**...dumpblock**

```

5      (void) putc('\n', fx);
      for (i = 0; i < 2; i++) {
          if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' ')) {
              if (i == 0)
                  nums(i);
              if (i == 0 && *out[1])
                  stars();
10         putline(i);
              if (i == 0 && *out[1])
                  fprintf(fx, star);
              if (i == 1)
                  nums(i);
15         }
      }
  }

20  /*
   * put out a number line: dumpblock()
   */
   static
   nums(ix)
25  {
       int      ix;      /* index in out[ ] holding seq line */

       char      nline[P_LINE];
       register  i, j;
       register char *pn, *px, *py;
30
       for (pn = nline, i = 0; i < lmax+P_SPC; i++, pn++)
           *pn = ' ';
       for (i = nc[ix], py = out[ix]; *py; py++, pn++) {
           if (*py == ' ' || *py == '?')
35             *pn = ' ';
           else {
               if (i%10 == 0 || (i == 1 && nc[ix] != 1)) {
                   j = (i < 0)? -i : i;
                   for (px = pn; j; j /= 10, px--)
40                     *px = j%10 + '0';
                   if (i < 0)
                       *px = '?';
               }
               else
45                 *pn = ' ';
               i++;
           }
       }
       *pn = '\0';
       nc[ix] = i;
       for (pn = nline; *pn; pn++)
           (void) putc(*pn, fx);
       (void) putc('\n', fx);
55  }

   /*
   * put out a line (name, [num], seq, [num]): dumpblock()
   */
   static
   putline(ix)
60  {
       int      ix;

```

nums**putline**

Table 1 (cont')**...putline**

```

5      int          i;
      register char *px;

      for (px = namex[ix], i = 0; *px && *px != ':'; px++, i++)
          (void) putc(*px, fx);
10     for (; i < lmax+P_SPC; i++)
          (void) putc(' ', fx);

      /* these count from 1:
       * ni[ ] is current element (from 1)
       * nc[ ] is number at start of current line
       */
15     for (px = out[ix]; *px; px++)
          (void) putc(*px&0x7F, fx);
      (void) putc('\n', fx);
20 }

/*
 * put a line of stars (seqs always in out[0], out[1]): dumpblock()
 */
25 static
stars()
{
    stars
    {
30         int          i;
        register char *p0, *p1, cx, *px;

        if (!*out[0] || (*out[0] == '' && *(po[0]) == '') ||
            !*out[1] || (*out[1] == '' && *(po[1]) == ''))
            return;
35         px = star;
        for (i = lmax+P_SPC; i; i--)
            *px++ = ' ';

        for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++) {
40             if (isalpha(*p0) && isalpha(*p1)) {

                if (xbm[*p0-'A'] & xbm[*p1-'A']) {
                    cx = '*';
                    nm++;
45                 }
                else if (!dna && _day[*p0-'A'][*p1-'A'] > 0)
                    cx = '.';
                else
                    cx = ' ';
50             }
            else
                cx = ' ';
            *px++ = cx;
55         }
        *px++ = '\n';
        *px = '\0';
    }
60

```

Table 1 (cont')

```

/*
 * strip path or prefix from pn, return len: pr_align()
 */
5  static
  stripname(pn)
      stripname
      char    *pn;    /* file name (may be path) */
10  {
      register char    *px, *py;

      py = 0;
      for (px = pn; *px; px++)
          if (*px == '/')
15          py = px + 1;

      if (py)
          (void) strcpy(pn, py);
      return(strlen(pn));
20  }

```

25

30

35

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50

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60

Table 1 (cont')

```

/*
 * cleanup() -- cleanup any tmp file
 * getseq() -- read in seq, set dna, len, maxlen
5  * g_alloc() -- calloc() with error checkin
 * readjumps() -- get the good jumps, from tmp file if necessary
 * writejumps() -- write a filled array of jumps to a tmp file: nw()
 */
#include "nw.h"
10 #include <sys/file.h>

char    *jname = "/tmp/homgXXXXXX";          /* tmp file for jumps */
FILE    *fj;

15 int    cleanup();                          /* cleanup tmp file */
long    lseek();

/*
 * remove any tmp file if we blow
20 */
cleanup(i)
    int    i;
{
    if (fj)
25     (void) unlink(jname);
    exit(i);
}

/*
30 * read, return ptr to seq, set dna, len, maxlen
 * skip lines starting with ';', '<', or '>'
 * seq in upper or lower case
 */
char    *
35 getseq(file, len)
    char    *file;    /* file name */
    int     *len;     /* seq len */
{
    char    line[1024], *pseq;
40     register char    *px, *py;
    int     natgc, tlen;
    FILE    *fp;

    if ((fp = fopen(file, "r")) == 0) {
45         fprintf(stderr, "%s: can't read %s\n", prog, file);
        exit(1);
    }
    tlen = natgc = 0;
    while (fgets(line, 1024, fp)) {
50         if (*line == ';' || *line == '<' || *line == '>')
            continue;
        for (px = line; *px != '\n'; px++)
            if (isupper(*px) || islower(*px))
                tlen++;
55     }
    if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
        fprintf(stderr, "%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);
        exit(1);
    }
60     pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';

```

cleanup

getseq

Table 1 (cont')

...getseq

```

5      py = pseq + 4;
      *len = tlen;
      rewind(fp);

      while (fgets(line, 1024, fp)) {
          if (*line == ';' || *line == '<' || *line == '>')
              continue;
10         for (px = line; *px != '\n'; px++) {
              if (isupper(*px))
                  *py++ = *px;
              else if (islower(*px))
                  *py++ = toupper(*px);
15         if (index("ATGCU", *(py-1)))
            natgc++;
        }
    }
    *py++ = '\0';
    *py = '\0';
    (void) fclose(fp);
    dna = natgc > (tlen/3);
    return(pseq+4);
25 }

char *
g_alloc(msg, nx, sz)
char *msg;          /* program, calling routine */
int nx, sz;          /* number and size of elements */
30 {
    char *px, *calloc();

    if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
        if (*msg) {
35             fprintf(stderr, "%s: g_alloc() failed %s (n=%d, sz=%d)\n", prog, msg, nx, sz);
            exit(1);
        }
    }
    return(px);
40 }

/*
 * get final jmps from dx[ ] or tmp file, set pp[ ], reset dmax: main()
 */
45 readjmps()
    readjmps
{
    int fd = -1;
    int siz, i0, i1;
50 register i, j, xx;

    if (fj) {
        (void) fclose(fj);
        if ((fd = open(jname, O_RDONLY, 0)) < 0) {
55             fprintf(stderr, "%s: can't open() %s\n", prog, jname);
            cleanup(1);
        }
    }
    for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; ; i++) {
60         while (1) {
            for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)

```

g_alloc

Table 1 (cont')**...readjumps**

```

5      if (j < 0 && dx[dmax].offset && fj) {
        (void) lseek(fd, dx[dmax].offset, 0);
        (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
        (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
        dx[dmax].ijmp = MAXJMP-1;
      }
10     else
        break;
    }
    if (i >= JMPS) {
        fprintf(stderr, "%s: too many gaps in alignment\n", prog);
        cleanup(1);
15    }
    if (j >= 0) {
        siz = dx[dmax].jp.n[j];
        xx = dx[dmax].jp.x[j];
        dmax += siz;
20        if (siz < 0) { /* gap in second seq */
            pp[1].n[i1] = -siz;
            xx += siz;
            /* id = xx - yy + len1 - 1
            */
            pp[1].x[i1] = xx - dmax + len1 - 1;
            gapy++;
            ngapy -= siz;
            /* ignore MAXGAP when doing endgaps */
            siz = (-siz < MAXGAP || endgaps)? -siz : MAXGAP;
30            i1++;
        }
        else if (siz > 0) { /* gap in first seq */
            pp[0].n[i0] = siz;
            pp[0].x[i0] = xx;
            gapx++;
            ngapx += siz;
            /* ignore MAXGAP when doing endgaps */
            siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
35            i0++;
        }
    }
40    }
    else
        break;
}

45    /* reverse the order of jumps
    */
    for (j = 0, i0--; j < i0; j++, i0--) {
        i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
50        i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
    }
    for (j = 0, i1--; j < i1; j++, i1--) {
        i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
        i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
55    }
    if (fd >= 0)
        (void) close(fd);
    if (fj) {
        (void) unlink(jname);
60        fj = 0;
        offset = 0;
    }
}

```

Table 1 (cont')

```

5  /*
   * write a filled jmp struct offset of the prev one (if any): nw()
   */
   writejumps(ix)
       writejumps
       int      ix;
10  {
       char      *mktemp();

       if (!fj) {
           if (mktemp(jname) < 0) {
               fprintf(stderr, "%s: can't mktemp() %s\n", prog, jname);
               cleanup(1);
15           }
           if ((fj = fopen(jname, "w")) == 0) {
               fprintf(stderr, "%s: can't write %s\n", prog, jname);
               exit(1);
20           }
       }
       (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
       (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
25  }

```

Table 2

5 PRO XXXXXXXXXXXXXXXX (Length = 15 amino acids)
 Comparison Protein XXXXXYYYYYYY (Length = 12 amino acids)
 % amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as
 10 determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =
 5 divided by 15 = 33.3%

Table 3

15 PRO XXXXXXXXXX (Length = 10 amino acids)
 Comparison Protein XXXXXYYYYYYZZYZ (Length = 15 amino acids)
 % amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as
 20 determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =
 5 divided by 10 = 50%

Table 4

25 PRO-DNA NNNNNNNNNNNNNN (Length = 14 nucleotides)
 Comparison DNA NNNNNNLLLLLLLLLL (Length = 16 nucleotides)
 % nucleic acid sequence identity =

30 (the number of identically matching nucleotides between the two nucleic acid sequences as determined by
 ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =
 6 divided by 14 = 42.9%

Table 5

35 PRO-DNA NNNNNNNNNNNN (Length = 12 nucleotides)
 Comparison DNA NNNNLLLVV (Length = 9 nucleotides)

% nucleic acid sequence identity =
 40

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =
4 divided by 12 = 33.3%

5 II. Compositions and Methods of the Invention

A. Full-Length PRO Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO polypeptides. In particular, cDNAs encoding various PRO polypeptides have been identified and isolated, as disclosed in further detail in the Examples
10 below. It is noted that proteins produced in separate expression rounds may be given different PRO numbers but the UNQ number is unique for any given DNA and the encoded protein, and will not be changed. However, for sake of simplicity, in the present specification the protein encoded by the full length native nucleic acid molecules disclosed herein as well as all further native homologues and variants included in the foregoing definition of PRO, will be referred to as "PRO/number", regardless of their origin or mode of
15 preparation.

As disclosed in the Examples below, various cDNA clones have been deposited with the ATCC. The actual nucleotide sequences of those clones can readily be determined by the skilled artisan by sequencing of the deposited clone using routine methods in the art. The predicted amino acid sequence can be determined from the nucleotide sequence using routine skill. For the PRO polypeptides and encoding
20 nucleic acids described herein, Applicants have identified what is believed to be the reading frame best identifiable with the sequence information available at the time.

B. PRO Polypeptide Variants

In addition to the full-length native sequence PRO polypeptides described herein, it is contemplated that PRO variants can be prepared. PRO variants can be prepared by introducing appropriate nucleotide
25 changes into the PRO DNA, and/or by synthesis of the desired PRO polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the PRO, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

Variations in the native full-length sequence PRO or in various domains of the PRO described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations may be a
30 substitution, deletion or insertion of one or more codons encoding the PRO that results in a change in the amino acid sequence of the PRO as compared with the native sequence PRO. Optionally, the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the PRO. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely
35 affecting the desired activity may be found by comparing the sequence of the PRO with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of about 1
40 to 5 amino acids. The variation allowed may be determined by systematically making insertions, deletions

or substitutions of amino acids in the sequence and testing the resulting variants for activity exhibited by the full-length or mature native sequence.

PRO polypeptide fragments are provided herein. Such fragments may be truncated at the N-terminus or C-terminus, or may lack internal residues, for example, when compared with a full length native protein. Certain fragments lack amino acid residues that are not essential for a desired biological activity of the PRO polypeptide.

PRO fragments may be prepared by any of a number of conventional techniques. Desired peptide fragments may be chemically synthesized. An alternative approach involves generating PRO fragments by enzymatic digestion, e.g., by treating the protein with an enzyme known to cleave proteins at sites defined by particular amino acid residues, or by digesting the DNA with suitable restriction enzymes and isolating the desired fragment. Yet another suitable technique involves isolating and amplifying a DNA fragment encoding a desired polypeptide fragment, by polymerase chain reaction (PCR). Oligonucleotides that define the desired termini of the DNA fragment are employed at the 5' and 3' primers in the PCR. Preferably, PRO polypeptide fragments share at least one biological and/or immunological activity with the native PRO polypeptide disclosed herein.

In particular embodiments, conservative substitutions of interest are shown in Table 6 under the heading of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 6, or as further described below in reference to amino acid classes, are introduced and the products screened.

20

Table 6

	Original Residue	Exemplary Substitutions	Preferred Substitutions
5	Ala (A)	val; leu; ile	val
	Arg (R)	lys; gln; asn	lys
	Asn (N)	gln; his; lys; arg	gln
	Asp (D)	glu	glu
10	Cys (C)	ser	ser
	Gln (Q)	asn	asn
	Glu (E)	asp	asp
	Gly (G)	pro; ala	ala
	His (H)	asn; gln; lys; arg	arg
15	Ile (I)	leu; val; met; ala; phe; norleucine	leu
	Leu (L)	norleucine; ile; val; met; ala; phe	ile
	Lys (K)	arg; gln; asn	arg
20	Met (M)	leu; phe; ile	leu
	Phe (F)	leu; val; ile; ala; tyr	leu
	Pro (P)	ala	ala
	Ser (S)	thr	thr
	Thr (T)	ser	ser
25	Trp (W)	tyr; phe	tyr
	Tyr (Y)	trp; phe; thr; ser	phe
	Val (V)	ile; leu; met; phe; ala; norleucine	leu

30 Substantial modifications in function or immunological identity of the PRO polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

- 35 (1) hydrophobic: norleucine, met, ala, val, leu, ile;
 (2) neutral hydrophilic: cys, ser, thr;
 (3) acidic: asp, glu;
 (4) basic: asn, gln, his, lys, arg;
 (5) residues that influence chain orientation: gly, pro; and
 40 (6) aromatic: trp, tyr, phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

45 The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., *Nucl. Acids Res.*, 13:4331 (1986); Zoller et al., *Nucl. Acids Res.*, 10:6487 (1987)], cassette mutagenesis [Wells et al., *Gene*, 34:315 (1985)], restriction selection mutagenesis [Wells et al., *Philos. Trans. R. Soc. London SerA*, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the PRO variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, Science, 244: 1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins, (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

C. Modifications of PRO

Covalent modifications of PRO are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a PRO polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of the PRO. Derivatization with bifunctional agents is useful, for instance, for crosslinking PRO to a water-insoluble support matrix or surface for use in the method for purifying anti-PRO antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimide.

Other modifications include deamidation of glutamyl and asparaginy residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the PRO polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence PRO (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence PRO. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

Addition of glycosylation sites to the PRO polypeptide may be accomplished by altering the amino acid sequence. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence PRO (for O-linked glycosylation sites). The PRO amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the PRO polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the PRO polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

5 Removal of carbohydrate moieties present on the PRO polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved
10 by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of PRO comprises linking the PRO polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417;
15 4,791,192 or 4,179,337.

The PRO of the present invention may also be modified in a way to form a chimeric molecule comprising PRO fused to another, heterologous polypeptide or amino acid sequence.

In one embodiment, such a chimeric molecule comprises a fusion of the PRO with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is
20 generally placed at the amino- or carboxyl- terminus of the PRO. The presence of such epitope-tagged forms of the PRO can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the PRO to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine
25 (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide
30 [Martin et al., Science, 255:192-194 (1992)]; an alpha-tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

In an alternative embodiment, the chimeric molecule may comprise a fusion of the PRO with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule
35 (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of a PRO polypeptide in place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CH1, CH2 and CH3 regions of an IgG1 molecule. For the production of immunoglobulin fusions see also US
40 Patent No. 5,428,130 issued June 27, 1995.

D. Preparation of PRO

The description below relates primarily to production of PRO by culturing cells transformed or transfected with a vector containing PRO nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare PRO. For instance, the PRO sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., Solid-Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, J. Am. Chem. Soc., 85:2149-2154 (1963)]. *In vitro* protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the PRO may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length PRO.

1. Isolation of DNA Encoding PRO

DNA encoding PRO may be obtained from a cDNA library prepared from tissue believed to possess the PRO mRNA and to express it at a detectable level. Accordingly, human PRO DNA can be conveniently obtained from a cDNA library prepared from human tissue, such as described in the Examples. The PRO-encoding gene may also be obtained from a genomic library or by known synthetic procedures (e.g., automated nucleic acid synthesis).

Libraries can be screened with probes (such as antibodies to the PRO or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding PRO is to use PCR methodology [Sambrook et al., supra; Dieffenbach et al., PCR Primer: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1995)].

The Examples below describe techniques for screening a cDNA library. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like ³²P-labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined using methods known in the art and as described herein.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

2. Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for PRO production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in Mammalian Cell Biotechnology: a Practical Approach, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

Methods of eukaryotic cell transfection and prokaryotic cell transformation are known to the ordinarily skilled artisan, for example, CaCl_2 , CaPO_4 , liposome-mediated and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., Gene, 23:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transfections have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., J. Bact., 130:946 (1977) and Hsiao et al., Proc. Natl. Acad. Sci. (USA), 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., Methods in Enzymology, 185:527-537 (1990) and Mansour et al., Nature, 336:348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacteriaceae such as *Escherichia*, e.g., *E. coli*, *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella*, e.g., *Salmonella typhimurium*, *Serratia*, e.g., *Serratia marcescens*, and *Shigella*, as well as *Bacilli* such as *B. subtilis* and *B. licheniformis* (e.g., *B. licheniformis* 41P disclosed in DD 266,710 published 12 April 1989), *Pseudomonas* such as *P. aeruginosa*, and *Streptomyces*. These examples are illustrative rather than limiting. Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110 strain 1A2, which has the complete genotype *tonA*; *E. coli* W3110 strain 9E4, which has the complete genotype *tonA ptr3*; *E. coli* W3110 strain 27C7 (ATCC 55,244), which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT kan'*; *E. coli* W3110 strain 37D6, which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG kan'*; *E. coli* W3110 strain 40B4, which is strain

37D6 with a non-kanamycin resistant *degP* deletion mutation; and an *E. coli* strain having mutant periplasmic protease disclosed in U.S. Patent No. 4,946,783 issued 7 August 1990. Alternatively, *in vitro* methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.

In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for PRO-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include *Schizosaccharomyces pombe* (Beach and Nurse, Nature, 290: 140 [1981]; EP 139,383 published 2 May 1985); *Kluyveromyces* hosts (U.S. Patent No. 4,943,529; Fleer et al., Bio/Technology, 9:968-975 (1991)) such as, e.g., *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt et al., J. Bacteriol., 154(2):737-742 [1983]), *K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickerhamii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilae* (ATCC 36,906; Van den Berg et al., Bio/Technology, 8:135 (1990)), *K. thermotolerans*, and *K. marxianus*; *yarrowia* (EP 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna et al., J. Basic Microbiol., 28:265-278 [1988]); *Candida*; *Trichoderma reesia* (EP 244,234); *Neurospora crassa* (Case et al., Proc. Natl. Acad. Sci. USA, 76:5259-5263 [1979]); *Schwanniomyces* such as *Schwanniomyces occidentalis* (EP 394,538 published 31 October 1990); and filamentous fungi such as, e.g., *Neurospora*, *Penicillium*, *Tolypocladium* (WO 91/00357 published 10 January 1991), and *Aspergillus* hosts such as *A. nidulans* (Ballance et al., Biochem. Biophys. Res. Commun., 112:284-289 [1983]; Tilburn et al., Gene, 26:205-221 [1983]; Yelton et al., Proc. Natl. Acad. Sci. USA, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, EMBO J., 4:475-479 [1985]). Methylophilic yeasts are suitable herein and include, but are not limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula*, *Candida*, *Kloeckera*, *Pichia*, *Saccharomyces*, *Torulopsis*, and *Rhodotorula*. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, The Biochemistry of Methylophilics, 269 (1982).

Suitable host cells for the expression of glycosylated PRO are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as *Drosophila* S2 and *Spodoptera* Sf9, as well as plant cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen. Virol., 36:59 (1977)); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77:4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod., 23:243-251 (1980)); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

3. Selection and Use of a Replicable Vector

The nucleic acid (e.g., cDNA or genomic DNA) encoding PRO may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination

sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

The PRO may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the PRO-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces* α -factor leaders, the latter described in U.S. Patent No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published 4 April 1990), or the signal described in WO 90/13646 published 15 November 1990. In mammalian cell expression, mammalian signal sequences may be used to direct secretion of the protein, such as signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2 μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells.

Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the PRO-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., Proc. Natl. Acad. Sci. USA, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp1* gene present in the yeast plasmid YRp7 [Stinchcomb et al., Nature, 282:39 (1979); Kingsman et al., Gene, 7:141 (1979); Tschemper et al., Gene, 10:157 (1980)]. The *trp1* gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, Genetics, 85:12 (1977)].

Expression and cloning vectors usually contain a promoter operably linked to the PRO-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include the β -lactamase and lactose promoter systems [Chang et al., Nature, 275:615 (1978); Goeddel et al., Nature, 281:544 (1979)], alkaline phosphatase, a tryptophan (*trp*) promoter system [Goeddel, Nucleic Acids Res., 8:4057 (1980); EP 36,776], and hybrid promoters such as the *tac* promoter [deBoer et al., Proc. Natl. Acad. Sci. USA, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding PRO.

Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., *J. Biol. Chem.*, 255:2073 (1980)] or other glycolytic enzymes [Hess et al., *J. Adv. Enzyme Reg.*, 7:149 (1968); Holland, *Biochemistry*, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytocrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

PRO transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

Transcription of a DNA encoding the PRO by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the PRO coding sequence, but is preferably located at a site 5' from the promoter.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding PRO.

Still other methods, vectors, and host cells suitable for adaptation to the synthesis of PRO in recombinant vertebrate cell culture are described in Gething et al., *Nature*, 293:620-625 (1981); Mantei et al., *Nature*, 281:40-46 (1979); EP 117,060; and EP 117,058.

4. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, *Proc. Natl. Acad. Sci. USA*, 77:5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be

employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

5 Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence PRO polypeptide or against a
10 synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to PRO DNA and encoding a specific antibody epitope.

5. Purification of Polypeptide

Forms of PRO may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by
15 enzymatic cleavage. Cells employed in expression of PRO can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

It may be desired to purify PRO from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as
20 DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the PRO. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, Methods in Enzymology, 182 (1990); Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York
25 (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular PRO produced.

E. Tissue Distribution

The location of tissues expressing the PRO can be identified by determining mRNA expression in various human tissues. The location of such genes provides information about which tissues are most likely
30 to be affected by the stimulating and inhibiting activities of the PRO polypeptides. The location of a gene in a specific tissue also provides sample tissue for the activity blocking assays discussed below.

As noted before, gene expression in various tissues may be measured by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA (Thomas, *Proc. Natl. Acad. Sci. USA*,
77:5201-5205 [1980]), dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled
35 probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes.

Gene expression in various tissues, alternatively, may be measured by immunological methods, such as immunohistochemical staining of tissue sections and assay of cell culture or body fluids, to
40 quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining

and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence of a PRO polypeptide or against a synthetic peptide based on the DNA sequences encoding the PRO polypeptide or against an exogenous sequence fused to a DNA encoding a PRO polypeptide and encoding a specific antibody epitope. General techniques for generating antibodies, and special protocols for Northern blotting and *in situ* hybridization are provided below.

F. Antibody Binding Studies

The activity of the PRO polypeptides can be further verified by antibody binding studies, in which the ability of anti-PRO antibodies to inhibit the effect of the PRO polypeptides, respectively, on tissue cells is tested. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies, the preparation of which will be described hereinbelow.

Antibody binding studies may be carried out in any known assay method, such as competitive binding assays, direct and indirect sandwich assays, and immunoprecipitation assays. Zola, *Monoclonal Antibodies: A Manual of Techniques*, pp.147-158 (CRC Press, Inc., 1987).

Competitive binding assays rely on the ability of a labeled standard to compete with the test sample analyte for binding with a limited amount of antibody. The amount of target protein in the test sample is inversely proportional to the amount of standard that becomes bound to the antibodies. To facilitate determining the amount of standard that becomes bound, the antibodies preferably are insolubilized before or after the competition, so that the standard and analyte that are bound to the antibodies may conveniently be separated from the standard and analyte which remain unbound.

Sandwich assays involve the use of two antibodies, each capable of binding to a different immunogenic portion, or epitope, of the protein to be detected. In a sandwich assay, the test sample analyte is bound by a first antibody which is immobilized on a solid support, and thereafter a second antibody binds to the analyte, thus forming an insoluble three-part complex. See, *e.g.*, US Pat No. 4,376,110. The second antibody may itself be labeled with a detectable moiety (direct sandwich assays) or may be measured using an anti-immunoglobulin antibody that is labeled with a detectable moiety (indirect sandwich assay). For example, one type of sandwich assay is an ELISA assay, in which case the detectable moiety is an enzyme.

For immunohistochemistry, the tissue sample may be fresh or frozen or may be embedded in paraffin and fixed with a preservative such as formalin, for example.

G. Cell-Based Assays

Cell-based assays and animal models for immune related diseases can be used to further understand the relationship between the genes and polypeptides identified herein and the development and pathogenesis of immune related disease.

In a different approach, cells of a cell type known to be involved in a particular immune related disease are transfected with the cDNAs described herein, and the ability of these cDNAs to stimulate or inhibit immune function is analyzed. Suitable cells can be transfected with the desired gene, and monitored for immune function activity. Such transfected cell lines can then be used to test the ability of poly- or monoclonal antibodies or antibody compositions to inhibit or stimulate immune function, for example to modulate T-cell proliferation or inflammatory cell infiltration. Cells transfected with the coding sequences of the genes identified herein can further be used to identify drug candidates for the treatment of immune

related diseases.

In addition, primary cultures derived from transgenic animals (as described below) can be used in the cell-based assays herein, although stable cell lines are preferred. Techniques to derive continuous cell lines from transgenic animals are well known in the art (see, e.g., Small *et al.*, *Mol. Cell. Biol.* 5: 642-648 [1985]).

One suitable cell based assay is the mixed lymphocyte reaction (MLR). *Current Protocols in Immunology*, unit 3.12; edited by J E Coligan, A M Kruisbeek, D H Marglies, E M Shevach, W Strober, National Institutes of Health, Published by John Wiley & Sons, Inc. In this assay, the ability of a test compound to stimulate or inhibit the proliferation of activated T cells is assayed. A suspension of responder T cells is cultured with allogeneic stimulator cells and the proliferation of T cells is measured by uptake of tritiated thymidine. This assay is a general measure of T cell reactivity. Since the majority of T cells respond to and produce IL-2 upon activation, differences in responsiveness in this assay in part reflect differences in IL-2 production by the responding cells. The MLR results can be verified by a standard lymphokine (IL-2) detection assay. *Current Protocols in Immunology*, above, 3.15, 6.3.

A proliferative T cell response in an MLR assay may be due to direct mitogenic properties of an assayed molecule or to external antigen induced activation. Additional verification of the T cell stimulatory activity of the PRO polypeptides can be obtained by a costimulation assay. T cell activation requires an antigen specific signal mediated through the T-cell receptor (TCR) and a costimulatory signal mediated through a second ligand binding interaction, for example, the B7 (CD80, CD86)/CD28 binding interaction. CD28 crosslinking increases lymphokine secretion by activated T cells. T cell activation has both negative and positive controls through the binding of ligands which have a negative or positive effect. CD28 and CTLA-4 are related glycoproteins in the Ig superfamily which bind to B7. CD28 binding to B7 has a positive costimulation effect of T cell activation; conversely, CTLA-4 binding to B7 has a T cell deactivating effect. Chambers, C. A. and Allison, J. P., *Curr. Opin. Immunol.* (1997) 9:396. Schwartz, R. H., *Cell* (1992) 71:1065; Linsey, P. S. and Ledbetter, J. A., *Annu. Rev. Immunol.* (1993) 11:191; June, C. H. *et al*, *Immunol. Today* (1994) 15:321; Jenkins, M. K., *Immunity* (1994) 1:405. In a costimulation assay, the PRO polypeptides are assayed for T cell costimulatory or inhibitory activity.

Direct use of a stimulating compound as in the invention has been validated in experiments with 4-1BB glycoprotein, a member of the tumor necrosis factor receptor family, which binds to a ligand (4-1BBL) expressed on primed T cells and signals T cell activation and growth. Alderson, M. E. *et al.*, *J. Immunol.* (1994) 24:2219.

The use of an agonist stimulating compound has also been validated experimentally. Activation of 4-1BB by treatment with an agonist anti-4-1BB antibody enhances eradication of tumors. Hellstrom, I. and Hellstrom, K. E., *Crit. Rev. Immunol.* (1998) 18:1. Immunoadjuvant therapy for treatment of tumors, described in more detail below, is another example of the use of the stimulating compounds of the invention.

Alternatively, an immune stimulating or enhancing effect can also be achieved by administration of a PRO which has vascular permeability enhancing properties. Enhanced vascular permeability would be beneficial to disorders which can be attenuated by local infiltration of immune cells (e.g., monocytes, eosinophils, PMNs) and inflammation.

On the other hand, PRO polypeptides, as well as other compounds of the invention, which are direct inhibitors of T cell proliferation/activation, lymphokine secretion, and/or vascular permeability can be directly used to suppress the immune response. These compounds are useful to reduce the degree of the immune response and to treat immune related diseases characterized by a hyperactive, superoptimal, or autoimmune response. This use of the compounds of the invention has been validated by the experiments described above in which CTLA-4 binding to receptor B7 deactivates T cells. The direct inhibitory compounds of the invention function in an analogous manner. The use of compound which suppress vascular permeability would be expected to reduce inflammation. Such uses would be beneficial in treating conditions associated with excessive inflammation.

Alternatively, compounds, *e.g.*, antibodies, which bind to stimulating PRO polypeptides and block the stimulating effect of these molecules produce a net inhibitory effect and can be used to suppress the T cell mediated immune response by inhibiting T cell proliferation/activation and/or lymphokine secretion. Blocking the stimulating effect of the polypeptides suppresses the immune response of the mammal. This use has been validated in experiments using an anti-IL2 antibody. In these experiments, the antibody binds to IL2 and blocks binding of IL2 to its receptor thereby achieving a T cell inhibitory effect.

H. Animal Models

The results of the cell based *in vitro* assays can be further verified using *in vivo* animal models and assays for T-cell function. A variety of well known animal models can be used to further understand the role of the genes identified herein in the development and pathogenesis of immune related disease, and to test the efficacy of candidate therapeutic agents, including antibodies, and other antagonists of the native polypeptides, including small molecule antagonists. The *in vivo* nature of such models makes them predictive of responses in human patients. Animal models of immune related diseases include both non-recombinant and recombinant (transgenic) animals. Non-recombinant animal models include, for example, rodent, *e.g.*, murine models. Such models can be generated by introducing cells into syngeneic mice using standard techniques, *e.g.*, subcutaneous injection, tail vein injection, spleen implantation, intraperitoneal implantation, implantation under the renal capsule, *etc.*

Graft-versus-host disease occurs when immunocompetent cells are transplanted into immunosuppressed or tolerant patients. The donor cells recognize and respond to host antigens. The response can vary from life threatening severe inflammation to mild cases of diarrhea and weight loss. Graft-versus-host disease models provide a means of assessing T cell reactivity against MHC antigens and minor transplant antigens. A suitable procedure is described in detail in *Current Protocols in Immunology*, above, unit 4.3.

An animal model for skin allograft rejection is a means of testing the ability of T cells to mediate *in vivo* tissue destruction and a measure of their role in transplant rejection. The most common and accepted models use murine tail-skin grafts. Repeated experiments have shown that skin allograft rejection is mediated by T cells, helper T cells and killer-effector T cells, and not antibodies. Auchincloss, H. Jr. and Sachs, D. H., *Fundamental Immunology*, 2nd ed., W. E. Paul ed., Raven Press, NY, 1989, 889-992. A suitable procedure is described in detail in *Current Protocols in Immunology*, above, unit 4.4. Other transplant rejection models which can be used to test the compounds of the invention are the allogeneic heart

transplant models described by Tanabe, M. *et al*, *Transplantation* (1994) 58:23 and Tinubu, S. A. *et al*, *J. Immunol.* (1994) 4330-4338.

Animal models for delayed type hypersensitivity provides an assay of cell mediated immune function as well. Delayed type hypersensitivity reactions are a T cell mediated *in vivo* immune response characterized by inflammation which does not reach a peak until after a period of time has elapsed after challenge with an antigen. These reactions also occur in tissue specific autoimmune diseases such as multiple sclerosis (MS) and experimental autoimmune encephalomyelitis (EAE, a model for MS). A suitable procedure is described in detail in *Current Protocols in Immunology*, above, unit 4.5.

EAE is a T cell mediated autoimmune disease characterized by T cell and mononuclear cell inflammation and subsequent demyelination of axons in the central nervous system. EAE is generally considered to be a relevant animal model for MS in humans. Bolton, C., *Multiple Sclerosis* (1995) 1:143. Both acute and relapsing-remitting models have been developed. The compounds of the invention can be tested for T cell stimulatory or inhibitory activity against immune mediated demyelinating disease using the protocol described in *Current Protocols in Immunology*, above, units 15.1 and 15.2. See also the models for myelin disease in which oligodendrocytes or Schwann cells are grafted into the central nervous system as described in Duncan, I. D. *et al*, *Molec. Med. Today* (1997) 554-561.

Contact hypersensitivity is a simple delayed type hypersensitivity *in vivo* assay of cell mediated immune function. In this procedure, cutaneous exposure to exogenous haptens which gives rise to a delayed type hypersensitivity reaction which is measured and quantitated. Contact sensitivity involves an initial sensitizing phase followed by an elicitation phase. The elicitation phase occurs when the T lymphocytes encounter an antigen to which they have had previous contact. Swelling and inflammation occur, making this an excellent model of human allergic contact dermatitis. A suitable procedure is described in detail in *Current Protocols in Immunology*, Eds. J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach and W. Strober, John Wiley & Sons, Inc., 1994, unit 4.2. See also Grabbe, S. and Schwarz, T, *Immun. Today* 19 (1): 37-44 (1998).

An animal model for arthritis is collagen-induced arthritis. This model shares clinical, histological and immunological characteristics of human autoimmune rheumatoid arthritis and is an acceptable model for human autoimmune arthritis. Mouse and rat models are characterized by synovitis, erosion of cartilage and subchondral bone. The compounds of the invention can be tested for activity against autoimmune arthritis using the protocols described in *Current Protocols in Immunology*, above, units 15.5. See also the model using a monoclonal antibody to CD18 and VLA-4 integrins described in Issekutz, A.C. *et al*, *Immunology* (1996) 88:569.

A model of asthma has been described in which antigen-induced airway hyper-reactivity, pulmonary eosinophilia and inflammation are induced by sensitizing an animal with ovalbumin and then challenging the animal with the same protein delivered by aerosol. Several animal models (guinea pig, rat, non-human primate) show symptoms similar to atopic asthma in humans upon challenge with aerosol antigens. Murine models have many of the features of human asthma. Suitable procedures to test the compounds of the invention for activity and effectiveness in the treatment of asthma are described by Wolyniec, W. W. *et al*, *Am. J. Respir. Cell Mol. Biol.* (1998) 18:777 and the references cited therein.

Additionally, the compounds of the invention can be tested on animal models for psoriasis like diseases. Evidence suggests a T cell pathogenesis for psoriasis. The compounds of the invention can be tested in the scid/scid mouse model described by Schon, M. P. *et al*, *Nat. Med.* (1997) 3:183, in which the mice demonstrate histopathologic skin lesions resembling psoriasis. Another suitable model is the human skin/scid mouse chimera prepared as described by Nickoloff, B. J. *et al*, *Am. J. Path.* (1995) 146:580.

Recombinant (transgenic) animal models can be engineered by introducing the coding portion of the genes identified herein into the genome of animals of interest, using standard techniques for producing transgenic animals. Animals that can serve as a target for transgenic manipulation include, without limitation, mice, rats, rabbits, guinea pigs, sheep, goats, pigs, and non-human primates, *e.g.*, baboons, chimpanzees and monkeys. Techniques known in the art to introduce a transgene into such animals include pronucleic microinjection (Hoppe and Wanger, U.S. Patent No. 4,873,191); retrovirus-mediated gene transfer into germ lines (*e.g.*, Van der Putten *et al.*, *Proc. Natl. Acad. Sci. USA* 82, 6148-615 [1985]); gene targeting in embryonic stem cells (Thompson *et al.*, *Cell* 56, 313-321 [1989]); electroporation of embryos (Lo, *Mol. Cel. Biol.* 3, 1803-1814 [1983]); sperm-mediated gene transfer (Lavitrano *et al.*, *Cell* 57, 717-73 [1989]). For review, see, for example, U.S. Patent No. 4,736,866.

For the purpose of the present invention, transgenic animals include those that carry the transgene only in part of their cells ("mosaic animals"). The transgene can be integrated either as a single transgene, or in concatamers, *e.g.*, head-to-head or head-to-tail tandems. Selective introduction of a transgene into a particular cell type is also possible by following, for example, the technique of Lasko *et al.*, *Proc. Natl. Acad. Sci. USA* 89, 6232-636 (1992).

The expression of the transgene in transgenic animals can be monitored by standard techniques. For example, Southern blot analysis or PCR amplification can be used to verify the integration of the transgene. The level of mRNA expression can then be analyzed using techniques such as *in situ* hybridization, Northern blot analysis, PCR, or immunocytochemistry.

The animals may be further examined for signs of immune disease pathology, for example by histological examination to determine infiltration of immune cells into specific tissues. Blocking experiments can also be performed in which the transgenic animals are treated with the compounds of the invention to determine the extent of the T cell proliferation stimulation or inhibition of the compounds. In these experiments, blocking antibodies which bind to the PRO polypeptide, prepared as described above, are administered to the animal and the effect on immune function is determined.

Alternatively, "knock out" animals can be constructed which have a defective or altered gene encoding a polypeptide identified herein, as a result of homologous recombination between the endogenous gene encoding the polypeptide and altered genomic DNA encoding the same polypeptide introduced into an embryonic cell of the animal. For example, cDNA encoding a particular polypeptide can be used to clone genomic DNA encoding that polypeptide in accordance with established techniques. A portion of the genomic DNA encoding a particular polypeptide can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see *e.g.*, Thomas and Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (*e.g.*, by electroporation) and cells in which the introduced DNA

has homologously recombined with the endogenous DNA are selected [see *e.g.*, Li *et al.*, *Cell*, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (*e.g.*, a mouse or rat) to form aggregation chimeras [see *e.g.*, Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be
5 implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to
10 absence of the polypeptide.

I. ImmunoAdjuvant Therapy

In one embodiment, the immunostimulating compounds of the invention can be used in immunoAdjuvant therapy for the treatment of tumors (cancer). It is now well established that T cells recognize human tumor specific antigens. One group of tumor antigens, encoded by the MAGE, BAGE and
15 GAGE families of genes, are silent in all adult normal tissues, but are expressed in significant amounts in tumors, such as melanomas, lung tumors, head and neck tumors, and bladder carcinomas. DeSmet, C. *et al.*, (1996) *Proc. Natl. Acad. Sci. USA*, 93:7149. It has been shown that costimulation of T cells induces tumor regression and an antitumor response both *in vitro* and *in vivo*. Melero, I. *et al.*, *Nature Medicine* (1997) 3:682; Kwon, E. D. *et al.*, *Proc. Natl. Acad. Sci. USA* (1997) 94: 8099; Lynch, D. H. *et al.*, *Nature Medicine*
20 (1997) 3:625; Finn, O. J. and Lotze, M. T., *J. Immunol.* (1998) 21:114. The stimulatory compounds of the invention can be administered as adjuvants, alone or together with a growth regulating agent, cytotoxic agent or chemotherapeutic agent, to stimulate T cell proliferation/activation and an antitumor response to tumor antigens. The growth regulating, cytotoxic, or chemotherapeutic agent may be administered in conventional amounts using known administration regimes. Immunostimulating activity by the compounds of the
25 invention allows reduced amounts of the growth regulating, cytotoxic, or chemotherapeutic agents thereby potentially lowering the toxicity to the patient.

J. Screening Assays for Drug Candidates

Screening assays for drug candidates are designed to identify compounds that bind to or complex with the polypeptides encoded by the genes identified herein or a biologically active fragment thereof, or
30 otherwise interfere with the interaction of the encoded polypeptides with other cellular proteins. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds, including peptides, preferably soluble peptides, (poly)peptide-immunoglobulin fusions, and, in particular, antibodies including, without limitation, poly- and
35 monoclonal antibodies and antibody fragments, single-chain antibodies, anti-idiotypic antibodies, and chimeric or humanized versions of such antibodies or fragments, as well as human antibodies and antibody fragments. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the art. All assays are common in that they call for contacting the drug candidate with a polypeptide encoded by a
40 nucleic acid identified herein under conditions and for a time sufficient to allow these two components to

interact.

In binding assays, the interaction is binding and the complex formed can be isolated or detected in the reaction mixture. In a particular embodiment, the polypeptide encoded by the gene identified herein or the drug candidate is immobilized on a solid phase, *e.g.*, on a microtiter plate, by covalent or non-covalent attachments. Non-covalent attachment generally is accomplished by coating the solid surface with a solution of the polypeptide and drying. Alternatively, an immobilized antibody, *e.g.*, a monoclonal antibody, specific for the polypeptide to be immobilized can be used to anchor it to a solid surface. The assay is performed by adding the non-immobilized component, which may be labeled by a detectable label, to the immobilized component, *e.g.*, the coated surface containing the anchored component. When the reaction is complete, the non-reacted components are removed, *e.g.*, by washing, and complexes anchored on the solid surface are detected. When the originally non-immobilized component carries a detectable label, the detection of label immobilized on the surface indicates that complexing occurred. Where the originally non-immobilized component does not carry a label, complexing can be detected, for example, by using a labelled antibody specifically binding the immobilized complex.

If the candidate compound interacts with but does not bind to a particular protein encoded by a gene identified herein, its interaction with that protein can be assayed by methods well known for detecting protein-protein interactions. Such assays include traditional approaches, such as, cross-linking, co-immunoprecipitation, and co-purification through gradients or chromatographic columns. In addition, protein-protein interactions can be monitored by using a yeast-based genetic system described by Fields and co-workers [Fields and Song, *Nature (London)* 340, 245-246 (1989); Chien *et al.*, *Proc. Natl. Acad. Sci. USA* 88, 9578-9582 (1991)] as disclosed by Chevray and Nathans, *Proc. Natl. Acad. Sci. USA* 89, 5789-5793 (1991). Many transcriptional activators, such as yeast GAL4, consist of two physically discrete modular domains, one acting as the DNA-binding domain, while the other one functioning as the transcription activation domain. The yeast expression system described in the foregoing publications (generally referred to as the "two-hybrid system") takes advantage of this property, and employs two hybrid proteins, one in which the target protein is fused to the DNA-binding domain of GAL4, and another, in which candidate activating proteins are fused to the activation domain. The expression of a GAL1-*lacZ* reporter gene under control of a GAL4-activated promoter depends on reconstitution of GAL4 activity via protein-protein interaction. Colonies containing interacting polypeptides are detected with a chromogenic substrate for β -galactosidase. A complete kit (MATCHMAKERTM) for identifying protein-protein interactions between two specific proteins using the two-hybrid technique is commercially available from Clontech. This system can also be extended to map protein domains involved in specific protein interactions as well as to pinpoint amino acid residues that are crucial for these interactions.

In order to find compounds that interfere with the interaction of a gene identified herein and other intra- or extracellular components can be tested, a reaction mixture is usually prepared containing the product of the gene and the intra- or extracellular component under conditions and for a time allowing for the interaction and binding of the two products. To test the ability of a test compound to inhibit binding, the reaction is run in the absence and in the presence of the test compound. In addition, a placebo may be added to a third reaction mixture, to serve as positive control. The binding (complex formation) between the test compound and the intra- or extracellular component present in the mixture is monitored as described above.

The formation of a complex in the control reaction(s) but not in the reaction mixture containing the test compound indicates that the test compound interferes with the interaction of the test compound and its reaction partner.

K. Compositions and Methods for the Treatment of Immune Related Diseases

5 The compositions useful in the treatment of immune related diseases include, without limitation, proteins, antibodies, small organic molecules, peptides, phosphopeptides, antisense and ribozyme molecules, triple helix molecules, *etc.* that inhibit or stimulate immune function, for example, T cell proliferation/activation, lymphokine release, or immune cell infiltration.

For example, antisense RNA and RNA molecules act to directly block the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. When antisense DNA is used, 10 oligodeoxyribonucleotides derived from the translation initiation site, *e.g.*, between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by 15 endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques. For further details see, *e.g.*, Rossi, *Current Biology* 4, 469-471 (1994), and PCT publication No. WO 97/33551 (published September 18, 1997).

Nucleic acid molecules in triple helix formation used to inhibit transcription should be single-stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is designed 20 such that it promotes triple helix formation via Hoogsteen base pairing rules, which generally require sizeable stretches of purines or pyrimidines on one strand of a duplex. For further details see, *e.g.*, PCT publication No. WO 97/33551, *supra*.

These molecules can be identified by any or any combination of the screening assays discussed above and/or by any other screening techniques well known for those skilled in the art.

25 L. Anti-PRO Antibodies

The present invention further provides anti-PRO antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

1. Polyclonal Antibodies

30 The anti-PRO antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the PRO polypeptide or a fusion protein thereof. It may be useful to 35 conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without 40 undue experimentation.

2. Monoclonal Antibodies

The anti-PRO antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.

The immunizing agent will typically include the PRO polypeptide or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against PRO. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, supra]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown *in vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Patent No. 4,816,567; Morrison et al., *supra*] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

In vitro methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

3. Human and Humanized Antibodies

The anti-PRO antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.*, 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-327 (1988); Verhoeyen et al., *Science*, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*, 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985) and Boerner et al., *J. Immunol.*, 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks et al., *Bio/Technology* 10, 779-783 (1992); Lonberg et al., *Nature* 368 856-859 (1994); Morrison, *Nature* 368, 812-13 (1994); Fishwild et al., *Nature Biotechnology* 14, 845-51 (1996); Neuberger, *Nature Biotechnology* 14, 826 (1996); Lonberg and Huszar, *Intern. Rev. Immunol.* 13 65-93 (1995).

The antibodies may also be affinity matured using known selection and/or mutagenesis methods as described above. Preferred affinity matured antibodies have an affinity which is five times, more preferably 10 times, even more preferably 20 or 30 times greater than the starting antibody (generally murine, humanized or human) from which the matured antibody is prepared.

4. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the PRO, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuello, *Nature*, 305:537-539 (1983)]. Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by

affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., EMBO J., 10:3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Fab' fragments may be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various technique for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form

the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger *et al.*, Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber *et al.*, J. Immunol. 152:5368 (1994). Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt *et al.*, J. Immunol. 147:60 (1991).

Exemplary bispecific antibodies may bind to two different epitopes on a given PRO polypeptide herein. Alternatively, an anti-PRO polypeptide arm may be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular PRO polypeptide. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express a particular PRO polypeptide. These antibodies possess a PRO-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the PRO polypeptide and further binds tissue factor (TF).

5. Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Patent No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

6. Effector Function Engineering

It may be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) may be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron *et al.*; J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff *et al.* Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson *et al.*, Anti-Cancer Drug Design, 3: 219-230 (1989).

7. Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

5 Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A
10 variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT),
15 bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in
20 Vitetta *et al.*, Science, **238**: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody may be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient,
25 followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is conjugated to a cytotoxic agent (e.g., a radionucleotide).

8. Immunoliposomes

The antibodies disclosed herein may also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein *et al.*, Proc. Natl. Acad. Sci. USA, **82**: 3688 (1985); Hwang *et al.*, Proc. Natl. Acad. Sci. USA, **77**: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized
35 phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin *et al.*, J. Biol. Chem., **257**: 286-288 (1982) via a disulfide-interchange reaction. A chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. See Gabizon *et al.*, J. National Cancer Inst., **81**(19): 1484 (1989).

40 M. Pharmaceutical Compositions

The active PRO molecules of the invention (*e.g.*, PRO polypeptides, anti-PRO antibodies, and/or variants of each) as well as other molecules identified by the screening assays disclosed above, can be administered for the treatment of immune related diseases, in the form of pharmaceutical compositions.

Therapeutic formulations of the active PRO molecule, preferably a polypeptide or antibody of the invention, are prepared for storage by mixing the active molecule having the desired degree of purity with optional pharmaceutically acceptable carriers, excipients or stabilizers (*Remington's Pharmaceutical Sciences* 16th edition, Osol, A. Ed. [1980]), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (*e.g.*, Zn-protein complexes); and/or non-ionic surfactants such as TWEENTM, PLURONICSTM or polyethylene glycol (PEG).

Compounds identified by the screening assays disclosed herein can be formulated in an analogous manner, using standard techniques well known in the art.

Lipofections or liposomes can also be used to deliver the PRO molecule into cells. Where antibody fragments are used, the smallest inhibitory fragment which specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable region sequences of an antibody, peptide molecules can be designed which retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology (see, *e.g.*, Marasco *et al.*, *Proc. Natl. Acad. Sci. USA* 90, 7889-7893 [1993]).

The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition may comprise a cytotoxic agent, cytokine or growth inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

The active PRO molecules may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in *Remington's Pharmaceutical Sciences* 16th edition, Osol, A. Ed. (1980).

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

Sustained-release preparations or the PRO molecules may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, *e.g.*, films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ -ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOTTM (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated antibodies remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S-S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

N. Methods of Treatment

It is contemplated that the polypeptides, antibodies and other active compounds of the present invention may be used to treat various immune related diseases and conditions, such as T cell mediated diseases, including those characterized by infiltration of inflammatory cells into a tissue, stimulation of T-cell proliferation, inhibition of T-cell proliferation, increased or decreased vascular permeability or the inhibition thereof.

Exemplary conditions or disorders to be treated with the polypeptides, antibodies and other compounds of the invention, include, but are not limited to systemic lupus erythematosus, rheumatoid arthritis, juvenile chronic arthritis, osteoarthritis, spondyloarthropathies, systemic sclerosis (scleroderma), idiopathic inflammatory myopathies (dermatomyositis, polymyositis), Sjögren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic anemia (immune pancytopenia, paroxysmal nocturnal hemoglobinuria), autoimmune thrombocytopenia (idiopathic thrombocytopenic purpura, immune-mediated thrombocytopenia), thyroiditis (Grave's disease, Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, atrophic thyroiditis), diabetes mellitus, immune-mediated renal disease (glomerulonephritis, tubulointerstitial nephritis), demyelinating diseases of the central and peripheral nervous systems such as multiple sclerosis, idiopathic demyelinating polyneuropathy or Guillain-Barré syndrome, and chronic inflammatory demyelinating polyneuropathy, hepatobiliary diseases such as infectious hepatitis (hepatitis A, B, C, D, E and other non-hepatotropic viruses), autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, and sclerosing cholangitis, inflammatory bowel disease (ulcerative colitis: Crohn's disease), gluten-sensitive enteropathy, and Whipple's disease, autoimmune or immune-mediated skin diseases including bullous skin diseases, erythema multiforme and contact dermatitis, psoriasis, allergic diseases such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria, immunologic diseases of the lung such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonitis, transplantation associated diseases including graft rejection and graft-versus-host-disease.

In systemic lupus erythematosus, the central mediator of disease is the production of auto-reactive antibodies to self proteins/tissues and the subsequent generation of immune-mediated inflammation. Antibodies either directly or indirectly mediate tissue injury. Though T lymphocytes have not been shown to be directly involved in tissue damage, T lymphocytes are required for the development of auto-reactive antibodies. The genesis of the disease is thus T lymphocyte dependent. Multiple organs and systems are affected clinically including kidney, lung, musculoskeletal system, mucocutaneous, eye, central nervous system, cardiovascular system, gastrointestinal tract, bone marrow and blood.

Rheumatoid arthritis (RA) is a chronic systemic autoimmune inflammatory disease that mainly involves the synovial membrane of multiple joints with resultant injury to the articular cartilage. The pathogenesis is T lymphocyte dependent and is associated with the production of rheumatoid factors, auto-antibodies directed against self IgG, with the resultant formation of immune complexes that attain high levels in joint fluid and blood. These complexes in the joint may induce the marked infiltrate of lymphocytes and monocytes into the synovium and subsequent marked synovial changes; the joint space/fluid is infiltrated by similar cells with the addition of numerous neutrophils. Tissues affected are primarily the joints, often in symmetrical pattern. However, extra-articular disease also occurs in two major forms. One form is the development of extra-articular lesions with ongoing progressive joint disease and typical lesions of pulmonary fibrosis, vasculitis, and cutaneous ulcers. The second form of extra-articular disease is the so called Felty's syndrome which occurs late in the RA disease course, sometimes after joint disease has become quiescent, and involves the presence of neutropenia, thrombocytopenia and splenomegaly. This can be accompanied by vasculitis in multiple organs with formations of infarcts, skin ulcers and gangrene. Patients often also develop rheumatoid nodules in the subcutis tissue overlying affected joints; the nodules late stage have necrotic centers surrounded by a mixed inflammatory cell infiltrate. Other manifestations which can occur in RA include: pericarditis, pleuritis, coronary arteritis, interstitial pneumonitis with pulmonary fibrosis, keratoconjunctivitis sicca, and rheumatoid nodules.

Juvenile chronic arthritis is a chronic idiopathic inflammatory disease which begins often at less than 16 years of age. Its phenotype has some similarities to RA; some patients which are rheumatoid factor positive are classified as juvenile rheumatoid arthritis. The disease is sub-classified into three major categories: pauciarticular, polyarticular, and systemic. The arthritis can be severe and is typically destructive and leads to joint ankylosis and retarded growth. Other manifestations can include chronic anterior uveitis and systemic amyloidosis.

Spondyloarthropathies are a group of disorders with some common clinical features and the common association with the expression of HLA-B27 gene product. The disorders include: ankylosing spondylitis, Reiter's syndrome (reactive arthritis), arthritis associated with inflammatory bowel disease, spondylitis associated with psoriasis, juvenile onset spondyloarthropathy and undifferentiated spondyloarthropathy. Distinguishing features include sacroileitis with or without spondylitis; inflammatory asymmetric arthritis; association with HLA-B27 (a serologically defined allele of the HLA-B locus of class I MHC); ocular inflammation, and absence of autoantibodies associated with other rheumatoid disease. The cell most implicated as key to induction of the disease is the CD8+ T lymphocyte, a cell which targets antigen presented by class I MHC molecules. CD8+ T cells may react against the class I MHC allele HLA-B27 as if it were a foreign peptide expressed by MHC class I molecules. It has been hypothesized that an

epitope of HLA-B27 may mimic a bacterial or other microbial antigenic epitope and thus induce a CD8+ T cells response.

Systemic sclerosis (scleroderma) has an unknown etiology. A hallmark of the disease is induration of the skin; likely this is induced by an active inflammatory process. Scleroderma can be localized or systemic; vascular lesions are common and endothelial cell injury in the microvasculature is an early and important event in the development of systemic sclerosis; the vascular injury may be immune mediated. An immunologic basis is implied by the presence of mononuclear cell infiltrates in the cutaneous lesions and the presence of anti-nuclear antibodies in many patients. ICAM-1 is often upregulated on the cell surface of fibroblasts in skin lesions suggesting that T cell interaction with these cells may have a role in the pathogenesis of the disease. Other organs involved include: the gastrointestinal tract: smooth muscle atrophy and fibrosis resulting in abnormal peristalsis/motility; kidney: concentric subendothelial intimal proliferation affecting small arcuate and interlobular arteries with resultant reduced renal cortical blood flow, results in proteinuria, azotemia and hypertension; skeletal muscle: atrophy, interstitial fibrosis; inflammation; lung: interstitial pneumonitis and interstitial fibrosis; and heart: contraction band necrosis, scarring/fibrosis.

Idiopathic inflammatory myopathies including dermatomyositis, polymyositis and others are disorders of chronic muscle inflammation of unknown etiology resulting in muscle weakness. Muscle injury/inflammation is often symmetric and progressive. Autoantibodies are associated with most forms. These myositis-specific autoantibodies are directed against and inhibit the function of components, proteins and RNA's, involved in protein synthesis.

Sjögren's syndrome is due to immune-mediated inflammation and subsequent functional destruction of the tear glands and salivary glands. The disease can be associated with or accompanied by inflammatory connective tissue diseases. The disease is associated with autoantibody production against Ro and La antigens, both of which are small RNA-protein complexes. Lesions result in keratoconjunctivitis sicca, xerostomia, with other manifestations or associations including biliary cirrhosis, peripheral or sensory neuropathy, and palpable purpura.

Systemic vasculitis are diseases in which the primary lesion is inflammation and subsequent damage to blood vessels which results in ischemia/necrosis/degeneration to tissues supplied by the affected vessels and eventual end-organ dysfunction in some cases. Vasculitides can also occur as a secondary lesion or sequelae to other immune-inflammatory mediated diseases such as rheumatoid arthritis, systemic sclerosis, etc., particularly in diseases also associated with the formation of immune complexes. Diseases in the primary systemic vasculitis group include: systemic necrotizing vasculitis: polyarteritis nodosa, allergic angiitis and granulomatosis, polyangiitis; Wegener's granulomatosis; lymphomatoid granulomatosis; and giant cell arteritis. Miscellaneous vasculitides include: mucocutaneous lymph node syndrome (MLNS or Kawasaki's disease), isolated CNS vasculitis, Behet's disease, thromboangiitis obliterans (Buerger's disease) and cutaneous necrotizing venulitis. The pathogenic mechanism of most of the types of vasculitis listed is believed to be primarily due to the deposition of immunoglobulin complexes in the vessel wall and subsequent induction of an inflammatory response either via ADCC, complement activation, or both.

Sarcoidosis is a condition of unknown etiology which is characterized by the presence of epithelioid granulomas in nearly any tissue in the body; involvement of the lung is most common. The pathogenesis

involves the persistence of activated macrophages and lymphoid cells at sites of the disease with subsequent chronic sequelae resultant from the release of locally and systemically active products released by these cell types.

Autoimmune hemolytic anemia including autoimmune hemolytic anemia, immune pancytopenia, and paroxysmal nocturnal hemoglobinuria is a result of production of antibodies that react with antigens expressed on the surface of red blood cells (and in some cases other blood cells including platelets as well) and is a reflection of the removal of those antibody coated cells via complement mediated lysis and/or ADCC/Fc-receptor-mediated mechanisms.

In autoimmune thrombocytopenia including thrombocytopenic purpura, and immune-mediated thrombocytopenia in other clinical settings, platelet destruction/removal occurs as a result of either antibody or complement attaching to platelets and subsequent removal by complement lysis, ADCC or FC-receptor mediated mechanisms.

Thyroiditis including Grave's disease, Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, and atrophic thyroiditis, are the result of an autoimmune response against thyroid antigens with production of antibodies that react with proteins present in and often specific for the thyroid gland. Experimental models exist including spontaneous models: rats (BUF and BB rats) and chickens (obese chicken strain); inducible models: immunization of animals with either thyroglobulin, thyroid microsomal antigen (thyroid peroxidase).

Type I diabetes mellitus or insulin-dependent diabetes is the autoimmune destruction of pancreatic islet β cells; this destruction is mediated by auto-antibodies and auto-reactive T cells. Antibodies to insulin or the insulin receptor can also produce the phenotype of insulin-non-responsiveness.

Immune mediated renal diseases, including glomerulonephritis and tubulointerstitial nephritis, are the result of antibody or T lymphocyte mediated injury to renal tissue either directly as a result of the production of autoreactive antibodies or T cells against renal antigens or indirectly as a result of the deposition of antibodies and/or immune complexes in the kidney that are reactive against other, non-renal antigens. Thus other immune-mediated diseases that result in the formation of immune-complexes can also induce immune mediated renal disease as an indirect sequelae. Both direct and indirect immune mechanisms result in inflammatory response that produces/induces lesion development in renal tissues with resultant organ function impairment and in some cases progression to renal failure. Both humoral and cellular immune mechanisms can be involved in the pathogenesis of lesions.

Demyelinating diseases of the central and peripheral nervous systems, including Multiple Sclerosis; idiopathic demyelinating polyneuropathy or Guillain-Barré syndrome; and Chronic Inflammatory Demyelinating Polyneuropathy, are believed to have an autoimmune basis and result in nerve demyelination as a result of damage caused to oligodendrocytes or to myelin directly. In MS there is evidence to suggest that disease induction and progression is dependent on T lymphocytes. Multiple Sclerosis is a demyelinating disease that is T lymphocyte-dependent and has either a relapsing-remitting course or a chronic progressive course. The etiology is unknown; however, viral infections, genetic predisposition, environment, and autoimmunity all contribute. Lesions contain infiltrates of predominantly T lymphocyte mediated, microglial cells and infiltrating macrophages; CD4+ T lymphocytes are the predominant cell type at lesions.

The mechanism of oligodendrocyte cell death and subsequent demyelination is not known but is likely T lymphocyte driven.

Inflammatory and Fibrotic Lung Disease, including Eosinophilic Pneumonias; Idiopathic Pulmonary Fibrosis, and Hypersensitivity Pneumonitis may involve a dysregulated immune-inflammatory response. Inhibition of that response would be of therapeutic benefit.

Autoimmune or Immune-mediated Skin Disease including Bullous Skin Diseases, Erythema Multiforme, and Contact Dermatitis are mediated by auto-antibodies, the genesis of which is T lymphocyte-dependent.

Psoriasis is a T lymphocyte-mediated inflammatory disease. Lesions contain infiltrates of T lymphocytes, macrophages and antigen processing cells, and some neutrophils.

Allergic diseases, including asthma; allergic rhinitis; atopic dermatitis; food hypersensitivity; and urticaria are T lymphocyte dependent. These diseases are predominantly mediated by T lymphocyte induced inflammation, IgE mediated-inflammation or a combination of both.

Transplantation associated diseases, including Graft rejection and Graft-Versus-Host-Disease (GVHD) are T lymphocyte-dependent; inhibition of T lymphocyte function is ameliorative.

Other diseases in which intervention of the immune and/or inflammatory response have benefit are infectious disease including but not limited to viral infection (including but not limited to AIDS, hepatitis A, B, C, D, E and herpes) bacterial infection, fungal infections, and protozoal and parasitic infections (molecules (or derivatives/agonists) which stimulate the MLR can be utilized therapeutically to enhance the immune response to infectious agents), diseases of immunodeficiency (molecules/derivatives/agonists) which stimulate the MLR can be utilized therapeutically to enhance the immune response for conditions of inherited, acquired, infectious induced (as in HIV infection), or iatrogenic (*i.e.*, as from chemotherapy) immunodeficiency, and neoplasia.

It has been demonstrated that some human cancer patients develop an antibody and/or T lymphocyte response to antigens on neoplastic cells. It has also been shown in animal models of neoplasia that enhancement of the immune response can result in rejection or regression of that particular neoplasm. Molecules that enhance the T lymphocyte response in the MLR have utility *in vivo* in enhancing the immune response against neoplasia. Molecules which enhance the T lymphocyte proliferative response in the MLR (or small molecule agonists or antibodies that affected the same receptor in an agonistic fashion) can be used therapeutically to treat cancer. Molecules that inhibit the lymphocyte response in the MLR also function *in vivo* during neoplasia to suppress the immune response to a neoplasm; such molecules can either be expressed by the neoplastic cells themselves or their expression can be induced by the neoplasm in other cells. Antagonism of such inhibitory molecules (either with antibody, small molecule antagonists or other means) enhances immune-mediated tumor rejection.

Additionally, inhibition of molecules with proinflammatory properties may have therapeutic benefit in reperfusion injury; stroke; myocardial infarction; atherosclerosis; acute lung injury; hemorrhagic shock; burn; sepsis/septic shock; acute tubular necrosis; endometriosis; degenerative joint disease and pancreatitis.

The compounds of the present invention, *e.g.*, polypeptides or antibodies, are administered to a mammal, preferably a human, in accord with known methods, such as intravenous administration as a bolus or by continuous infusion over a period of time, by intramuscular, intraperitoneal, intracerebrospinal,

subcutaneous, intra-articular, intrasynovial, intrathecal, oral, topical, or inhalation (intranasal, intrapulmonary) routes. Intravenous or inhaled administration of polypeptides and antibodies is preferred.

In immunoadjuvant therapy, other therapeutic regimens, such administration of an anti-cancer agent, may be combined with the administration of the proteins, antibodies or compounds of the instant invention. For example, the patient to be treated with a the immunoadjuvant of the invention may also receive an anti-cancer agent (chemotherapeutic agent) or radiation therapy. Preparation and dosing schedules for such chemotherapeutic agents may be used according to manufacturers' instructions or as determined empirically by the skilled practitioner. Preparation and dosing schedules for such chemotherapy are also described in *Chemotherapy Service* Ed., M.C. Perry, Williams & Wilkins, Baltimore, MD (1992). The chemotherapeutic agent may precede, or follow administration of the immunoadjuvant or may be given simultaneously therewith. Additionally, an anti-estrogen compound such as tamoxifen or an anti-progesterone such as onapristone (see, EP 616812) may be given in dosages known for such molecules.

It may be desirable to also administer antibodies against other immune disease associated or tumor associated antigens, such as antibodies which bind to CD20, CD11a, CD18, ErbB2, EGFR, ErbB3, ErbB4, or vascular endothelial factor (VEGF). Alternatively, or in addition, two or more antibodies binding the same or two or more different antigens disclosed herein may be coadministered to the patient. Sometimes, it may be beneficial to also administer one or more cytokines to the patient. In one embodiment, the PRO polypeptides are coadministered with a growth inhibitory agent. For example, the growth inhibitory agent may be administered first, followed by a PRO polypeptide. However, simultaneous administration or administration first is also contemplated. Suitable dosages for the growth inhibitory agent are those presently used and may be lowered due to the combined action (synergy) of the growth inhibitory agent and the PRO polypeptide.

For the treatment or reduction in the severity of immune related disease, the appropriate dosage of an a compound of the invention will depend on the type of disease to be treated, as defined above, the severity and course of the disease, whether the agent is administered for preventive or therapeutic purposes, previous therapy, the patient's clinical history and response to the compound, and the discretion of the attending physician. The compound is suitably administered to the patient at one time or over a series of treatments.

For example, depending on the type and severity of the disease, about 1 µg/kg to 15 mg/kg (e.g., 0.1-20 mg/kg) of polypeptide or antibody is an initial candidate dosage for administration to the patient, whether, for example, by one or more separate administrations, or by continuous infusion. A typical daily dosage might range from about 1 µg/kg to 100 mg/kg or more, depending on the factors mentioned above. For repeated administrations over several days or longer, depending on the condition, the treatment is sustained until a desired suppression of disease symptoms occurs. However, other dosage regimens may be useful. The progress of this therapy is easily monitored by conventional techniques and assays.

O. Articles of Manufacture

In another embodiment of the invention, an article of manufacture containing materials (e.g., comprising a PRO molecule) useful for the diagnosis or treatment of the disorders described above is provided. The article of manufacture comprises a container and an instruction. Suitable containers include, for example, bottles, vials, syringes, and test tubes. The containers may be formed from a variety of

materials such as glass or plastic. The container holds a composition which is effective for diagnosing or treating the condition and may have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). The active agent in the composition is usually a polypeptide or an antibody of the invention. An instruction or label on, or associated with, the container indicates that the composition is used for diagnosing or treating the condition of choice. The article of manufacture may further comprise a second container comprising a pharmaceutically-acceptable buffer, such as phosphate-buffered saline, Ringer's solution and dextrose solution. It may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, syringes, and package inserts with instructions for use.

P. Diagnosis and Prognosis of Immune Related Disease

Cell surface proteins, such as proteins which are overexpressed in certain immune related diseases, are excellent targets for drug candidates or disease treatment. The same proteins along with secreted proteins encoded by the genes amplified in immune related disease states find additional use in the diagnosis and prognosis of these diseases. For example, antibodies directed against the protein products of genes amplified in multiple sclerosis, rheumatoid arthritis, or another immune related disease, can be used as diagnostics or prognostics.

For example, antibodies, including antibody fragments, can be used to qualitatively or quantitatively detect the expression of proteins encoded by amplified or overexpressed genes ("marker gene products"). The antibody preferably is equipped with a detectable, *e.g.*, fluorescent label, and binding can be monitored by light microscopy, flow cytometry, fluorimetry, or other techniques known in the art. These techniques are particularly suitable, if the overexpressed gene encodes a cell surface protein. Such binding assays are performed essentially as described above.

In situ detection of antibody binding to the marker gene products can be performed, for example, by immunofluorescence or immunoelectron microscopy. For this purpose, a histological specimen is removed from the patient, and a labeled antibody is applied to it, preferably by overlaying the antibody on a biological sample. This procedure also allows for determining the distribution of the marker gene product in the tissue examined. It will be apparent for those skilled in the art that a wide variety of histological methods are readily available for *in situ* detection.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, VA.

EXAMPLE 1: Microarray analysis of stimulated T-cells

Nucleic acid microarrays, often containing thousands of gene sequences, are useful for identifying differentially expressed genes in diseased tissues as compared to their normal counterparts. Using nucleic acid microarrays, test and control mRNA samples from test and control tissue samples are reverse transcribed and labeled to generate cDNA probes. The cDNA probes are then hybridized to an array of nucleic acids immobilized on a solid support. The array is configured such that the sequence and position of each member of the array is known. For example, a selection of genes known to be expressed in certain disease states may be arrayed on a solid support. Hybridization of a labeled probe with a particular array member indicates that the sample from which the probe was derived expresses that gene. If the hybridization signal of a probe from a test (in this instance, activated CD4+ T cells) sample is greater than hybridization signal of a probe from a control (in this instance, non-stimulated CD4 + T cells) sample, the gene or genes overexpressed in the test tissue are identified. The implication of this result is that an overexpressed protein in a test tissue is useful not only as a diagnostic marker for the presence of the disease condition, but also as a therapeutic target for treatment of the disease condition.

The methodology of hybridization of nucleic acids and microarray technology is well known in the art. In one example, the specific preparation of nucleic acids for hybridization and probes, slides, and hybridization conditions are all detailed in PCT Patent Application Serial No. PCT/US01/10482, filed on March 30, 2001 and which is herein incorporated by reference.

In this experiment, CD4+ T cells were purified from a single donor using the RossetteSep™ protocol from (Stem Cell Technologies, Vancouver BC) which contains anti-CD8, anti-CD16, anti-CD19, anti-CD36 and anti-CD56 antibodies used to produce a population of isolated CD4 + T cells. Isolated CD4+ T cells were activated with an anti-CD3 antibody (used at a concentration that does not stimulate proliferation) together with either ICAM-1, anti-CD28 antibody or a combination of both ICAM-1, anti-CD28. At 24 or 72 hours cells were harvested, RNA extracted and analysis run on Affimax (Affymetrix Inc., Santa Clara, CA) U95A chips. Non-stimulated (resting) cells were harvested immediately after purification, and subjected to the same analysis. Genes were compared whose expression was upregulated at either of the two timepoints in activated vs. resting cells. These genes were also compared to a panel of normal tissues. A normal "universal" tissue control sample was prepared by pooling non-cancerous, human tissues including liver, kidney, and lung. Microarray hybridization experiments using the universal control samples generated a linear plot in a 2-color analysis. The slope of the line generated in a 2-color analysis was then used to normalize the ratios of (test:control detection) within each experiment. The normalized ratios from various experiments were then compared and used to identify clustering of gene expression. Thus, the universal control sample not only allowed effective relative gene expression determinations in a simple 2-sample comparison, it also allowed multi-sample comparisons across several experiments.

Below are the results of these experiments, demonstrating that various PRO polypeptides of the present invention are significantly overexpressed in isolated CD4 + T cells activated by ICAM-1, anti-CD 28, or a combination of ICAM-1/anti-CD28 as compared to isolated resting CD4+ T cells. As described above, these data demonstrate that the PRO polypeptides of the present invention are useful not only as diagnostic markers for the presence of one or more immune disorders, but also serve as therapeutic targets for the treatment of those immune disorders.

Figures 1-280 are the PRO polypeptides increased by ICAM-1/anti-CD28.

Figures 281-496 are the PRO polypeptides increased by ICAM-1.

Figures 497-742 are the PRO polypeptides increased by anti-CD28.

5 EXAMPLE 2: Use of PRO as a hybridization probe

The following method describes use of a nucleotide sequence encoding PRO as a hybridization probe.

DNA comprising the coding sequence of full-length or mature PRO as disclosed herein is employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of PRO) in
10 human tissue cDNA libraries or human tissue genomic libraries.

Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled PRO-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing
15 of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

DNAs having a desired sequence identity with the DNA encoding full-length native sequence PRO can then be identified using standard techniques known in the art.

EXAMPLE 3: Expression of PRO in *E. coli*

20 This example illustrates preparation of an unglycosylated form of PRO by recombinant expression in *E. coli*.

The DNA sequence encoding PRO is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is
25 pBR322 (derived from *E. coli*; see Bolivar et al., *Gene*, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the PRO coding region, lambda transcriptional terminator,
30 and an argU gene.

The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., *supra*. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and
DNA sequencing.

35 Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the

solubilized PRO protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

PRO may be expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding PRO is initially amplified using selected PCR primers. The primers will contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences are then ligated into an expression vector, which is used to transform an *E. coli* host based on strain 52 (W3110 fuhA(tonA) lon galE rpoHts(htpRts) clpP(lacIq). Transformants are first grown in LB containing 50 mg/ml carbenicillin at 30°C with shaking until an O.D.600 of 3-5 is reached. Cultures are then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g (NH₄)₂SO₄, 0.71 g sodium citrate•2H₂O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM MgSO₄) and grown for approximately 20-30 hours at 30°C with shaking. Samples are removed to verify expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets are frozen until purification and refolding.

E. coli paste from 0.5 to 1 L fermentations (6-10 g pellets) is resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution is stirred overnight at 4°C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution is centrifuged at 40,000 rpm in a Beckman Ultracentrifuge for 30 min. The supernatant is diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. The clarified extract is loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column is washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein is eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein are pooled and stored at 4°C. Protein concentration is estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

The proteins are refolded by diluting the sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes are chosen so that the final protein concentration is between 50 to 100 micrograms/ml. The refolding solution is stirred gently at 4°C for 12-36 hours. The refolding reaction is quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution is filtered through a 0.22 micron filter and acetonitrile is added to 2-10% final concentration. The refolded protein is chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance are analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein are pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

Fractions containing the desired folded PRO polypeptide are pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins are formulated into 20 mM Hepes, pH 6.8 with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

5 Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 4: Expression of PRO in mammalian cells

This example illustrates preparation of a potentially glycosylated form of PRO by recombinant expression in mammalian cells.

10 The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector. Optionally, the PRO DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the PRO DNA using ligation methods such as described in Sambrook et al., *supra*. The resulting vector is called pRK5-PRO.

15 In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 µg pRK5-PRO DNA is mixed with about 1 µg DNA encoding the VA RNA gene [Thimmappaya et al., *Cell*, 31:543 (1982)] and dissolved in 500 µl of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M CaCl₂. To this mixture is added, dropwise, 500 µl of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM NaPO₄, and a precipitate is allowed to form for 10 minutes
20 at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

Approximately 24 hours after the transfections, the culture medium is removed and replaced with
25 culture medium (alone) or culture medium containing 200 µCi/ml ³⁵S-cysteine and 200 µCi/ml ³⁵S-methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of PRO polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

30 In an alternative technique, PRO may be introduced into 293 cells transiently using the dextran sulfate method described by Somparyrac et al., *Proc. Natl. Acad. Sci.*, 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 µg pRK5-PRO DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue
35 culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 µg/ml bovine insulin and 0.1 µg/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed PRO can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

In another embodiment, PRO can be expressed in CHO cells. The pRK5-PRO can be transfected
40 into CHO cells using known reagents such as CaPO₄ or DEAE-dextran. As described above, the cell

cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as ^{35}S -methionine. After determining the presence of PRO polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO can then be concentrated and purified by any selected method.

Epitope-tagged PRO may also be expressed in host CHO cells. The PRO may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO insert can then be subcloned into a SV40 promoter/enhancer containing vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 promoter/enhancer containing vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO can then be concentrated and purified by any selected method, such as by Ni^{2+} -chelate affinity chromatography.

PRO may also be expressed in CHO and/or COS cells by a transient expression procedure or in CHO cells by another stable expression procedure.

Stable expression in CHO cells is performed using the following procedure. The proteins are expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins are fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

Following PCR amplification, the respective DNAs are subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., Current Protocols of Molecular Biology, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., Nucl. Acids Res. 24:9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect® (Quiagen), Dospers® or Eugene® (Boehringer Mannheim). The cells are grown as described in Lucas et al., supra. Approximately 3×10^7 cells are frozen in an ampule for further growth and production as described below.

The ampules containing the plasmid DNA are thawed by placement into water bath and mixed by vortexing. The contents are pipetted into a centrifuge tube containing 10 mL of media and centrifuged at 1000 rpm for 5 minutes. The supernatant is aspirated and the cells are resuspended in 10 mL of selective media (0.2 μm filtered PS20 with 5% 0.2 μm diafiltered fetal bovine serum). The cells are then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells are transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37°C. After another 2-3 days, 250 mL, 500 mL and 2000 mL spinners are seeded with 3×10^5 cells/mL. The cell media is exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in U.S. Patent No. 5,122,469, issued June 16, 1992 may actually be used. A 3L production spinner is seeded at 1.2×10^6 cells/mL. On day 0, pH is determined. On

day 1, the spinner is sampled and sparging with filtered air is commenced. On day 2, the spinner is sampled, the temperature shifted to 33°C, and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion) taken. Throughout the production, the pH is adjusted as necessary to keep it at around 7.2. After 10 days, or until the viability
5 dropped below 70%, the cell culture is harvested by centrifugation and filtering through a 0.22 µm filter. The filtrate was either stored at 4°C or immediately loaded onto columns for purification.

For the poly-His tagged constructs, the proteins are purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer
10 containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column is washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

15 Immunoadhesin (Fc-containing) constructs are purified from the conditioned media as follows. The conditioned medium is pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 ml fractions into tubes containing 275 µl of 1 M Tris buffer, pH 9. The highly purified protein
20 is subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity is assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

25 EXAMPLE 5: Expression of PRO in Yeast

The following method describes recombinant expression of PRO in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of PRO from the ADH2/GAPDH promoter. DNA encoding PRO and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of PRO. For secretion, DNA encoding
30 PRO can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, a native PRO signal peptide or other mammalian signal peptide, or, for example, a yeast alpha-factor or invertase secretory signal/leader sequence, and linker sequences (if needed) for expression of PRO.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be
35 analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

Recombinant PRO can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing PRO may further be purified using selected column chromatography resins.

40 Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 6: Expression of PRO in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of PRO in Baculovirus-infected insect cells.

5 The sequence coding for PRO is fused upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the sequence encoding PRO or the desired portion of the coding sequence of PRO such as the sequence encoding the extracellular domain of a transmembrane protein
10 or the sequence encoding the mature protein if the protein is extracellular is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™
15 virus DNA (Pharmlingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4 - 5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley et al., Baculovirus expression vectors: A Laboratory Manual, Oxford: Oxford University Press (1994).

20 Expressed poly-his tagged PRO can then be purified, for example, by Ni²⁺-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., Nature, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl₂; 0.1 mM EDTA; 10% glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is
25 diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% glycerol, pH 7.8) and filtered through a 0.45 µm filter. A Ni²⁺-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A₂₈₀ with loading buffer, at which point fraction collection is started. Next, the column is washed with a
30 secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A₂₈₀ baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or Western blot with Ni²⁺-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His₁₀-tagged PRO are pooled and dialyzed against loading buffer.

35 Alternatively, purification of the IgG tagged (or Fc tagged) PRO can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 7: Preparation of Antibodies that Bind PRO

40 This example illustrates preparation of monoclonal antibodies which can specifically bind PRO.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, supra. Immunogens that may be employed include purified PRO, fusion proteins containing PRO, and cells expressing recombinant PRO on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

5 Mice, such as Balb/c, are immunized with the PRO immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the
10 mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-PRO antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of PRO. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected
15 murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against PRO. Determination of
20 "positive" hybridoma cells secreting the desired monoclonal antibodies against PRO is within the skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the
25 ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

EXAMPLE 8: Purification of PRO Polypeptides Using Specific Antibodies

30 Native or recombinant PRO polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-PRO polypeptide, mature PRO polypeptide, or pre-PRO polypeptide is purified by immunoaffinity chromatography using antibodies specific for the PRO polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-PRO polypeptide antibody to an activated chromatographic resin.

35 Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB

Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

Such an immunoaffinity column is utilized in the purification of PRO polypeptide by preparing a fraction from cells containing PRO polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble PRO polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

A soluble PRO polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PRO polypeptide (*e.g.*, high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/PRO polypeptide binding (*e.g.*, a low pH buffer such as approximately pH 2-3, or a high concentration of a chaotrope such as urea or thiocyanate ion), and PRO polypeptide is collected.

EXAMPLE 9: Drug Screening

This invention is particularly useful for screening compounds by using PRO polypeptides or binding fragment thereof in any of a variety of drug screening techniques. The PRO polypeptide or fragment employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the PRO polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between PRO polypeptide or a fragment and the agent being tested. Alternatively, one can examine the diminution in complex formation between the PRO polypeptide and its target cell or target receptors caused by the agent being tested.

Thus, the present invention provides methods of screening for drugs or any other agents which can affect a PRO polypeptide-associated disease or disorder. These methods comprise contacting such an agent with an PRO polypeptide or fragment thereof and assaying (i) for the presence of a complex between the agent and the PRO polypeptide or fragment, or (ii) for the presence of a complex between the PRO polypeptide or fragment and the cell, by methods well known in the art. In such competitive binding assays, the PRO polypeptide or fragment is typically labeled. After suitable incubation, free PRO polypeptide or fragment is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of the particular agent to bind to PRO polypeptide or to interfere with the PRO polypeptide/cell complex.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to a polypeptide and is described in detail in WO 84/03564, published on September 13, 1984. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. As applied to a PRO polypeptide, the peptide test compounds are reacted with PRO polypeptide and washed. Bound PRO polypeptide is detected by methods well known in the art. Purified PRO polypeptide can also be coated directly onto plates for use in the

aforementioned drug screening techniques. In addition, non-neutralizing antibodies can be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding PRO polypeptide specifically compete with a test compound for binding to PRO polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PRO polypeptide.

EXAMPLE 10: Rational Drug Design

The goal of rational drug design is to produce structural analogs of biologically active polypeptide of interest (*i.e.*, a PRO polypeptide) or of small molecules with which they interact, *e.g.*, agonists, antagonists, or inhibitors. Any of these examples can be used to fashion drugs which are more active or stable forms of the PRO polypeptide or which enhance or interfere with the function of the PRO polypeptide *in vivo* (*c.f.*, Hodgson, Bio/Technology, 9: 19-21 (1991)).

In one approach, the three-dimensional structure of the PRO polypeptide, or of a PRO polypeptide-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the PRO polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of the PRO polypeptide may be gained by modeling based on the structure of homologous proteins. In both cases, relevant structural information is used to design analogous PRO polypeptide-like molecules or to identify efficient inhibitors. Useful examples of rational drug design may include molecules which have improved activity or stability as shown by Braxton and Wells, Biochemistry, 31:7796-7801 (1992) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda *et al.*, J. Biochem., 113:742-746 (1993).

It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then act as the pharmacore.

By virtue of the present invention, sufficient amounts of the PRO polypeptide may be made available to perform such analytical studies as X-ray crystallography. In addition, knowledge of the PRO polypeptide amino acid sequence provided herein will provide guidance to those employing computer modeling techniques in place of or in addition to x-ray crystallography.

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by the construct deposited, since the deposited embodiment is intended as a single illustration of certain aspects of the invention and any constructs that are functionally equivalent are within the scope of this invention. The deposit of material herein does not constitute an admission that the written description herein contained is inadequate to enable the practice of any aspect of the invention, including the best mode thereof, nor is it to be construed as

limiting the scope of the claims to the specific illustrations that it represents. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

What is claimed:

1. Isolated nucleic acid having at least 80% nucleic acid sequence identity to:
- 5 (a) a nucleotide sequence encoding the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 8 (SEQ ID NO:14), Figure 8 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244)

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2. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 11 (SEQ ID NO:11), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21

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(SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25), Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49),
5 Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figure 59 (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63 (SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69), Figure 71 (SEQ ID NO:71), Figure 73 (SEQ ID NO:73), Figure 75 (SEQ ID NO:75), Figure 77 (SEQ ID NO:77), Figure 79 (SEQ ID NO:79), Figure 81 (SEQ ID NO:81), Figure 83 (SEQ ID NO:83), Figure 85 (SEQ ID NO:85), Figure 87 (SEQ ID NO:87), Figure 89 (SEQ ID NO:89), Figure 91 (SEQ ID NO:91), Figure 93 (SEQ ID NO:93), Figure 95 (SEQ ID NO:95), Figure 97 (SEQ ID NO:97), Figure 99 (SEQ ID NO:99), Figure 101 (SEQ ID NO:101), Figure 103 (SEQ ID NO:103), Figure 105 (SEQ ID NO:105), Figure 107 (SEQ ID NO:107), Figure 109 (SEQ ID NO:109), Figure 111 (SEQ ID NO:111), Figure 113 (SEQ ID NO:113), Figure 115 (SEQ ID NO:115), Figure 117 (SEQ ID NO:117), Figure 119 (SEQ ID NO:119), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:139), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177), Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189),
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40 Figure 289 (SEQ ID NO:289), Figure 291 (SEQ ID NO:291), Figure 293 (SEQ ID NO:293), Figure 295

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3. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the full-length coding sequence of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 11 (SEQ ID NO:11), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21 (SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25), Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49), Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figure 59 (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63

(SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69),
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NO:99), Figure 101 (SEQ ID NO:101), Figure 103 (SEQ ID NO:103), Figure 105 (SEQ ID NO:105), Figure
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25 NO:491), Figure 493 (SEQ ID NO:493), Figure 495 (SEQ ID NO:495), Figure 497 (SEQ ID NO:497),
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35 Figure 559 (SEQ ID NO:559), Figure 561 (SEQ ID NO:561), Figure 563 (SEQ ID NO:563), Figure 565
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Figure 579 (SEQ ID NO:579), Figure 581 (SEQ ID NO:581), Figure 583 (SEQ ID NO:583), Figure 585
(SEQ ID NO:585), Figure 587 (SEQ ID NO:587), Figure 589 (SEQ ID NO:589), Figure 591 (SEQ ID
40 NO:591), Figure 593 (SEQ ID NO:593), Figure 595 (SEQ ID NO:595), Figure 597 (SEQ ID NO:597),

Figure 599 (SEQ ID NO:599), Figure 601 (SEQ ID NO:601), Figure 603 (SEQ ID NO:603), Figure 605 (SEQ ID NO:605), Figure 607 (SEQ ID NO:607), Figure 609 (SEQ ID NO:609), Figure 611 (SEQ ID NO:611), Figure 613 (SEQ ID NO:613), Figure 615 (SEQ ID NO:615), Figure 617 (SEQ ID NO:617), Figure 619 (SEQ ID NO:619), Figure 621 (SEQ ID NO:621), Figure 623 (SEQ ID NO:623), Figure 625 (SEQ ID NO:625), Figure 627 (SEQ ID NO:627), Figure 629 (SEQ ID NO:629), Figure 631 (SEQ ID NO:631), Figure 633 (SEQ ID NO:633), Figure 635 (SEQ ID NO:635), Figure 637 (SEQ ID NO:637), Figure 639 (SEQ ID NO:639), Figure 641 (SEQ ID NO:641), Figure 643 (SEQ ID NO:643), Figure 645 (SEQ ID NO:645), Figure 647 (SEQ ID NO:647), Figure 649 (SEQ ID NO:649), Figure 651 (SEQ ID NO:651), Figure 653 (SEQ ID NO:653), Figure 655 (SEQ ID NO:655), Figure 657 (SEQ ID NO:657), Figure 659 (SEQ ID NO:659), Figure 661 (SEQ ID NO:661), Figure 663 (SEQ ID NO:663), Figure 665 (SEQ ID NO:665), Figure 667 (SEQ ID NO:667), Figure 669 (SEQ ID NO:669), Figure 671 (SEQ ID NO:671), Figure 673 (SEQ ID NO:673), Figure 675 (SEQ ID NO:675), Figure 677 (SEQ ID NO:677), Figure 679 (SEQ ID NO:679), Figure 681 (SEQ ID NO:681), Figure 683 (SEQ ID NO:683), Figure 685 (SEQ ID NO:685), Figure 687 (SEQ ID NO:687), Figure 689 (SEQ ID NO:689), Figure 691 (SEQ ID NO:691), Figure 693 (SEQ ID NO:693), Figure 695 (SEQ ID NO:695), Figure 697 (SEQ ID NO:697), Figure 699 (SEQ ID NO:699), Figure 701 (SEQ ID NO:701), Figure 703 (SEQ ID NO:703), Figure 705 (SEQ ID NO:705), Figure 707 (SEQ ID NO:707), Figure 709 (SEQ ID NO:709), Figure 711 (SEQ ID NO:711), Figure 713 (SEQ ID NO:713), Figure 715 (SEQ ID NO:715), Figure 717 (SEQ ID NO:717), Figure 719 (SEQ ID NO:719), Figure 721 (SEQ ID NO:721), Figure 723 (SEQ ID NO:723), Figure 725 (SEQ ID NO:725), Figure 727 (SEQ ID NO:727), Figure 729 (SEQ ID NO:729), Figure 731 (SEQ ID NO:731), Figure 733 (SEQ ID NO:733), Figure 735 (SEQ ID NO:735), Figure 737 (SEQ ID NO:737), Figure 739 (SEQ ID NO:739), and Figure 741 (SEQ ID NO:741).

5. A vector comprising the nucleic acid of Claim 1.
6. The vector of Claim 5 operably linked to control sequences recognized by a host cell transformed with the vector.
7. A host cell comprising the vector of Claim 5.
8. The host cell of Claim 7, wherein said cell is a CHO cell, an *E.coli* cell or a yeast cell.
9. A process for producing a PRO polypeptide comprising culturing the host cell of Claim 7 under conditions suitable for expression of said PRO polypeptide and recovering said PRO polypeptide from the cell culture.
10. An isolated polypeptide having at least 80% amino acid sequence identity to:
 - (a) an amino acid sequence of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 8 (SEQ ID NO:14), Figure 8 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure

18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24),
Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID
NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40
(SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46),
5 Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID
NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62
(SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68),
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NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84
10 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90),
Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID
NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure
106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID
NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118),
15 Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126
(SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID
NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138),
Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146
(SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID
20 NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158),
Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166
(SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID
NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178),
Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186
25 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID
NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198),
Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206
(SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID
NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218),
30 Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226
(SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID
NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238),
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35 NO:252), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256), Figure 258 (SEQ ID NO:258),
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5 Figure 320 (SEQ ID NO:320), Figure 322 (SEQ ID NO:322), Figure 324 (SEQ ID NO:324), Figure 326
(SEQ ID NO:326), Figure 328 (SEQ ID NO:328), Figure 330 (SEQ ID NO:330), Figure 332 (SEQ ID
NO:332), Figure 334 (SEQ ID NO:334), Figure 336 (SEQ ID NO:336), Figure 338 (SEQ ID NO:338),
Figure 340 (SEQ ID NO:340), Figure 342 (SEQ ID NO:342), Figure 344 (SEQ ID NO:344), Figure 346
(SEQ ID NO:346), Figure 348 (SEQ ID NO:348), Figure 350 (SEQ ID NO:350), Figure 352 (SEQ ID
10 NO:352), Figure 354 (SEQ ID NO:354), Figure 356 (SEQ ID NO:356), Figure 358 (SEQ ID NO:358),
Figure 360 (SEQ ID NO:360), Figure 362 (SEQ ID NO:362), Figure 364 (SEQ ID NO:364), Figure 366
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Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386
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NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400),
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(SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID
NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420),
20 Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428
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25 NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460),
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(SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID
NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480),
Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488
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NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500),
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35 Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528
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Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548), Figure 550
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40 NO:556), Figure 558 (SEQ ID NO:558), Figure 560 (SEQ ID NO:560), Figure 562 (SEQ ID NO:562),

Figure 564 (SEQ ID NO:564), Figure 566 (SEQ ID NO:566), Figure 568 (SEQ ID NO:568), Figure 570 (SEQ ID NO:570), Figure 572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580 (SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), Figure 610 (SEQ ID NO:610), Figure 612 (SEQ ID NO:612), Figure 614 (SEQ ID NO:614), Figure 616 (SEQ ID NO:616), Figure 618 (SEQ ID NO:618), Figure 620 (SEQ ID NO:620), Figure 622 (SEQ ID NO:622), Figure 624 (SEQ ID NO:624), Figure 626 (SEQ ID NO:626), Figure 628 (SEQ ID NO:628), Figure 630 (SEQ ID NO:630), Figure 632 (SEQ ID NO:632), Figure 634 (SEQ ID NO:634), Figure 636 (SEQ ID NO:636), Figure 638 (SEQ ID NO:638), Figure 640 (SEQ ID NO:640), Figure 642 (SEQ ID NO:642), Figure 644 (SEQ ID NO:644), Figure 646 (SEQ ID NO:646), Figure 648 (SEQ ID NO:648), Figure 650 (SEQ ID NO:650), Figure 652 (SEQ ID NO:652), Figure 654 (SEQ ID NO:654), Figure 656 (SEQ ID NO:656), Figure 658 (SEQ ID NO:658), Figure 660 (SEQ ID NO:660), Figure 662 (SEQ ID NO:662), Figure 664 (SEQ ID NO:664), Figure 666 (SEQ ID NO:666), Figure 668 (SEQ ID NO:668), Figure 670 (SEQ ID NO:670), Figure 672 (SEQ ID NO:672), Figure 674 (SEQ ID NO:674), Figure 676 (SEQ ID NO:676), Figure 678 (SEQ ID NO:678), Figure 680 (SEQ ID NO:680), Figure 682 (SEQ ID NO:682), Figure 684 (SEQ ID NO:684), Figure 686 (SEQ ID NO:686), Figure 688 (SEQ ID NO:688), Figure 690 (SEQ ID NO:690), Figure 692 (SEQ ID NO:692), Figure 694 (SEQ ID NO:694), Figure 696 (SEQ ID NO:696), Figure 698 (SEQ ID NO:698), Figure 700 (SEQ ID NO:700), Figure 702 (SEQ ID NO:702), Figure 704 (SEQ ID NO:704), Figure 706 (SEQ ID NO:706), Figure 708 (SEQ ID NO:708), Figure 710 (SEQ ID NO:710), Figure 712 (SEQ ID NO:712), Figure 714 (SEQ ID NO:714), Figure 716 (SEQ ID NO:716), Figure 718 (SEQ ID NO:718), Figure 720 (SEQ ID NO:720), Figure 722 (SEQ ID NO:722), Figure 724 (SEQ ID NO:724), Figure 726 (SEQ ID NO:726), Figure 728 (SEQ ID NO:728), Figure 730 (SEQ ID NO:730), Figure 732 (SEQ ID NO:732), Figure 734 (SEQ ID NO:734), Figure 736 (SEQ ID NO:736), Figure 740 (SEQ ID NO:740), or Figure 742 (SEQ ID NO:742).

12. A chimeric molecule comprising a polypeptide according to Claim 10 fused to a heterologous amino acid sequence.

13. The chimeric molecule of Claim 12, wherein said heterologous amino acid sequence is an epitope tag sequence or an Fc region of an immunoglobulin.

14. An antibody which specifically binds to a polypeptide according to Claim 10.

15. The antibody of Claim 14, wherein said antibody is a monoclonal antibody, a humanized antibody or a single-chain antibody.

16. A composition of matter comprising (a) a polypeptide of Claim 10, (b) an agonist of said polypeptide, (c) an antagonist of said polypeptide, or (d) an antibody that binds to said polypeptide, in combination with a carrier.

5 17. The composition of matter of Claim 16, wherein said carrier is a pharmaceutically acceptable carrier.

18. The composition of matter of Claim 16 comprising a therapeutically effective amount of (a), (b), (c) or (d).

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19. An article of manufacture, comprising:

a container;

a label on said container; and

15 a composition of matter comprising (a) a polypeptide of Claim 10, (b) an agonist of said polypeptide, (c) an antagonist of said polypeptide, or (d) an antibody that binds to said polypeptide, contained within said container, wherein label on said container indicates that said composition of matter can be used for treating an immune related disease.

20 20. A method of treating an immune related disorder in a mammal in need thereof comprising administering to said mammal a therapeutically effective amount of (a) a polypeptide of Claim 10, (b) an agonist of said polypeptide, (c) an antagonist of said polypeptide, or (d) an antibody that binds to said polypeptide.

21. The method of Claim 20, wherein the immune related disorder is systemic lupus
25 erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, Sjögren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic anemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Guillain-Barré syndrome, a chronic inflammatory demyelinating
30 polyneuropathy, a hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, erythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, eosinophilic pneumonias,
35 idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host-disease.

22. A method for determining the presence of a PRO69457
PRO69458, PRO52268, PRO69459, PRO62927, PRO59136, PRO37121, PRO69460, PRO60475,
40 PRO34451, PRO38070, PRO23756, PRO10404, PRO69461, PRO70006, PRO69462, PRO2081,

PRO70007, PRO69463, PRO62908, PRO69464, PRO52804, PRO60438, PRO69465, PRO37421,
PRO37596, PRO36124, PRO69466, PRO60499, PRO69467, PRO61824, PRO69468, PRO21341,
PRO38213, PRO69469, PRO37172, PRO35991, PRO36905, PRO69470, PRO36451, PRO69471,
PRO37492, PRO70008, PRO69472, PRO69473, PRO36996, PRO22613, PRO69475, PRO61755,
5 PRO70009, PRO69476, PRO4881, PRO12876, PRO70010, PRO37534, PRO21928, PRO69478,
PRO69479, PRO69480, PRO69481, PRO69482, PRO69483, PRO38642, PRO69484, PRO66269,
PRO1723, PRO22297, PRO61349, PRO69485, PRO69486, PRO69487, PRO36963, PRO23814,
PRO57980, PRO20128, PRO4551, PRO69488, PRO39268, PRO69489, PRO69490, PRO69491,
PRO69492, PRO37713, PRO58993, PRO69493, PRO69494, PRO69495, PRO70011, PRO62861,
10 PRO36640, PRO36766, PRO69497, PRO69498, PRO69499, PRO69500, PRO69501, PRO70012,
PRO69503, PRO69474, PRO69505, PRO69506, PRO69507, PRO51301, PRO69508, PRO69509,
PRO69510, PRO69511, PRO51309, PRO50578, PRO69512, PRO69513, PRO69514, PRO10607,
PRO61705, PRO49214, PRO39648, PRO69515, PRO38497, PRO29371, PRO70013, PRO69516,
PRO69517, PRO69518, PRO70014, PRO69520, PRO69521, PRO69522, PRO69523, PRO60513,
15 PRO2512, PRO69524, PRO12569, PRO69525, PRO69526, PRO69527, PRO69528, PRO69529,
PRO12166, PRO2154, PRO69530, PRO51916, PRO52174, PRO69531, PRO69532, PRO69533,
PRO69534, PRO54728, PRO70015, PRO69536, PRO69537, PRO37498, PRO22175, PRO69538,
PRO37015, PRO12187, PRO69539, PRO69880, PRO69541, PRO69542, PRO69543, PRO70016,
PRO69545, PRO50197, PRO69546, PRO69547, PRO69548, PRO69549, PRO69550, PRO69551,
20 PRO69552, PRO37460, PRO42223, PRO69553, PRO69554, PRO69555, PRO61014, PRO59915,
PRO37891, PRO69556, PRO12875, PRO70017, PRO70018, PRO4426, PRO69558, PRO69559,
PRO37676, PRO69560, PRO69561, PRO69562, PRO63204, PRO70019, PRO69564, PRO62830,
PRO69565, PRO69566, PRO69567, PRO49675, PRO69568, PRO2013, PRO69569, PRO69570,
PRO69571, PRO36403, PRO4676, PRO37657, PRO62097, PRO38081, PRO69572, PRO69573,
25 PRO69574, PRO69883, PRO69576, PRO37584, PRO11603, PRO70020, PRO51695, PRO69579,
PRO69580, PRO69581, PRO69582, PRO69583, PRO69584, PRO69585, PRO69586, PRO69587,
PRO69588, PRO69589, PRO70021, PRO69590, PRO70022, PRO69592, PRO37029, PRO69593,
PRO69594, PRO69595, PRO1207, PRO69596, PRO69597, PRO51139, PRO62545, PRO3615,
PRO38036, PRO69598, PRO4701, PRO69599, PRO69600, PRO69601, PRO69887, PRO69603,
30 PRO69604, PRO70023, PRO69606, PRO69607, PRO69608, PRO69609, PRO69610, PRO9902,
PRO69611, PRO69612, PRO69613, PRO69614, PRO69615, PRO70024, PRO69616, PRO49619,
PRO69617, PRO69618, PRO38040, PRO69619, PRO69620, PRO69621, PRO69622, PRO4401,
PRO70025, PRO69625, PRO12025, PRO70026, PRO69627, PRO69628, PRO22637, PRO69629,
PRO70027, PRO70028, PRO69632, PRO69634, PRO36857, PRO69893, PRO69635, PRO6180,
35 PRO69637, PRO69638, PRO69639, PRO69640, PRO69641, PRO62766, PRO53782, PRO61472,
PRO38179, PRO69642, PRO69643, PRO69644, PRO69645, PRO11608, PRO69646, PRO59825,
PRO69647, PRO69648, PRO70029, PRO1213, PRO70030, PRO50195, PRO69651, PRO37538,
PRO69652, PRO59210, PRO23374, PRO24844, PRO70031, PRO69653, PRO69654, PRO69655,
PRO69656, PRO70032, PRO69659, PRO69660, PRO58054, PRO69661, PRO69662, PRO69898,
40 PRO69664, PRO69665, PRO69666, PRO69667, PRO69669, PRO69671, PRO69672, PRO58204,

PRO49419, PRO69673, PRO69674, PRO49810, PRO70033, PRO69676, PRO58076, PRO69677, PRO69678, PRO69679, PRO1718, PRO51161, PRO69680, PRO59281, PRO36102, PRO61799, PRO69681, PRO69682, PRO69901, PRO69684, PRO69685, PRO69686, PRO69687, PRO38469, PRO69688, PRO70034, PRO59354, PRO59189, PRO38197, PRO69902, PRO69690, PRO61569, 5 PRO69903, or PRO1970 polypeptide in a sample suspected of containing said polypeptide, said method comprising exposing said sample to an anti-PRO69457, anti-PRO69458, anti-PRO52268, anti-PRO69459, anti-PRO62927, anti-PRO59136, anti-PRO37121, anti-PRO69460, anti-PRO60475, anti-PRO34451, anti-PRO38070, anti-PRO23756, anti-PRO10404, anti-PRO69461, anti-PRO70006, anti-PRO69462, anti-PRO2081, anti-PRO70007, anti-PRO69463, anti-PRO62908, anti-PRO69464, anti-PRO52804, anti-10 PRO60438, anti-PRO69465, anti-PRO37421, anti-PRO37596, anti-PRO36124, anti-PRO69466, anti-PRO60499, anti-PRO69467, anti-PRO61824, anti-PRO69468, anti-PRO21341, anti-PRO38213, anti-PRO69469, anti-PRO37172, anti-PRO35991, anti-PRO36905, anti-PRO69470, anti-PRO36451, anti-PRO69471, anti-PRO37492, anti-PRO70008, anti-PRO69472, anti-PRO69473, anti-PRO36996, anti-PRO22613, anti-PRO69475, anti-PRO61755, anti-PRO70009, anti-PRO69476, anti-PRO4881, anti-15 PRO12876, anti-PRO70010, anti-PRO37534, anti-PRO21928, anti-PRO69478, anti-PRO69479, anti-PRO69480, anti-PRO69481, anti-PRO69482, anti-PRO69483, anti-PRO38642, anti-PRO69484, anti-PRO66269, anti-PRO1723, anti-PRO22297, anti-PRO61349, anti-PRO69485, anti-PRO69486, anti-PRO69487, anti-PRO36963, anti-PRO23814, anti-PRO57980, anti-PRO20128, anti-PRO4551, anti-PRO69488, anti-PRO39268, anti-PRO69489, anti-PRO69490, anti-PRO69491, anti-PRO69492, anti-20 PRO37713, anti-PRO58993, anti-PRO69493, anti-PRO69494, anti-PRO69495, anti-PRO70011, anti-PRO62861, anti-PRO36640, anti-PRO36766, anti-PRO69497, anti-PRO69498, anti-PRO69499, anti-PRO69500, anti-PRO69501, anti-PRO70012, anti-PRO69503, anti-PRO69474, anti-PRO69505, anti-PRO69506, anti-PRO69507, anti-PRO51301, anti-PRO69508, anti-PRO69509, anti-PRO69510, anti-PRO69511, anti-PRO51309, anti-PRO50578, anti-PRO69512, anti-PRO69513, anti-PRO69514, anti-25 PRO10607, anti-PRO61705, anti-PRO49214, anti-PRO39648, anti-PRO69515, anti-PRO38497, anti-PRO29371, anti-PRO70013, anti-PRO69516, anti-PRO69517, anti-PRO69518, anti-PRO70014, anti-PRO69520, anti-PRO69521, anti-PRO69522, anti-PRO69523, anti-PRO60513, anti-PRO2512, anti-PRO69524, anti-PRO12569, anti-PRO69525, anti-PRO69526, anti-PRO69527, anti-PRO69528, anti-PRO69529, anti-PRO12166, anti-PRO2154, anti-PRO69530, anti-PRO51916, anti-PRO52174, anti-30 PRO69531, anti-PRO69532, anti-PRO69533, anti-PRO69534, anti-PRO54728, anti-PRO70015, anti-PRO69536, anti-PRO69537, anti-PRO37498, anti-PRO22175, anti-PRO69538, anti-PRO37015, anti-PRO12187, anti-PRO69539, anti-PRO69880, anti-PRO69541, anti-PRO69542, anti-PRO69543, anti-PRO70016, anti-PRO69545, anti-PRO50197, anti-PRO69546, anti-PRO69547, anti-PRO69548, anti-PRO69549, anti-PRO69550, anti-PRO69551, anti-PRO69552, anti-PRO37460, anti-PRO42223, anti-35 PRO69553, anti-PRO69554, anti-PRO69555, anti-PRO61014, anti-PRO59915, anti-PRO37891, anti-PRO69556, anti-PRO12875, anti-PRO70017, anti-PRO70018, anti-PRO4426, anti-PRO69558, anti-PRO69559, anti-PRO37676, anti-PRO69560, anti-PRO69561, anti-PRO69562, anti-PRO63204, anti-PRO70019, anti-PRO69564, anti-PRO62830, anti-PRO69565, anti-PRO69566, anti-PRO69567, anti-PRO49675, anti-PRO69568, anti-PRO2013, anti-PRO69569, anti-PRO69570, anti-PRO69571, anti-40 PRO36403, anti-PRO4676, anti-PRO37657, anti-PRO62097, anti-PRO38081, anti-PRO69572, anti-

PRO69573, anti-PRO69574, anti-PRO69883, anti-PRO69576, anti-PRO37584, anti-PRO11603, anti-PRO70020, anti-PRO51695, anti-PRO69579, anti-PRO69580, anti-PRO69581, anti-PRO69582, anti-PRO69583, anti-PRO69584, anti-PRO69585, anti-PRO69586, anti-PRO69587, anti-PRO69588, anti-PRO69589, anti-PRO70021, anti-PRO69590, anti-PRO70022, anti-PRO69592, anti-PRO37029, anti-PRO69593, anti-PRO69594, anti-PRO69595, anti-PRO1207, anti-PRO69596, anti-PRO69597, anti-PRO51139, anti-PRO62545, anti-PRO3615, anti-PRO38036, anti-PRO69598, anti-PRO4701, anti-PRO69599, anti-PRO69600, anti-PRO69601, anti-PRO69887, anti-PRO69603, anti-PRO69604, anti-PRO70023, anti-PRO69606, anti-PRO69607, anti-PRO69608, anti-PRO69609, anti-PRO69610, anti-PRO9902, anti-PRO69611, anti-PRO69612, anti-PRO69613, anti-PRO69614, anti-PRO69615, anti-PRO70024, anti-PRO69616, anti-PRO49619, anti-PRO69617, anti-PRO69618, anti-PRO38040, anti-PRO69619, anti-PRO69620, anti-PRO69621, anti-PRO69622, anti-PRO4401, anti-PRO70025, anti-PRO69625, anti-PRO12025, anti-PRO70026, anti-PRO69627, anti-PRO69628, anti-PRO22637, anti-PRO69629, anti-PRO70027, anti-PRO70028, anti-PRO69632, anti-PRO69634, anti-PRO36857, anti-PRO69893, anti-PRO69635, anti-PRO6180, anti-PRO69637, anti-PRO69638, anti-PRO69639, anti-PRO69640, anti-PRO69641, anti-PRO62766, anti-PRO53782, anti-PRO61472, anti-PRO38179, anti-PRO69642, anti-PRO69643, anti-PRO69644, anti-PRO69645, anti-PRO11608, anti-PRO69646, anti-PRO59825, anti-PRO69647, anti-PRO69648, anti-PRO70029, anti-PRO1213, anti-PRO70030, anti-PRO50195, anti-PRO69651, anti-PRO37538, anti-PRO69652, anti-PRO59210, anti-PRO23374, anti-PRO24844, anti-PRO70031, anti-PRO69653, anti-PRO69654, anti-PRO69655, anti-PRO69656, anti-PRO70032, anti-PRO69659, anti-PRO69660, anti-PRO58054, anti-PRO69661, anti-PRO69662, anti-PRO69898, anti-PRO69664, anti-PRO69665, anti-PRO69666, anti-PRO69667, anti-PRO69669, anti-PRO69671, anti-PRO69672, anti-PRO58204, anti-PRO49419, anti-PRO69673, anti-PRO69674, anti-PRO49810, anti-PRO70033, anti-PRO69676, anti-PRO58076, anti-PRO69677, anti-PRO69678, anti-PRO69679, anti-PRO1718, anti-PRO51161, anti-PRO69680, anti-PRO59281, anti-PRO36102, anti-PRO61799, anti-PRO69681, anti-PRO69682, anti-PRO69901, anti-PRO69684, anti-PRO69685, anti-PRO69686, anti-PRO69687, anti-PRO38469, anti-PRO69688, anti-PRO70034, anti-PRO59354, anti-PRO59189, anti-PRO38197, anti-PRO69902, anti-PRO69690, anti-PRO61569, anti-PRO69903, or anti-PRO1970 antibody and determining binding of said antibody to a component of said sample.

23. A method of diagnosing an immune related disease in a mammal, said method comprising detecting the level of expression of a gene encoding PRO69457, PRO69458, PRO52268, PRO69459, PRO62927, PRO59136, PRO37121, PRO69460, PRO60475, PRO34451, PRO38070, PRO23756, PRO10404, PRO69461, PRO70006, PRO69462, PRO2081, PRO70007, PRO69463, PRO62908, PRO69464, PRO52804, PRO60438, PRO69465, PRO37421, PRO37596, PRO36124, PRO69466, PRO60499, PRO69467, PRO61824, PRO69468, PRO21341, PRO38213, PRO69469, PRO37172, PRO35991, PRO36905, PRO69470, PRO36451, PRO69471, PRO37492, PRO70008, PRO69472, PRO69473, PRO36996, PRO22613, PRO69475, PRO61755, PRO70009, PRO69476, PRO4881, PRO12876, PRO70010, PRO37534, PRO21928, PRO69478, PRO69479, PRO69480, PRO69481, PRO69482, PRO69483, PRO38642, PRO69484, PRO66269, PRO1723, PRO22297, PRO61349, PRO69485, PRO69486, PRO69487, PRO36963, PRO23814, PRO57980, PRO20128, PRO4551,

PRO69488, PRO39268, PRO69489, PRO69490, PRO69491, PRO69492, PRO37713, PRO58993,
 PRO69493, PRO69494, PRO69495, PRO70011, PRO62861, PRO36640, PRO36766, PRO69497,
 PRO69498, PRO69499, PRO69500, PRO69501, PRO70012, PRO69503, PRO69474, PRO69505,
 PRO69506, PRO69507, PRO51301, PRO69508, PRO69509, PRO69510, PRO69511, PRO51309,
 5 PRO50578, PRO69512, PRO69513, PRO69514, PRO10607, PRO61705, PRO49214, PRO39648,
 PRO69515, PRO38497, PRO29371, PRO70013, PRO69516, PRO69517, PRO69518, PRO70014,
 PRO69520, PRO69521, PRO69522, PRO69523, PRO60513, PRO2512, PRO69524, PRO12569,
 PRO69525, PRO69526, PRO69527, PRO69528, PRO69529, PRO12166, PRO2154, PRO69530,
 PRO51916, PRO52174, PRO69531, PRO69532, PRO69533, PRO69534, PRO54728, PRO70015,
 10 PRO69536, PRO69537, PRO37498, PRO22175, PRO69538, PRO37015, PRO12187, PRO69539,
 PRO69880, PRO69541, PRO69542, PRO69543, PRO70016, PRO69545, PRO50197, PRO69546,
 PRO69547, PRO69548, PRO69549, PRO69550, PRO69551, PRO69552, PRO37460, PRO42223,
 PRO69553, PRO69554, PRO69555, PRO61014, PRO59915, PRO37891, PRO69556, PRO12875,
 PRO70017, PRO70018, PRO4426, PRO69558, PRO69559, PRO37676, PRO69560, PRO69561,
 15 PRO69562, PRO63204, PRO70019, PRO69564, PRO62830, PRO69565, PRO69566, PRO69567,
 PRO49675, PRO69568, PRO2013, PRO69569, PRO69570, PRO69571, PRO36403, PRO4676,
 PRO37657, PRO62097, PRO38081, PRO69572, PRO69573, PRO69574, PRO69883, PRO69576,
 PRO37584, PRO11603, PRO70020, PRO51695, PRO69579, PRO69580, PRO69581, PRO69582,
 PRO69583, PRO69584, PRO69585, PRO69586, PRO69587, PRO69588, PRO69589, PRO70021,
 20 PRO69590, PRO70022, PRO69592, PRO37029, PRO69593, PRO69594, PRO69595, PRO1207,
 PRO69596, PRO69597, PRO51139, PRO62545, PRO3615, PRO38036, PRO69598, PRO4701,
 PRO69599, PRO69600, PRO69601, PRO69887, PRO69603, PRO69604, PRO70023, PRO69606,
 PRO69607, PRO69608, PRO69609, PRO69610, PRO9902, PRO69611, PRO69612, PRO69613,
 PRO69614, PRO69615, PRO70024, PRO69616, PRO49619, PRO69617, PRO69618, PRO38040,
 25 PRO69619, PRO69620, PRO69621, PRO69622, PRO4401, PRO70025, PRO69625, PRO12025,
 PRO70026, PRO69627, PRO69628, PRO22637, PRO69629, PRO70027, PRO70028, PRO69632,
 PRO69634, PRO36857, PRO69893, PRO69635, PRO6180, PRO69637, PRO69638, PRO69639,
 PRO69640, PRO69641, PRO62766, PRO53782, PRO61472, PRO38179, PRO69642, PRO69643,
 PRO69644, PRO69645, PRO11608, PRO69646, PRO59825, PRO69647, PRO69648, PRO70029,
 30 PRO1213, PRO70030, PRO50195, PRO69651, PRO37538, PRO69652, PRO59210, PRO23374,
 PRO24844, PRO70031, PRO69653, PRO69654, PRO69655, PRO69656, PRO70032, PRO69659,
 PRO69660, PRO58054, PRO69661, PRO69662, PRO69898, PRO69664, PRO69665, PRO69666,
 PRO69667, PRO69669, PRO69671, PRO69672, PRO58204, PRO49419, PRO69673, PRO69674,
 PRO49810, PRO70033, PRO69676, PRO58076, PRO69677, PRO69678, PRO69679, PRO1718,
 35 PRO51161, PRO69680, PRO59281, PRO36102, PRO61799, PRO69681, PRO69682, PRO69901,
 PRO69684, PRO69685, PRO69686, PRO69687, PRO38469, PRO69688, PRO70034, PRO59354,
 PRO59189, PRO38197, PRO69902, PRO69690, PRO61569, PRO69903 or PRO1970 polypeptide (a) in a
 test sample of tissue cells obtained from the mammal, and (b) in a control sample of known normal tissue
 cells of the same cell type, wherein a higher or lower level of expression of said gene in the test sample as

compared to the control sample is indicative of the presence of an immune related disease in the mammal from which the test tissue cells were obtained.

24. A method of diagnosing an immune related disease in a mammal, said method comprising
- 5 (a) contacting an an anti-PRO69457, anti-PRO69458, anti-PRO52268, anti-PRO69459, anti-PRO62927, anti-PRO59136, anti-PRO37121, anti-PRO69460, anti-PRO60475, anti-PRO34451, anti-PRO38070, anti-PRO23756, anti-PRO10404, anti-PRO69461, anti-PRO70006, anti-PRO69462, anti-PRO2081, anti-PRO70007, anti-PRO69463, anti-PRO62908, anti-PRO69464, anti-PRO52804, anti-PRO60438, anti-PRO69465, anti-PRO37421, anti-PRO37596, anti-PRO36124, anti-PRO69466, anti-PRO60499, anti-PRO69467, anti-PRO61824, anti-PRO69468, anti-PRO21341, anti-PRO38213, anti-PRO69469, anti-PRO37172, anti-PRO35991, anti-PRO36905, anti-PRO69470, anti-PRO36451, anti-PRO69471, anti-PRO37492, anti-PRO70008, anti-PRO69472, anti-PRO69473, anti-PRO36996, anti-PRO22613, anti-PRO69475, anti-PRO61755, anti-PRO70009, anti-PRO69476, anti-PRO4881, anti-PRO12876, anti-PRO70010, anti-PRO37534, anti-PRO21928, anti-PRO69478, anti-PRO69479, anti-PRO69480, anti-PRO69481, anti-PRO69482, anti-PRO69483, anti-PRO38642, anti-PRO69484, anti-PRO66269, anti-PRO1723, anti-PRO22297, anti-PRO61349, anti-PRO69485, anti-PRO69486, anti-PRO69487, anti-PRO36963, anti-PRO23814, anti-PRO57980, anti-PRO20128, anti-PRO4551, anti-PRO69488, anti-PRO39268, anti-PRO69489, anti-PRO69490, anti-PRO69491, anti-PRO69492, anti-PRO37713, anti-PRO58993, anti-PRO69493, anti-PRO69494, anti-PRO69495, anti-PRO70011, anti-PRO62861, anti-PRO36640, anti-PRO36766, anti-PRO69497, anti-PRO69498, anti-PRO69499, anti-PRO69500, anti-PRO69501, anti-PRO70012, anti-PRO69503, anti-PRO69474, anti-PRO69505, anti-PRO69506, anti-PRO69507, anti-PRO51301, anti-PRO69508, anti-PRO69509, anti-PRO69510, anti-PRO69511, anti-PRO51309, anti-PRO50578, anti-PRO69512, anti-PRO69513, anti-PRO69514, anti-PRO10607, anti-PRO61705, anti-PRO49214, anti-PRO39648, anti-PRO69515, anti-PRO38497, anti-PRO29371, anti-PRO70013, anti-PRO69516, anti-PRO69517, anti-PRO69518, anti-PRO70014, anti-PRO69520, anti-PRO69521, anti-PRO69522, anti-PRO69523, anti-PRO60513, anti-PRO2512, anti-PRO69524, anti-PRO12569, anti-PRO69525, anti-PRO69526, anti-PRO69527, anti-PRO69528, anti-PRO69529, anti-PRO12166, anti-PRO2154, anti-PRO69530, anti-PRO51916, anti-PRO52174, anti-PRO69531, anti-PRO69532, anti-PRO69533, anti-PRO69534, anti-PRO54728, anti-PRO70015, anti-PRO69536, anti-PRO69537, anti-PRO37498, anti-PRO22175, anti-PRO69538, anti-PRO37015, anti-PRO12187, anti-PRO69539, anti-PRO69880, anti-PRO69541, anti-PRO69542, anti-PRO69543, anti-PRO70016, anti-PRO69545, anti-PRO50197, anti-PRO69546, anti-PRO69547, anti-PRO69548, anti-PRO69549, anti-PRO69550, anti-PRO69551, anti-PRO69552, anti-PRO37460, anti-PRO42223, anti-PRO69553, anti-PRO69554, anti-PRO69555, anti-PRO61014, anti-PRO59915, anti-PRO37891, anti-PRO69556, anti-PRO12875, anti-PRO70017, anti-PRO70018, anti-PRO4426, anti-PRO69558, anti-PRO69559, anti-PRO37676, anti-PRO69560, anti-PRO69561, anti-PRO69562, anti-PRO63204, anti-PRO70019, anti-PRO69564, anti-PRO62830, anti-PRO69565, anti-PRO69566, anti-PRO69567, anti-PRO49675, anti-PRO69568, anti-PRO2013, anti-PRO69569, anti-PRO69570, anti-PRO69571, anti-PRO36403, anti-PRO4676, anti-PRO37657, anti-PRO62097, anti-PRO38081, anti-PRO69572, anti-PRO69573, anti-PRO69574, anti-PRO69883, anti-PRO69576, anti-PRO37584, anti-PRO11603, anti-PRO70020, anti-

PRO51695, anti-PRO69579, anti-PRO69580, anti-PRO69581, anti-PRO69582, anti-PRO69583, anti-PRO69584, anti-PRO69585, anti-PRO69586, anti-PRO69587, anti-PRO69588, anti-PRO69589, anti-PRO70021, anti-PRO69590, anti-PRO70022, anti-PRO69592, anti-PRO37029, anti-PRO69593, anti-PRO69594, anti-PRO69595, anti-PRO1207, anti-PRO69596, anti-PRO69597, anti-PRO51139, anti-PRO62545, anti-PRO3615, anti-PRO38036, anti-PRO69598, anti-PRO4701, anti-PRO69599, anti-PRO69600, anti-PRO69601, anti-PRO69887, anti-PRO69603, anti-PRO69604, anti-PRO70023, anti-PRO69606, anti-PRO69607, anti-PRO69608, anti-PRO69609, anti-PRO69610, anti-PRO9902, anti-PRO69611, anti-PRO69612, anti-PRO69613, anti-PRO69614, anti-PRO69615, anti-PRO70024, anti-PRO69616, anti-PRO49619, anti-PRO69617, anti-PRO69618, anti-PRO38040, anti-PRO69619, anti-PRO69620, anti-PRO69621, anti-PRO69622, anti-PRO4401, anti-PRO70025, anti-PRO69625, anti-PRO12025, anti-PRO70026, anti-PRO69627, anti-PRO69628, anti-PRO22637, anti-PRO69629, anti-PRO70027, anti-PRO70028, anti-PRO69632, anti-PRO69634, anti-PRO36857, anti-PRO69893, anti-PRO69635, anti-PRO6180, anti-PRO69637, anti-PRO69638, anti-PRO69639, anti-PRO69640, anti-PRO69641, anti-PRO62766, anti-PRO53782, anti-PRO61472, anti-PRO38179, anti-PRO69642, anti-PRO69643, anti-PRO69644, anti-PRO69645, anti-PRO11608, anti-PRO69646, anti-PRO59825, anti-PRO69647, anti-PRO69648, anti-PRO70029, anti-PRO1213, anti-PRO70030, anti-PRO50195, anti-PRO69651, anti-PRO37538, anti-PRO69652, anti-PRO59210, anti-PRO23374, anti-PRO24844, anti-PRO70031, anti-PRO69653, anti-PRO69654, anti-PRO69655, anti-PRO69656, anti-PRO70032, anti-PRO69659, anti-PRO69660, anti-PRO58054, anti-PRO69661, anti-PRO69662, anti-PRO69898, anti-PRO69664, anti-PRO69665, anti-PRO69666, anti-PRO69667, anti-PRO69669, anti-PRO69671, anti-PRO69672, anti-PRO58204, anti-PRO49419, anti-PRO69673, anti-PRO69674, anti-PRO49810, anti-PRO70033, anti-PRO69676, anti-PRO58076, anti-PRO69677, anti-PRO69678, anti-PRO69679, anti-PRO1718, anti-PRO51161, anti-PRO69680, anti-PRO59281, anti-PRO36102, anti-PRO61799, anti-PRO69681, anti-PRO69682, anti-PRO69901, anti-PRO69684, anti-PRO69685, anti-PRO69686, anti-PRO69687, anti-PRO38469, anti-PRO69688, anti-PRO70034, anti-PRO59354, anti-PRO59189, anti-PRO38197, anti-PRO69902, anti-PRO69690, anti-PRO61569, anti-PRO69903 or anti-PRO1970, antibody with a test sample of tissue cells obtained from said mammal and (b) detecting the formation of a complex between the antibody and the polypeptide in the test sample, wherein formation of said complex is indicative of the presence of an immune related disease in the mammal from which the test tissue cells were obtained.

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25. A method of identifying a compound that inhibits the activity of PRO69457

PRO69458, PRO52268, PRO69459, PRO62927, PRO59136, PRO37121, PRO69460, PRO60475, PRO34451, PRO38070, PRO23756, PRO10404, PRO69461, PRO70006, PRO69462, PRO2081, PRO70007, PRO69463, PRO62908, PRO69464, PRO52804, PRO60438, PRO69465, PRO37421, PRO37596, PRO36124, PRO69466, PRO60499, PRO69467, PRO61824, PRO69468, PRO21341, PRO38213, PRO69469, PRO37172, PRO35991, PRO36905, PRO69470, PRO36451, PRO69471, PRO37492, PRO70008, PRO69472, PRO69473, PRO36996, PRO22613, PRO69475, PRO61755, PRO70009, PRO69476, PRO4881, PRO12876, PRO70010, PRO37534, PRO21928, PRO69478, PRO69479, PRO69480, PRO69481, PRO69482, PRO69483, PRO38642, PRO69484, PRO66269, PRO1723, PRO22297, PRO61349, PRO69485, PRO69486, PRO69487, PRO36963, PRO23814,

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PRO57980, PRO20128, PRO4551, PRO69488, PRO39268, PRO69489, PRO69490, PRO69491,
PRO69492, PRO37713, PRO58993, PRO69493, PRO69494, PRO69495, PRO70011, PRO62861,
PRO36640, PRO36766, PRO69497, PRO69498, PRO69499, PRO69500, PRO69501, PRO70012,
PRO69503, PRO69474, PRO69505, PRO69506, PRO69507, PRO51301, PRO69508, PRO69509,
5 PRO69510, PRO69511, PRO51309, PRO50578, PRO69512, PRO69513, PRO69514, PRO10607,
PRO61705, PRO49214, PRO39648, PRO69515, PRO38497, PRO29371, PRO70013, PRO69516,
PRO69517, PRO69518, PRO70014, PRO69520, PRO69521, PRO69522, PRO69523, PRO60513,
PRO2512, PRO69524, PRO12569, PRO69525, PRO69526, PRO69527, PRO69528, PRO69529,
PRO12166, PRO2154, PRO69530, PRO51916, PRO52174, PRO69531, PRO69532, PRO69533,
10 PRO69534, PRO54728, PRO70015, PRO69536, PRO69537, PRO37498, PRO22175, PRO69538,
PRO37015, PRO12187, PRO69539, PRO69880, PRO69541, PRO69542, PRO69543, PRO70016,
PRO69545, PRO50197, PRO69546, PRO69547, PRO69548, PRO69549, PRO69550, PRO69551,
PRO69552, PRO37460, PRO42223, PRO69553, PRO69554, PRO69555, PRO61014, PRO59915,
PRO37891, PRO69556, PRO12875, PRO70017, PRO70018, PRO4426, PRO69558, PRO69559,
15 PRO37676, PRO69560, PRO69561, PRO69562, PRO63204, PRO70019, PRO69564, PRO62830,
PRO69565, PRO69566, PRO69567, PRO49675, PRO69568, PRO2013, PRO69569, PRO69570,
PRO69571, PRO36403, PRO4676, PRO37657, PRO62097, PRO38081, PRO69572, PRO69573,
PRO69574, PRO69883, PRO69576, PRO37584, PRO11603, PRO70020, PRO51695, PRO69579,
PRO69580, PRO69581, PRO69582, PRO69583, PRO69584, PRO69585, PRO69586, PRO69587,
20 PRO69588, PRO69589, PRO70021, PRO69590, PRO70022, PRO69592, PRO37029, PRO69593,
PRO69594, PRO69595, PRO1207, PRO69596, PRO69597, PRO51139, PRO62545, PRO3615,
PRO38036, PRO69598, PRO4701, PRO69599, PRO69600, PRO69601, PRO69887, PRO69603,
PRO69604, PRO70023, PRO69606, PRO69607, PRO69608, PRO69609, PRO69610, PRO9902,
PRO69611, PRO69612, PRO69613, PRO69614, PRO69615, PRO70024, PRO69616, PRO49619,
25 PRO69617, PRO69618, PRO38040, PRO69619, PRO69620, PRO69621, PRO69622, PRO4401,
PRO70025, PRO69625, PRO12025, PRO70026, PRO69627, PRO69628, PRO22637, PRO69629,
PRO70027, PRO70028, PRO69632, PRO69634, PRO36857, PRO69893, PRO69635, PRO6180,
PRO69637, PRO69638, PRO69639, PRO69640, PRO69641, PRO62766, PRO53782, PRO61472,
PRO38179, PRO69642, PRO69643, PRO69644, PRO69645, PRO11608, PRO69646, PRO59825,
30 PRO69647, PRO69648, PRO70029, PRO1213, PRO70030, PRO50195, PRO69651, PRO37538,
PRO69652, PRO59210, PRO23374, PRO24844, PRO70031, PRO69653, PRO69654, PRO69655,
PRO69656, PRO70032, PRO69659, PRO69660, PRO58054, PRO69661, PRO69662, PRO69898,
PRO69664, PRO69665, PRO69666, PRO69667, PRO69669, PRO69671, PRO69672, PRO58204,
PRO49419, PRO69673, PRO69674, PRO49810, PRO70033, PRO69676, PRO58076, PRO69677,
35 PRO69678, PRO69679, PRO1718, PRO51161, PRO69680, PRO59281, PRO36102, PRO61799,
PRO69681, PRO69682, PRO69901, PRO69684, PRO69685, PRO69686, PRO69687, PRO38469,
PRO69688, PRO70034, PRO59354, PRO59189, PRO38197, PRO69902, PRO69690, PRO61569,
PRO69903 or PRO1970 polypeptide, said method comprising contacting cells which normally respond to
said polypeptide with (a) said polypeptide and (b) a candidate compound, and determining the lack
40 responsiveness by said cell to (a).

26. A method of identifying a compound that inhibits the expression of a gene encoding a
PRO69457, PRO69458, PRO52268, PRO69459, PRO62927, PRO59136, PRO37121, PRO69460,
PRO60475, PRO34451, PRO38070, PRO23756, PRO10404, PRO69461, PRO70006, PRO69462,
5 PRO2081, PRO70007, PRO69463, PRO62908, PRO69464, PRO52804, PRO60438, PRO69465,
PRO37421, PRO37596, PRO36124, PRO69466, PRO60499, PRO69467, PRO61824, PRO69468,
PRO21341, PRO38213, PRO69469, PRO37172, PRO35991, PRO36905, PRO69470, PRO36451,
PRO69471, PRO37492, PRO70008, PRO69472, PRO69473, PRO36996, PRO22613, PRO69475,
PRO61755, PRO70009, PRO69476, PRO4881, PRO12876, PRO70010, PRO37534, PRO21928,
10 PRO69478, PRO69479, PRO69480, PRO69481, PRO69482, PRO69483, PRO38642, PRO69484,
PRO66269, PRO1723, PRO22297, PRO61349, PRO69485, PRO69486, PRO69487, PRO36963,
PRO23814, PRO57980, PRO20128, PRO4551, PRO69488, PRO39268, PRO69489, PRO69490,
PRO69491, PRO69492, PRO37713, PRO58993, PRO69493, PRO69494, PRO69495, PRO70011,
PRO62861, PRO36640, PRO36766, PRO69497, PRO69498, PRO69499, PRO69500, PRO69501,
15 PRO70012, PRO69503, PRO69474, PRO69505, PRO69506, PRO69507, PRO51301, PRO69508,
PRO69509, PRO69510, PRO69511, PRO51309, PRO50578, PRO69512, PRO69513, PRO69514,
PRO10607, PRO61705, PRO49214, PRO39648, PRO69515, PRO38497, PRO29371, PRO70013,
PRO69516, PRO69517, PRO69518, PRO70014, PRO69520, PRO69521, PRO69522, PRO69523,
PRO60513, PRO2512, PRO69524, PRO12569, PRO69525, PRO69526, PRO69527, PRO69528,
20 PRO69529, PRO12166, PRO2154, PRO69530, PRO51916, PRO52174, PRO69531, PRO69532,
PRO69533, PRO69534, PRO54728, PRO70015, PRO69536, PRO69537, PRO37498, PRO22175,
PRO69538, PRO37015, PRO12187, PRO69539, PRO69880, PRO69541, PRO69542, PRO69543,
PRO70016, PRO69545, PRO50197, PRO69546, PRO69547, PRO69548, PRO69549, PRO69550,
PRO69551, PRO69552, PRO37460, PRO42223, PRO69553, PRO69554, PRO69555, PRO61014,
25 PRO59915, PRO37891, PRO69556, PRO12875, PRO70017, PRO70018, PRO4426, PRO69558,
PRO69559, PRO37676, PRO69560, PRO69561, PRO69562, PRO63204, PRO70019, PRO69564,
PRO62830, PRO69565, PRO69566, PRO69567, PRO49675, PRO69568, PRO2013, PRO69569,
PRO69570, PRO69571, PRO36403, PRO4676, PRO37657, PRO62097, PRO38081, PRO69572,
PRO69573, PRO69574, PRO69883, PRO69576, PRO37584, PRO11603, PRO70020, PRO51695,
30 PRO69579, PRO69580, PRO69581, PRO69582, PRO69583, PRO69584, PRO69585, PRO69586,
PRO69587, PRO69588, PRO69589, PRO70021, PRO69590, PRO70022, PRO69592, PRO37029,
PRO69593, PRO69594, PRO69595, PRO1207, PRO69596, PRO69597, PRO51139, PRO62545,
PRO3615, PRO38036, PRO69598, PRO4701, PRO69599, PRO69600, PRO69601, PRO69887,
PRO69603, PRO69604, PRO70023, PRO69606, PRO69607, PRO69608, PRO69609, PRO69610,
35 PRO9902, PRO69611, PRO69612, PRO69613, PRO69614, PRO69615, PRO70024, PRO69616,
PRO49619, PRO69617, PRO69618, PRO38040, PRO69619, PRO69620, PRO69621, PRO69622,
PRO4401, PRO70025, PRO69625, PRO12025, PRO70026, PRO69627, PRO69628, PRO22637,
PRO69629, PRO70027, PRO70028, PRO69632, PRO69634, PRO36857, PRO69893, PRO69635,
PRO6180, PRO69637, PRO69638, PRO69639, PRO69640, PRO69641, PRO62766, PRO53782,
40 PRO61472, PRO38179, PRO69642, PRO69643, PRO69644, PRO69645, PRO11608, PRO69646,

PRO59825, PRO69647, PRO69648, PRO70029, PRO1213, PRO70030, PRO50195, PRO69651, PRO37538, PRO69652, PRO59210, PRO23374, PRO24844, PRO70031, PRO69653, PRO69654, PRO69655, PRO69656, PRO70032, PRO69659, PRO69660, PRO58054, PRO69661, PRO69662, PRO69898, PRO69664, PRO69665, PRO69666, PRO69667, PRO69669, PRO69671, PRO69672, PRO58204, PRO49419, PRO69673, PRO69674, PRO49810, PRO70033, PRO69676, PRO58076, PRO69677, PRO69678, PRO69679, PRO1718, PRO51161, PRO69680, PRO59281, PRO36102, PRO61799, PRO69681, PRO69682, PRO69901, PRO69684, PRO69685, PRO69686, PRO69687, PRO38469, PRO69688, PRO70034, PRO59354, PRO59189, PRO38197, PRO69902, PRO69690, PRO61569, PRO69903 or PRO1970 polypeptide, said method comprising contacting cells which normally express said polypeptide with a candidate compound, and determining the lack of expression said gene.

27. The method of Claim 26, wherein said candidate compound is an antisense nucleic acid.

28. A method of identifying a compound that mimics the activity of a PRO69457

PRO69458, PRO52268, PRO69459, PRO62927, PRO59136, PRO37121, PRO69460, PRO60475, PRO34451, PRO38070, PRO23756, PRO10404, PRO69461, PRO70006, PRO69462, PRO2081, PRO70007, PRO69463, PRO62908, PRO69464, PRO52804, PRO60438, PRO69465, PRO37421, PRO37596, PRO36124, PRO69466, PRO60499, PRO69467, PRO61824, PRO69468, PRO21341, PRO38213, PRO69469, PRO37172, PRO35991, PRO36905, PRO69470, PRO36451, PRO69471, PRO37492, PRO70008, PRO69472, PRO69473, PRO36996, PRO22613, PRO69475, PRO61755, PRO70009, PRO69476, PRO4881, PRO12876, PRO70010, PRO37534, PRO21928, PRO69478, PRO69479, PRO69480, PRO69481, PRO69482, PRO69483, PRO38642, PRO69484, PRO66269, PRO1723, PRO22297, PRO61349, PRO69485, PRO69486, PRO69487, PRO36963, PRO23814, PRO57980, PRO20128, PRO4551, PRO69488, PRO39268, PRO69489, PRO69490, PRO69491, PRO69492, PRO37713, PRO58993, PRO69493, PRO69494, PRO69495, PRO70011, PRO62861, PRO36640, PRO36766, PRO69497, PRO69498, PRO69499, PRO69500, PRO69501, PRO70012, PRO69503, PRO69474, PRO69505, PRO69506, PRO69507, PRO51301, PRO69508, PRO69509, PRO69510, PRO69511, PRO51309, PRO50578, PRO69512, PRO69513, PRO69514, PRO10607, PRO61705, PRO49214, PRO39648, PRO69515, PRO38497, PRO29371, PRO70013, PRO69516, PRO69517, PRO69518, PRO70014, PRO69520, PRO69521, PRO69522, PRO69523, PRO60513, PRO2512, PRO69524, PRO12569, PRO69525, PRO69526, PRO69527, PRO69528, PRO69529, PRO12166, PRO2154, PRO69530, PRO51916, PRO52174, PRO69531, PRO69532, PRO69533, PRO69534, PRO54728, PRO70015, PRO69536, PRO69537, PRO37498, PRO22175, PRO69538, PRO37015, PRO12187, PRO69539, PRO69880, PRO69541, PRO69542, PRO69543, PRO70016, PRO69545, PRO50197, PRO69546, PRO69547, PRO69548, PRO69549, PRO69550, PRO69551, PRO69552, PRO37460, PRO42223, PRO69553, PRO69554, PRO69555, PRO61014, PRO59915, PRO37891, PRO69556, PRO12875, PRO70017, PRO70018, PRO4426, PRO69558, PRO69559, PRO37676, PRO69560, PRO69561, PRO69562, PRO63204, PRO70019, PRO69564, PRO62830, PRO69565, PRO69566, PRO69567, PRO49675, PRO69568, PRO2013, PRO69569, PRO69570, PRO69571, PRO36403, PRO4676, PRO37657, PRO62097, PRO38081, PRO69572, PRO69573,

PRO69574, PRO69883, PRO69576, PRO37584, PRO11603, PRO70020, PRO51695, PRO69579,
 PRO69580, PRO69581, PRO69582, PRO69583, PRO69584, PRO69585, PRO69586, PRO69587,
 PRO69588, PRO69589, PRO70021, PRO69590, PRO70022, PRO69592, PRO37029, PRO69593,
 PRO69594, PRO69595, PRO1207, PRO69596, PRO69597, PRO51139, PRO62545, PRO3615,
 5 PRO38036, PRO69598, PRO4701, PRO69599, PRO69600, PRO69601, PRO69887, PRO69603,
 PRO69604, PRO70023, PRO69606, PRO69607, PRO69608, PRO69609, PRO69610, PRO9902,
 PRO69611, PRO69612, PRO69613, PRO69614, PRO69615, PRO70024, PRO69616, PRO49619,
 PRO69617, PRO69618, PRO38040, PRO69619, PRO69620, PRO69621, PRO69622, PRO4401,
 PRO70025, PRO69625, PRO12025, PRO70026, PRO69627, PRO69628, PRO22637, PRO69629,
 10 PRO70027, PRO70028, PRO69632, PRO69634, PRO36857, PRO69893, PRO69635, PRO6180,
 PRO69637, PRO69638, PRO69639, PRO69640, PRO69641, PRO62766, PRO53782, PRO61472,
 PRO38179, PRO69642, PRO69643, PRO69644, PRO69645, PRO11608, PRO69646, PRO59825,
 PRO69647, PRO69648, PRO70029, PRO1213, PRO70030, PRO50195, PRO69651, PRO37538,
 PRO69652, PRO59210, PRO23374, PRO24844, PRO70031, PRO69653, PRO69654, PRO69655,
 15 PRO69656, PRO70032, PRO69659, PRO69660, PRO58054, PRO69661, PRO69662, PRO69898,
 PRO69664, PRO69665, PRO69666, PRO69667, PRO69669, PRO69671, PRO69672, PRO58204,
 PRO49419, PRO69673, PRO69674, PRO49810, PRO70033, PRO69676, PRO58076, PRO69677,
 PRO69678, PRO69679, PRO1718, PRO51161, PRO69680, PRO59281, PRO36102, PRO61799,
 PRO69681, PRO69682, PRO69901, PRO69684, PRO69685, PRO69686, PRO69687, PRO38469,
 20 PRO69688, PRO70034, PRO59354, PRO59189, PRO38197, PRO69902, PRO69690, PRO61569,
 PRO69903 or PRO1970 polypeptide, said method comprising contacting cells which normally respond to
 said polypeptide with a candidate compound, and determining the responsiveness by said cell to said
 candidate compound.

25 31. A method of stimulating the immune response in a mammal, said method comprising administering
 to said mammal an effective amount of a PRO69457, PRO69458, PRO52268, PRO69459, PRO62927,
 PRO59136, PRO37121, PRO69460, PRO60475, PRO34451, PRO38070, PRO23756, PRO10404,
 PRO69461, PRO70006, PRO69462, PRO2081, PRO70007, PRO69463, PRO62908, PRO69464,
 PRO52804, PRO60438, PRO69465, PRO37421, PRO37596, PRO36124, PRO69466, PRO60499,
 30 PRO69467, PRO61824, PRO69468, PRO21341, PRO38213, PRO69469, PRO37172, PRO35991,
 PRO36905, PRO69470, PRO36451, PRO69471, PRO37492, PRO70008, PRO69472, PRO69473,
 PRO36996, PRO22613, PRO69475, PRO61755, PRO70009, PRO69476, PRO4881, PRO12876,
 PRO70010, PRO37534, PRO21928, PRO69478, PRO69479, PRO69480, PRO69481, PRO69482,
 PRO69483, PRO38642, PRO69484, PRO66269, PRO1723, PRO22297, PRO61349, PRO69485,
 35 PRO69486, PRO69487, PRO36963, PRO23814, PRO57980, PRO20128, PRO4551, PRO69488,
 PRO39268, PRO69489, PRO69490, PRO69491, PRO69492, PRO37713, PRO58993, PRO69493,
 PRO69494, PRO69495, PRO70011, PRO62861, PRO36640, PRO36766, PRO69497, PRO69498,
 PRO69499, PRO69500, PRO69501, PRO70012, PRO69503, PRO69474, PRO69505, PRO69506,
 PRO69507, PRO51301, PRO69508, PRO69509, PRO69510, PRO69511, PRO51309, PRO50578,
 40 PRO69512, PRO69513, PRO69514, PRO10607, PRO61705, PRO49214, PRO39648, PRO69515,

PRO38497, PRO29371, PRO70013, PRO69516, PRO69517, PRO69518, PRO70014, PRO69520, PRO69521, PRO69522, PRO69523, PRO60513, PRO2512, PRO69524, PRO12569, PRO69525, PRO69526, PRO69527, PRO69528, PRO69529, PRO12166, PRO2154, PRO69530, PRO51916, PRO52174, PRO69531, PRO69532, PRO69533, PRO69534, PRO54728, PRO70015, PRO69536, PRO69537, PRO37498, PRO22175, PRO69538, PRO37015, PRO12187, PRO69539, PRO69880, PRO69541, PRO69542, PRO69543, PRO70016, PRO69545, PRO50197, PRO69546, PRO69547, PRO69548, PRO69549, PRO69550, PRO69551, PRO69552, PRO37460, PRO42223, PRO69553, PRO69554, PRO69555, PRO61014, PRO59915, PRO37891, PRO69556, PRO12875, PRO70017, PRO70018, PRO4426, PRO69558, PRO69559, PRO37676, PRO69560, PRO69561, PRO69562, PRO63204, PRO70019, PRO69564, PRO62830, PRO69565, PRO69566, PRO69567, PRO49675, PRO69568, PRO2013, PRO69569, PRO69570, PRO69571, PRO36403, PRO4676, PRO37657, PRO62097, PRO38081, PRO69572, PRO69573, PRO69574, PRO69883, PRO69576, PRO37584, PRO11603, PRO70020, PRO51695, PRO69579, PRO69580, PRO69581, PRO69582, PRO69583, PRO69584, PRO69585, PRO69586, PRO69587, PRO69588, PRO69589, PRO70021, PRO69590, PRO70022, PRO69592, PRO37029, PRO69593, PRO69594, PRO69595, PRO1207, PRO69596, PRO69597, PRO51139, PRO62545, PRO3615, PRO38036, PRO69598, PRO4701, PRO69599, PRO69600, PRO69601, PRO69887, PRO69603, PRO69604, PRO70023, PRO69606, PRO69607, PRO69608, PRO69609, PRO69610, PRO9902, PRO69611, PRO69612, PRO69613, PRO69614, PRO69615, PRO70024, PRO69616, PRO49619, PRO69617, PRO69618, PRO38040, PRO69619, PRO69620, PRO69621, PRO69622, PRO4401, PRO70025, PRO69625, PRO12025, PRO70026, PRO69627, PRO69628, PRO22637, PRO69629, PRO70027, PRO70028, PRO69632, PRO69634, PRO36857, PRO69893, PRO69635, PRO6180, PRO69637, PRO69638, PRO69639, PRO69640, PRO69641, PRO62766, PRO53782, PRO61472, PRO38179, PRO69642, PRO69643, PRO69644, PRO69645, PRO11608, PRO69646, PRO59825, PRO69647, PRO69648, PRO70029, PRO1213, PRO70030, PRO50195, PRO69651, PRO37538, PRO69652, PRO59210, PRO23374, PRO24844, PRO70031, PRO69653, PRO69654, PRO69655, PRO69656, PRO70032, PRO69659, PRO69660, PRO58054, PRO69661, PRO69662, PRO69898, PRO69664, PRO69665, PRO69666, PRO69667, PRO69669, PRO69671, PRO69672, PRO58204, PRO49419, PRO69673, PRO69674, PRO49810, PRO70033, PRO69676, PRO58076, PRO69677, PRO69678, PRO69679, PRO1718, PRO51161, PRO69680, PRO59281, PRO36102, PRO61799, PRO69681, PRO69682, PRO69901, PRO69684, PRO69685, PRO69686, PRO69687, PRO38469, PRO69688, PRO70034, PRO59354, PRO59189, PRO38197, PRO69902, PRO69690, PRO61569, PRO6990 or PRO1970 polypeptide antagonist, wherein said immune response is stimulated.

32. A method of diagnosing an inflammatory immune response in a mammal, said method comprising detecting the level of expression of a gene encoding PRO69457, PRO69458, PRO52268, PRO69459, PRO62927, PRO59136, PRO37121, PRO69460, PRO60475, PRO34451, PRO38070, PRO23756, PRO10404, PRO69461, PRO70006, PRO69462, PRO2081, PRO70007, PRO69463, PRO62908, PRO69464, PRO52804, PRO60438, PRO69465, PRO37421, PRO37596, PRO36124, PRO69466, PRO60499, PRO69467, PRO61824, PRO69468, PRO21341, PRO38213, PRO69469, PRO37172,

PRO35991, PRO36905, PRO69470, PRO36451, PRO69471, PRO37492, PRO70008, PRO69472,
PRO69473, PRO36996, PRO22613, PRO69475, PRO61755, PRO70009, PRO69476, PRO4881,
PRO12876, PRO70010, PRO37534, PRO21928, PRO69478, PRO69479, PRO69480, PRO69481,
PRO69482, PRO69483, PRO38642, PRO69484, PRO66269, PRO1723, PRO22297, PRO61349,
5 PRO69485, PRO69486, PRO69487, PRO36963, PRO23814, PRO57980, PRO20128, PRO4551,
PRO69488, PRO39268, PRO69489, PRO69490, PRO69491, PRO69492, PRO37713, PRO58993,
PRO69493, PRO69494, PRO69495, PRO70011, PRO62861, PRO36640, PRO36766, PRO69497,
PRO69498, PRO69499, PRO69500, PRO69501, PRO70012, PRO69503, PRO69474, PRO69505,
PRO69506, PRO69507, PRO51301, PRO69508, PRO69509, PRO69510, PRO69511, PRO51309,
10 PRO50578, PRO69512, PRO69513, PRO69514, PRO10607, PRO61705, PRO49214, PRO39648,
PRO69515, PRO38497, PRO29371, PRO70013, PRO69516, PRO69517, PRO69518, PRO70014,
PRO69520, PRO69521, PRO69522, PRO69523, PRO60513, PRO2512, PRO69524, PRO12569,
PRO69525, PRO69526, PRO69527, PRO69528, PRO69529, PRO12166, PRO2154, PRO69530,
PRO51916, PRO52174, PRO69531, PRO69532, PRO69533, PRO69534, PRO54728, PRO70015,
15 PRO69536, PRO69537, PRO37498, PRO22175, PRO69538, PRO37015, PRO12187, PRO69539,
PRO69880, PRO69541, PRO69542, PRO69543, PRO70016, PRO69545, PRO50197, PRO69546,
PRO69547, PRO69548, PRO69549, PRO69550, PRO69551, PRO69552, PRO37460, PRO42223,
PRO69553, PRO69554, PRO69555, PRO61014, PRO59915, PRO37891, PRO69556, PRO12875,
PRO70017, PRO70018, PRO4426, PRO69558, PRO69559, PRO37676, PRO69560, PRO69561,
20 PRO69562, PRO63204, PRO70019, PRO69564, PRO62830, PRO69565, PRO69566, PRO69567,
PRO49675, PRO69568, PRO2013, PRO69569, PRO69570, PRO69571, PRO36403, PRO4676,
PRO37657, PRO62097, PRO38081, PRO69572, PRO69573, PRO69574, PRO69883, PRO69576,
PRO37584, PRO11603, PRO70020, PRO51695, PRO69579, PRO69580, PRO69581, PRO69582,
PRO69583, PRO69584, PRO69585, PRO69586, PRO69587, PRO69588, PRO69589, PRO70021,
25 PRO69590, PRO70022, PRO69592, PRO37029, PRO69593, PRO69594, PRO69595, PRO1207,
PRO69596, PRO69597, PRO51139, PRO62545, PRO3615, PRO38036, PRO69598, PRO4701,
PRO69599, PRO69600, PRO69601, PRO69887, PRO69603, PRO69604, PRO70023, PRO69606,
PRO69607, PRO69608, PRO69609, PRO69610, PRO9902, PRO69611, PRO69612, PRO69613,
PRO69614, PRO69615, PRO70024, PRO69616, PRO49619, PRO69617, PRO69618, PRO38040,
30 PRO69619, PRO69620, PRO69621, PRO69622, PRO4401, PRO70025, PRO69625, PRO12025,
PRO70026, PRO69627, PRO69628, PRO22637, PRO69629, PRO70027, PRO70028, PRO69632,
PRO69634, PRO36857, PRO69893, PRO69635, PRO6180, PRO69637, PRO69638, PRO69639,
PRO69640, PRO69641, PRO62766, PRO53782, PRO61472, PRO38179, PRO69642, PRO69643,
PRO69644, PRO69645, PRO11608, PRO69646, PRO59825, PRO69647, PRO69648, PRO70029,
35 PRO1213, PRO70030, PRO50195, PRO69651, PRO37538, PRO69652, PRO59210, PRO23374,
PRO24844, PRO70031, PRO69653, PRO69654, PRO69655, PRO69656, PRO70032, PRO69659,
PRO69660, PRO58054, PRO69661, PRO69662, PRO69898, PRO69664, PRO69665, PRO69666,
PRO69667, PRO69669, PRO69671, PRO69672, PRO58204, PRO49419, PRO69673, PRO69674,
PRO49810, PRO70033, PRO69676, PRO58076, PRO69677, PRO69678, PRO69679, PRO1718,
40 PRO51161, PRO69680, PRO59281, PRO36102, PRO61799, PRO69681, PRO69682, PRO69901,

PRO69684, PRO69685, PRO69686, PRO69687, PRO38469, PRO69688, PRO70034, PRO59354, PRO59189, PRO38197, PRO69902, PRO69690, PRO61569, PRO69903 or PRO1970 polypeptide (a) in a test sample of tissue cells obtained from the mammal, and (b) in a control sample of known normal tissue cells of the same cell type, wherein a higher or lower level of expression of said gene in the test sample as compared to the control sample is indicative of the presence of an inflammatory immune response in the mammal from which the test tissue cells were obtained.

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FIGURE 1

GCGTGAAGCGCGGACCTTTCAACAAGGGCTTTATTAATTCTCACGCTGCGGCCCCGGAAAGCGATGAGGTGGCG
GCTAATTGCTCCCTACGGGTGAAGAGACCTCTGTTGGATCCCCGCTTCGAGGGTTACAAGCTCTCTCTTGAGCCG
CTGCCTTGTTACCAGCTGGAGCTTGACGCAGCTGTGGCAGAGGTAAACTTCGAGATGATCAATATACACTGGAA
CACATGCATGCTTTTGAATGTATAATTACCTGCCTGTGATTGATGATCAAGACAGTGTCTACTATATTGAT
ACCTTGGGAAGAATTATGAATTTAACAGTAATGCTGGACACTGCCTTAGGAAAACCACGAGAGGTGTTTCGACTT
CCTACAGATTGACAGCATGTGACAACCGTCTTTGTGCATCTATCCATTTCTCATCTTCTACCTGGGTACCTTG
TCAGATGGAAGTGAAGATTGTATGTCATTGGAACAGGTGAACGTGGAAATAGCGCTTCTGAAAAATGGGAGATT
ATGTTTAAATGAAGAAGTGGGGATCCTTTTATTATAATTCACAGTATCTCACTGCTAAATGCTGAAGAACATTCT
ATAGCTACCTACTTCTTCGAATAGAGAAAGAGGAATTGGATATGAAAGGAAGTGGTTTCTATGTTTCTCTGGAG
TGGGTCACTATCAGTAAGAAAAATCAAGATAATAAAAAATATGAAATTATTAAGCGTGATATTCTCCGTGGAAAG
TCAGTGCCACATTATGCTGCTATTGAGCCTGATGGAAATGGTCTAATGATTGTATCCTACAAGTCTTTAACATTT
GTTTCAGGCTGGTCAAGATCTTGAAGAAAATATGGATGAAGACATATCAGAGAAAATCAAAGAACCTCTGTATTAC
TGGCAACAGACTGAAGATGATTTGACAGTAACCATACGGCTTCCAGAAGACAGTACTAAGGAGGACATTCAAATA
CAGTTTTTGCCTGATCACATCAACATTGTACTGAAGGATCACCAGTTTTTAGAAGGAAAACCTCTATTCTCTATT
GATCATGAAAGCAGTACATGGATAATTAAAGAGAGTAATAGCTTGGAGATTTCTTGATTAAGAAGAATGAAGGA
CTGACCTGGCCAGAGCTAGTAATTGGAGATAACAAGGGGAACCTTATAAGAGATTCAGCCCAGTGTGCTGCAATA
GCTGAACGTTTGATGCATTTGACCTCTGAAGAAGTGAATCCAAATCCAGATAAAGAAAAACCACTTGCAGTGCT
CAAGAGTTAGAAGAATGTGATATTTTCTTTGAAGAGAGCTCCAGTTTATGCAGATTTGATGGCAATACATTAAAA
ACTACTCATGTGGTGAATCTTGAAGCAACCAGTACCTTTTCTCTGTCTAGTGGATCCTAAAGAAATGCCCTGC
TTCTGTTTGCGCCATGATGTTGATGCCCTACTCTGGCAACCACACTCCAGCAAACAAGATGATATGTGGGAGCAC
ATCGCAACTTTCAATGCTTTAGGCTATGTCCAAGCATCAAAGAGAGACAAAAAATTTTTGCTGTGCTCCAAAT
TACTCGTATGCAGCCCTTGTGAGTGCCTTCGTCGAGTATTCATCTATCGTCAGCCTGCTCCCATGTCCACTGTA
CTTTACAACAGAAAGGAAGGCAGGCAAGTAGGACAGGTTGCTAAGCAGCAAGTAGCAAGCCTAGAAACCAATGAT
CCTATTTTAGGATTTAGGCAACAAATGAGAGATTATTTGTTCTTACTACCAAAAACCTCTTTTAATAAAAGTA
AATACAGAGAATTAAATTATTCTAACATATTGGCCTCTTTGTACTGGAAAAGTATTCAGTGGTACCTGGAGGTCTG
GACAGTTATACTGTAACCTCTTAAGTTTTAATGTGCTAAATATATCTTGATGATTTTTTTATTTTAAATAACAT
TGGAATATATTCAAGAGATTATGATTCTGTAAAGCTGTGGAATGAAGCTGCAGATTTAGAGAACATTGGCTTCT
GAAAAAAAAAAGAGTGAAGATAGTACTAGCAAGTATACTTATTTTTTAAACAGGCTAGAATCTCATGTTTTAT
ATGAAAGATGTACAATTCAGTGTTTAAAAATAAAATATTTATTGTGT

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FIGURE 2

MEVAANCSLRVKRPLLDPRFEGYKLSLEPLPCYQLELDAAAVEVKLRDDQYTLEHMHAFGMYNYLHCDSWYQDSV
YYIDTLGRIMNLTVMMLDTALGKPREVFRLPDTLTACDNRLCASIHFSSSTWVTLSDGTGRLYVIGTGERGNSASE
KWEIMFNEELGDPFIIHSISLLNAEEHSIATLLLRIEKEELDMKSGSFYVSLEWVTISKKNQDNKKYEIIKRDI
LRGKSVPHYAAIEPDGNGLMIVSYKSLTFVQAGQDLEENMDEIDSEKIKEPLYWQQTEDDLTVTIRLPEDSTKE
DIQIQFLPDHINIVLKDHFLEGKLYSSIDHESSTWIKESNSLEISLIKNEGLTWPELVIGDKQGELIRDSAQ
CAAIAERLMHLTSEELNPNPDKEKPPCSAQELEECDIFFEESSLCRFDGNTLKTHVNVNLGSNQYLFVIVDPK
EMPCFCLRHDVDALLWQPHSSKQDDMWEHIATFNALGYVQASKRDKKFFACAPNYSYAALCECLRRVFIYRQPAP
MSTVLYNRKEGRQVGQVAKQQVASLETNDPILGFQATNERLEVLTTKNLFLIKVNTEN

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FIGURE 3

GAATTCCGGTGAAGTTGACCGGGTCCACCCGAAGCTTGTGCGCGTGCAGGTGCTCAGGGCGGACGCGGCACGGA
GACGGCGGCAGCCTGGACTAGGTGGCAGGCCCTGCATCATGGAAGAACTCTTCTAATGCAAGTGGTACTTTTGCCA
TACGCCCTTTTAAAGATACTGTGTCAAGATAACCCTTCGCACAACGTGTTCTGTTCTCCTGTGAGCATCTCCTCTG
CCCTGGCCATGGTTCTCCTAGGGGCAAAGGGAAACACCGCAACCCAGATGGCCCAGGCACTGTCTTTAAACACAG
AGGAAGACATTTCATCGGGCTTTCCAGTCGCTTCTCACTGAAGTGAACAAGGCTGGCACACAGTACCTGCTGAGAA
CGGCCAACAGGCTCTTTGGAGAGAAAACCTTGTGAGTTCTCTCAACGTTTAAGGAATCCTGTCTTCAATTCTACC
ATGCTGAGCTGAAGGAGCTTTTCTTTATCAGAGCTGCAGAAGAGTCCAGGAAACACATCAACACCTGGGTCTCAA
AAAAGACCGAAGGTAAAATTGAAGAGTTGTTGCCGGGTAGCTCAATTGATGCAGAAACCAGGCTGGTTCTTGTC
ATGCCATCTACTTCAAAGGAAAGTGAATGAACCGTTTGACGAAACATACACAAGGGAAATGCCCTTTAAATAA
ACCAGGAGGAGCAAAGGCCAGTGCAGATGATGTATCAGGAGGCCACGTTTAAGCTCGCCACGTTGGCGAGGTGC
GCGCGCAGCTGCTGGAGCTGCCCTACGCCAGGAAGGAGCTGAGCCTGCTGGTGCTGCTGCCTGACGACGGCGTGG
AGCTCAGCACGGTGGAAAAAAGTCTCACTTTTGAGAACTCACAGCCTGGACCAAGCCAGACTGTATGAAGAGTA
CTGAGGTTGAAGTTCTCCTTCCAAAATTTAACTACAAGAGGATTATGACATGGAATCTGTGCTTCGGCATTG
GAATTGTTGATGCCCTTCCAACAGGGCAAGGCTGACTTGTCGGCAATGTCAGCGGAGAGAGACCTGTGTCTGTCCA
AGTTTCGTGCACAAGAGTTTTGTGGAGGTGAATGAAGAAGGCACCGAGGCAGCGGCAGCGTCGAGCTGCTTTGTAG
TTGCAGAGTGCTGCATGGAATCTGGCCCCAGGTTCTGTGCTGACCACCCTTTCTTTTCTTCATCAGGCACAACA
GAGCCAACAGCATTCTGTTCTGTGGCAGGTTCTCATCGCCATTAAGGGTGCACCTACCGTGCACCTCGGCCATTT
CCTCTTCTGTGTCCCCAGATCCCCACTACAGCTCCAAGAGGATGGGCCTAGAAAGCCAAGTGCAAAGATGAGGG
CAGATTCTTACCTGTCTGCCCTCATGATTTGCCAGCATGAATTCATGATGCTCCACACTCGCTTATGCTACTTA
ATCAGAATCTTGAGAAAATAGACCATAATGATTCCCTGTTGTATTAAATTTGCCATCCCCGAATTCCTATAGGA
TGGCAAGCAAAGTTCTTCTAGAATTCCACATGCAATTCCTCTGGCGACCCTGTGCTTTCCTGACACTGCGAATA
CATTCCTTAACCCGCTGCCTCAGTGGAATAAATGGTGCTAGCCGGAATTC

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FIGURE 4

METLSNASGTFAIRLLKILCQDNPSHNVFCSPVSISSALAMVLLGAKGNTATQMAQALSLNTEEDIHRAFQSLLT
EVNKAGTQYLLRTANRLFGEKTCQFLSTFKESCLQFYHAELKELSFIRAAEESRKHINTWVSKKTEGKIEELLPG
SSIDAETRLVLVNAIYFKGKWNEPFDETYTREMPFKINQEEQRPVQMMYQEATFKLAHVGEVRAQLLELPYARKE
LSLLVLLPDDGVELSTVEKSLTFEKLTAWTKPDCMKSTEVEVLLPKFKLQEDYDMESVLRHLGIVDAFQQGKADL
SAMSAERDLCLSKFVHKSFVEVNEEGTEAAAASSCFVVAECCMESGPRFCADHPFLFFIRHNRANSILFCGRFSS
P

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FIGURE 5

GCTAAGCGTCCCAGCCGCATCCTCCCGCAGCGACGGCGGCCCGGGACCGGGCTGTGAACCATGAACACCCGCA
ATAGAGTGGTGAACTCCGGGCTCGGCGCCTCCCCTGCCTCCCGCCCCGACCCGGGATCCCCAGGACCCTTCTGGGC
GGCAAGGGGAGCTGAGCCCCGTGGAAGACCAGAGAGAGGGTTTGGAGGCAGCCCCTAAGGGCCCTTCGCGGGAGA
GCGTCGTGCACGCGGGCCAGAGGCGCACAAAGTGCATACACCTTGATAGCACCAAATATAAACCGGAGAAATGAGA
TACAAAGAATGCGGAGCAGGAGCTGGCCAACCTGGAGAAGTGAAGGAGCAGAACAGAGCTAAACCGGTTACCT
GGTGGCCAGACGGCTAGGTGGAAGCCAGTCAGAACTGAAGTCAGACAGAAACAACAACCTCCAGCTGATGCAATC
TAAATACAAGCAAAAGCTAAAAAGAGAAGAATCTGTAAGAATCAAGAAGGAAGCTGAAGAAGCTGAACCTCCAAAA
AATGAAGGCAATTGAGAGAGAGAAGAGCAATAAACTGGAGGAGAAAAAAGACTTCAAGAAAACCTTAGAAGAGA
AGCATTGTAGAGAGCATCAGCAATACAAAACCGCTGAGTTCTTGAGCAAACTGAACACAGAATCGCCAGACAGAAG
TGCCTGTCAAAGTGCTGTTTGTGGCCCAATCCTCAACATGGGCCAGAAGCTGGGCTTACAGAGATTCTCTAAA
GGCAGAAGAAAAACAGAAAATTGCAAAAGATGAAGGATGAACAACATCAAAAGAGTGAATTACTGGAAGTGAACG
GCAGCAGCAAGAGCAAGAAAGAGCCAAAATCCACCAGACTGAACACAGGAGGGTAAATAATGCTTTTCTGGACCG
ACTCCAAGGTAAAAGTCAACCAGGTGGCCTCGAGCAATCTGGAGGCTGTTGGAATATGAATAGTGGTAACAGCTG
GGGTATATAGAAAAATATTGACTCCTATCTGGCCTTCATCAACTGACCTCGAAAAGCCTCATGAGATGCTTTTTC
TTAATGTGATTTTGTTCAGCCTCACTGTTTTTACCTTAATTTCAACTGCCCACACACTTGACCGTGCAGTCAGGA
GTGACTGGCTTCTCCTTGTCCCTCATTTATGCAIGTTTGGAGGAGCTGATTCTGAACTCATATTTAATCTCTACT
GCCAGGGAAATGCTACATTATTTTTCTAATTGGAAGTATAATTAGAGTGATGTTGGTAGGGTGGAAAAAGAGGGA
GTCATTGATGCTTTTCAAGTTAATCAGAGCTATGGGTGCTACAGGCTTGTCTTTCTAAGTGACATATTCTTATCT
AATTCTCAGATCAGGTTTTGAAAAGCTTTGGGGTCTTTTTAGATTTTAAATCCCTACTTTCTTTATGGTACAAAT
ATGTACAAAAGAAAAAGTCTTATATTCTTTTACACAAATTTATAAATAAATTTTGAACCTCCTTCTGTAT

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FIGURE 6

MKAIQREKSNKLEEKRLQENLRREAFREHQYKTAEFLSKLNTESPDRSACQSAVCGPQSSTWARSWAYRDSLK
AEENRKLQKMKDEQHOKSELLELKROQQEQERAKIHQTEHRRVNNAFLDRLOGKSQPGGLEQSGGCWNMNSGNSW
GI

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FIGURE 7

TAGTTATTAAAGTTCCTATGCAGCTCCGCCTCCGTCCGGCCTCATTTCTCAAAAAATCCCTGCTTCCCCGCTC
GCCACGCCCTCCTGCTACCCGGCTTTAAAGCTAGTGAGGCACAGCCTGCGGGGAACGTAGCTAGCTGCAAGCAGA
GGCCGGC**ATG**ACCACCAGCAGCGACGCAGCCTGCAAGCCTTCAGGATTATATCCGGAAGACCCTGGACCCTAC
CTACATCCTGAGCTACATGGCCCCCTGGTTTAGGGAGGAAGAGGTGCAGTATATTAGGCTGAGAAAAACAACA
GGGCCCCAATGGAGGCTGCCACACTTTTTCTCAAGTTCCTGTTGGAGCTCCAGGAGGAAGGCTGGTTCCGTGGCTT
TTTGGATGCCCTAGACCATGCAGGTTATTCTGGACTTTATGAAGCCATTGAAAGTTGGGATTTCAAAAAAATTGA
AAAGTTGGAGGAGTATAGATTACTTTTAAACGTTTACAACCAGAATTTAAACCAGAATTATCCCAACCGATAT
CATTTCTGATCTGTCTGAATGTTTAATTAATCAGGAATGTGAAGAAATTCTACAGATTTGCTCTACTAAGGGGAT
GATGGCAGGTGCAGAGAAATTGGTGGAATGCCTTCTCAGATCAGACAAGGAAAACCTGGCCCCAAACCTTTGAAACT
TGCTTTGGAGAAAGAAAGGAACAAGTTCAGTGAACGTGTGGATTGTAGAGAAAGGTATAAAAGATGTTGAAACAGA
AGATCTTGAGGATAAGATGGAACTTCTGACATACAGATTTTCTACCAAGAAGATCCAGAATGCCAGAATCTTAG
TGAGAATTCAATGTCACCTTCAGAAAGTGTCTGATACAACTTGTACAGCCCATTAAACCAAGAAATTACCAATT
AGAGCTTGCTTTGCCTGCTATGAAAGGAAAAACAATAATATGTGCTCCTACAGGTTGTGGAAAAACCTTTGT
TTCAGTGTCTTATATGTGAACATCATCTTAAAAAATTTCCACAAAGGACAAAAGGGGAAAGTTGTCTTTTTTGCGAA
TCAGATCCCAGTGTATGAACAGCAGAAATCTGTATTTCTCAAAATACTTTGAAAGACATGGGTATAGAGTTACAGG
CATTTCTGGAGCAACAGCTGAGAATGTCCCAGTGGAACAGATTGTTGAGAACAATGACATCATCTTTAACTCC
ACAGATTCTTGGAACAACCTTAAAAAGGGAACGATTCCATCACTATCCATCTTTACTTTGATGATATTTGATGA
ATGCCACAACACTAGTAAACAACACCCGTACAATATGATCATGTTTAATTATCTAGATCAGAACTTGGAGGATC
TTCAGGCCCCACTGCCCCAGGTCAATGGGCTGACTGCCTCGGTTGGTGTGGGGATGCCAAAAACACAGATGAAGC
CTTGGATTATATCTGCAAGCTGTGTGCTTCTCTTGATGCGTCAGTGATAGCAACAGTCAAACACAATCTGGAGGA
ACTGGAGCAAGTTGTTTATAAGCCCCAGAAGTTTTTCAGGAAAGTGGAATCACGGATTAGCGACAAATTTAAATA
CATCATAGCTCAGCTGATGAGGGACACAGAGAGTCTGGCAAAGAGAATCTGCAAAGACCTCGAAAACCTTATCTCA
AATTCAAAATAGGGAATTTGGAACACAGAAATATGAACAATGGATTGTTACAGTTCAGAAAGCATGCATGGTGT
CCAGATGCCAGACAAAGATGAAGAGAGCAGGATTTGTAAAGCCCTGTTTTTATACACTTCACATTTGCGGAAATA
TAATGATGCCCTCATTATCAGTGAGCATGCACGAATGAAAGATGCTCTGGATTACTTGAAAGACTTCTTCAGCAA
TGTCCGAGCAGCAGGATTGGAAGAGATTGAGCAAGATCTTACTCAGAGATTGAAGAAAAGCTGCAGGAACTAGA
AAGTGTTCAGGGATCCCAGCAATGAGAATCCTAAACTTGAAGACCTCTGCTTCATCTTACAAGAAGAGTACCA
CTTAAACCCAGAGACAATAACAATTCTCTTTGTGAAAACCAGAGCACTTGTGGACGCTTTAAAAAATTGGATTGA
AGGAAATCCTAAACTCAGTTTTCTAAACCTGGCATATTGACTGGACGTGGCAAAAACAAATCAGAACACAGGAAT
GACCTCCCGGCACAGAAGTGTATATTGGATGCATTCAAAGCCAGTGGAGATCACAATATTCTGATTGCCACCTC
AGTTGCTGATGAAGGCATTGACATTGCACAGTGCAATCTTGTCTATCCTTTATGAGTATGTGGGCAATGTCATCAA
AATGATCCAAACCAGAGGCAGAGGAAGAGCAAGAGGTAGCAAGTGCTTCTTCTGACTAGTAATGCTGGTGTAAAT
TGAAAAAGAACAATAAACATGTACAAAGAAAAAATGATGAATGACTCTATTTACGCCCTTCAGACATGGGACGA
AGCAGTATTTAGGGAAAAGATTCTGCATATACAGACTCATGAAAAATTCATCAGAGATAGTCAAGAAAAACCAA
ACCTGTCCCTGATAAGGAAAATAAAAACTGCTCTGCAGAAAGTGCAAAGCCTTGGCATGTTACACAGCTGACGT
AAGAGTGATAGAGGAATGCCATTACACTGTGCTTGGAGATGCTTTTAAGGAATGCTTTGTGAGTAGACCACATCC
CAAGCCAAAGCAGTTTTCAAGTTTTGAAAAAGAGCAAAGATATTCTGTGCCCAGACAGAACTGCAGCCATGACTG
GGGAATCCATGTGAAGTACAAGACATTTGAGATTCAGTTATAAAAAATTGAAAGTTTTGTGGTGGAGGATATTGC
AACTGGAGTTCAGACACTGTACTCGAAGTGAAGGACTTTCAATTTTGAGAAGATACCATTTGATCCAGCAGAAAT
GTCCAAAT**AGAT**ATCAGGTCTCAATCTTCAGCTACAGGGAATGAGTAACCTTTGAGTGGAGAAGAAACAAACATAG
TGGGTATAATCATGGATCGCTTGTACCCCTGTGAAAATATATTTTTTAAAAATAAAAAAAAAAAAAA

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FIGURE 8

MTTEQRRSLQAFQDYIRKTLDPITYILSYMAPWFREEEVQYIIQAEKNNKGPMEEATLFLKFLLLELQEEGWFRGFLD
ALDHAGYSGLYEAIESWDFKKIEKLEEYRLLLKRLQPEFKTRIIPTDIISDLSECLINQECEEILQICSTKGMMMA
GAEKLVECLLRSDKENWPKTLKLALEKERNKFSELWIVEKGIKDVETEDLEDKMETSIDIQIFYQEDPECQNLSEN
SCPPSEVSDTNLYSPFKPRNYQLELALPAMKGKNTIICAPTGCCKTFVSLICEHHLKKFPQGQKGKVVFANQI
PVYEQQKSVFSKYFERHGYRVTGISGATAENVPEQIVENNDIIILTPQILVNNLKKGTIPSLSIFTLMIFDECH
NTSKQHPYNMIMFNLDQKLGGSSGPLPQVIGLTASVGVGDAKNTDEALDYICKLCASLDASVIATVKHNLEELE
QVYKPKQKFFRKVESRISDKFYIIAQLMRDTESLAKRICKDLENLSQIQNREFGTQKYEQWIVTVQKACMVQM
PDKDEESRICKALFLYTSHLRKYNDALIISEHARMKDALDYLDKDFFSNVRAAGFEEIEQDLTQRFEEKLQELSV
SRDPSNENPKLEDLCFILQEEYHLNPETITILFVKTRALVDALKNWIEGNPKLSFLKPGILTGRGKTNQNTGMTL
PAQKCILDAFKASGDHNLIIATSVADGIDIAQCNLVILYEVGNVIKMIQTRGRGRARGSKCFLLTSNAGVIEK
EQINMYKEKMMNDSILRLQTWDEAVFREKILHIQTHEKFIRDSQEKPKPVPDKENKKLLCRCKALACYTADVRV
IEECHYTVLGDAFKECFVSRPHPKPKQFSSFEKRAKIFCARQNCSDWGIHVKYKTFEIPVIKIESFVVEDIATG
VQTLYSKWKDFHFEKIPFDPAEMSK

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FIGURE 9

GGAAAAAAGCGACTTGTGGCGGTCGAGCGTGGCGCAGGCGAATCCTCGGCACTAAGCAAATATGACCTCGCGGC
GGCAGCGGAGCCGGGCGCCGGCAGCCAGCACCTGGAGGTCCGCGACGAGGTGGCCGAGAAGTGCCAGAACTGTT
CCTGGACTTCTTGGAGGAGTTTCAGAGCAGCGATGAGAAATTAAATACTTGCAATTAGCAGAGGAACTGATTGCG
TCCTGAGAGAAACACATTGGTTGTGAGTTTTGTGGACCTGGAACAATTTAACCCAGCAACTTTCCACCACCATTCA
AGAGGAGTTCTATAGAGTTTACCCCTTACCTGTGTCGGGCCTTGAAAACATTTCGTCAAAGACCGTAAAGAGATCCC
TCTTGCCAAGGATTTTTATGTTGCATTCCAAGACCTGCCTACCAGACACAAGATTTCGAGAGCTCACCTCATCCAG
AATTGGTTTGGCTCACTCGCATCAGTGGGCAGGTGGTGGGACTCACCCAGTTCACCCAGAGCTTGTGAGCGGAAC
TTTTCTGTGCTTGGACTGTCAGACAGTGATCAGGGATGTAGAACAGCAGTTCAAATACACACAGCCAAACATCTG
CCGAAATCCAGTTTGTGCCAACAGGAGGAGATTCTTACTGGATACAAATAAATCAAGATTTGTTGATTTTCAAAA
GGTTTCGTATTCAAGAGACCCAAGCTGAGCTTCCTCGAGGGAGTATCCCCCGCAGTTTAGAAGTAATTTTAAGGGC
TGAAGCTGTGGAATCAGCTCAAGCTGGTGACAAGTGTGACTTTACAGGGACACTGATTGTTGTGCCTGACGTCTC
CAAGCTTAGCACACCAGGAGCACGTGCAGAACTAATCCCCGTGTCAGTGGTGTGATGGATATGAGACAGAAGG
CATTTCGAGGACTCCGGGCCCTTGGTGTTAGGGACCTTTCTTATAGGCTGGTCTTTCTGCTGCTGTGTTGCGCC
AACCAACCCAAGGTTTGGGGGAAAGAGCTCAGAGATGAGGAACAGACAGCTGAGAGCATTAAGAACCAATGAC
TGTGAAAGAATGGGAGAAAGTGTGAGATGAGTCAAGATAAAAACTATACCACAATCTTTGTACCAGCCTGTT
CCCTACTATACATGGCAATGATGAAGTAAACGGGGTGTCTGCTGATGCTCTTTGGTGGCGTTCCAAAGACAAC
AGGAGAAGGGACCTCTCTTCGAGGGGACATAAATGTTTGCATTGTTGGTGACCCAAGTACAGCTAAGAGCCAATT
TCTCAAGCACGTGGAGGAGTTCAGCCCCAGAGCTGTCTACACCAGTGGTAAAGCGTCCAGTGCTGCTGGCTTAAC
AGCAGCTGTTGTGAGAGATGAAGAATCTCATGAGTTTGTGATTGAGGCTGGAGCTTTGATGTTGGCTGATAATGG
TGTGTGTTGATTGATGAATTTGATAAGATGGACGTGCGGGATCAAGTTGCTATTTCATGAAGCTATGGAACAGCA
GACCATATCCATCACTAAAGCAGGAGTGAAGGCTACTCTGAACGCCCGGACGTCCATTTTGGCAGCAGCAAACCC
AATCAGTGGACACTATGACAGATCAAAATCATTGAAACAGAATATAAATTTGTCAGCTCCCATCATGTCCCGATT
CGATCTCTTCTTTATCCTTGTGGATGAATGTAATGAGGTTACAGATTATGCCATTGCCAGGCGCATAGTAGATTT
GCATTCAAGAATTGAGGAATCAATTGATCGTGTCTATTCCCTCGATGATATCAGAAGATATCTCTCTTTGCAAG
ACAGTTTAAACCCAAGATTTCCAAAGAGTCAGAGGACTTCATTGTGGAGCAATATAAACATCTCCGCCAGAGAGA
TGGTTCTGGAGTGACCAAGTCTTCATGGAGGATTACAGTGCAGACAGCTTGAGAGCATGATTGCTCTCTCTGAAGC
TATGGCTCGGATGCACTGCTGTGATGAGGTCCAACCTAAACATGTGAAGGAAGCTTTCCGGTTACTGAATAAATC
AATCATCCGTGTGGAACACCTGATGTCAATCTAGATCAAGAGGAAGAGATCCAGATGGAGGTAGATGAGGGTGC
TGGTGGCATCAATGGTCATGCTGACAGCCCTGCTCCTGTGAACGGGATCAATGGCTACAATGAAGACATAAATCA
AGAGTCTGCTCCCAAAGCCTCCTTAAGGCTGGGCTTCTCTGAGTACTGCCGAATCTCTAACCTTATTGTGCTTCA
CCTCAGAAAGGTGGAAGAAGAAGAGGACGAGTCAGCATTAAAGAGGAGCGAGCTTGTTAACTGGTACTTGAAGGA
AATCGAATCAGAGATAGACTCTGAAGAAGAACTTATAAATAAAAAAAGAATCATAGAGAAAGTTATTCATCGACT
CACACACTATGATCATGTTCTAATTGAGCTCACCCAGGCTGGATTGAAAGGCTCCACAGAGGGAAGTGAGAGCTA
TGAAGAAGATCCCTACTTGGTAGTTAACCCTAACTACTTGCTCGAAGATTGAGATAGTGAAAGTAACTGACCAGA
GCTGAGGAAGTGTGGCACAGCACCTCGTGGCCTGGAGCCTGGCTGGAGCTCTGCTAGGGACAGAAGTGTCTTCTGG
AAGTGATGCTTCCAGGATTTGTTTTTCAGAAACAAGAATTGAGTTGATGGTCCTATGTGTACATTATCACAGGT
TTCATACCAACACAGGCTTCAGCACTTCCTTTGGTGTGTTTCTGTCCCAGTGAAGTTGGAACCAATAATGTGT
AGTCTCTATAACCAATACCTTTGTTTTCATGTGTAAGAAAAGGCCATTACTTTTAAGGTATGTGCTGTCTTATT
GAGCAAATAACTTTTTTTCAATTGCCAGCTACTGCTTTTATTCATCAAAATAAAATAACTTGTCTGT

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FIGURE 10

MDLAAAAEPGAGSQHLEVRDEVAEKCQKLFLDFLEEFQSSDGEIKYLQLAEELIRPERNTLVVSFVDLEQFNQQL
STTIQEEFYRVYPYLCRALKTFVKDRKEIPLAKDFYVAFQDLPTRHKIRELTSSRIGLLTRISGQVVRTHPVHPE
LVSGTFLCLDCQTVIRDVEQQFKYTQPNICRNPVCANRRRFLDTNKSRFVDFQKVRIQETQAELPRGSIPRSLE
VILRAEAVESAQAGDKCDFGTGLIVVPDVSKLSTPGARAETNSRVSGVDGYETEGIRGLRALGVRDLSYRLVFLA
CCVAPTNPFRGGKELRDEEQTAESIKNQMTVKEWEKVFEMSQDKNLYHNLCTSLFPTIHGNDEVKRGVLLMLFGG
VPKTTGEGTSLRGDINVCIVGDPSTAKSQFLKHVEEFSPRAVYTSKGASSAAGLTAAVVRDEESHEFVIEAGALM
LADNGVCCIDEFDKMDVRDQVAIHEAMEQQTISITKAGVKATLNARTSILAAANPISGHYDRSKSLKQNINLSAP
IMSRFDLFFILVDECNEVTDYAIARRIVDLHSRIEESIDRVYSLDDIRRYLLFARQFKPKISKESEDFIVEQYKH
LRQRDGSVGTKSSWRITVRQLESMIRLSEAMARMHCCDEVQPKHVKEAFRLLNKSIIRVETPDVNLDQEEEIOME
VDEGAGGINGHADSPAPVNGINGYNEDINQESAPKASLRIGFSEYCRISNLIVLHLRKVEEEEDESALKRSELVN
WYLKEIESEIDSEEELINKKRIIEKVIHRLTHYDHVLIELTQAGLKGSTEGSESYEEDPYLVVNPNYLLED

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FIGURE 11

ATATAACCGCGTGGCCCGCGCGCGCTTCCCTCCCGGCGCAGTCACCGGCGCGGTCTATGGCTGCGACTTCTCT
AATGTCTGCTTTGGCTGCCCCGGCTGCTGCAGCCCGCGCACAGCTGCTCCCTTCGCCTTCGCCCTTTCCACCTCGC
GGCAGTTCGAAATGAAGCTGTTGTCAATTTCTGGAAGGAACTGGCCCAGCAGATCAAGCAGGAAGTGCGGCAGGA
GGTAGAAGAGTGGGTGGCCTCAGGCAACAAACGGCCACACCTGAGTGTGATCCTGGTTGGCGAGAATCCTGCAAG
TCACTCCTATGTCTCAACAAAACCAGGGCAGCTGCAGTTGTGGGAATCAACAGTGAGACAATTATGAAACCAGC
TTCAATTTTCAGAGGAAGAATTGTTGAATTTAATCAATAAACTGAATAATGATGATAATGTAGATGGCCTCCTTGT
TCAGTTGCCTCTTCCAGAGCATATTGATGAGAGAAGGATCTGCAATGCTGTTTCTCCAGACAAGGATGTTGATGG
CTTTCATGTAATTAATGTAGGACGAATGTGTTTGGATCAGTATTCCATGTTACCGGCTACTCCATGGGGTGTGTG
GGAAATAATCAAGCGAAGTGGCATTCCAACCCTAGGGAAGAATGTGGTTGTGGCTGGAAGGTCAAAAAACGTTGG
AATGCCCATTGCAATGTTACTGCACACAGATGGGGCGCATGAACGTCCCGAGGTGATGCCACTGTTACAATATC
TCATCGATATACTCCCAAAGAGCAGTTGAAGAAACATACAATCTTGCAGATATTGTAATATCTGCTGCAGGTAT
TCCAAATCTGATCACAGCAGATATGATCAAGGAAGGAGCAGCAGTCATTGATGTGGGAATAAATAGAGTTCACGA
TCCTGTAAGTGCCAAACCAAGTTGGTTGGAGATGTGGATTTTGAAGGAGTCAGACAAAAGCTGGGTATATCAC
TCCAGTTCTGGAGGTGTTGGCCCCATGACAGTGGCAATGCTAATGAAGAATACCATTATGCTGCAAAAAGGT
GCTGAGGCTTGAAGAGCGAGAAGTGTGTAAGTCTAAAGAGCTTGGGGTAGCCACTAATTAACTACTGTGTCTTCT
GTGTCACAAACAGCACTCCAGGCCAGCTCAAGAAGCAAAGCAGGCCAATAGAAATGCAATATTTTAAATTTATTC
TACTGAAATGGTTTAAATGATGCCTTGTATTTATTGAAAGCTTAAATGGGTGGGTGTTTCTGCACATACCTCTG
CAGTACCTCACCAGGGAGCATTCCAGTATCATGCAGGTCCTGTGATCTAGCCAGGAGCAGCCATTAACTAGTG
ATTAATATGGGAGACATTACCATATGGAGGATGGATGCTTCACTTTGTCAAGCACCTCAGTTACACATTTCGCCTT
TTCTAGGATTGCATTTCCCAAGTCTATTGCAATAACAGTTGATACTCATTTTAGGTACCAGACCTTTTGAGTTC
AACTGATCAAACCAAAGGAAAAGTGTGCTAGAGAAAATTGGGAAAAGGTGAAAAGAAAAAATGGTAGTAATT
GAGCAGAAAAAATTAATTTATATATGTATTGATTGGCAACCAGATTTATCTAAGTAGAACTGAATTGGCTAGGA
AAAAAGAAAACTGCATGTTAATCATTTTCCTAAGCTGTCCTTTTGAGGCTTAGTCAGTTTATTGGGAAAATGTT
TAGGATTATTCCTTGCTATTAGTACTCATTTTATGTATGTTACCTTCAGTAAGTTCTCCCCATTTTAGTTTTCT
AGGACTGAAAGGATTCTTTTCTACATTATACATGTGTGTTGTCATATTTGGCTTTTGCTATATACTTTAACTTCA
TTGTTAAATTTTGTATTGTATAGTTTCTTTGGTGTATCTTAAACCTATTTTGA AAAACAACTTGGCTTGAT
AATCATTTGGGCAGCTTGGGTAAGTACGCAACTTACTTTTCCACCAAAGAACTGTCAGCAGCTGCCTGCTTTTCT
GTGATGTATGTATCCTGTTGACTTTTCCAGAAATTTTAAAGAGTTTGAGTTACTATTGAATTTAATCAGACTTT
CTGATTAAAGGGTTTTCTTTCTTTTTTAATAAAACACATCTGTCTGGTATGGTA

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FIGURE 12

MSALAARLLQPAHSCSLRLRPFHLAAVRNEAVVISGRKLAQQIKQEVQRQVEEWVASGNKRPHLSVILVGENPAS
HSYVLNKTAAAVVGINSETIMKPASISEEELNLINKLNDDNDVGLLVQLPLPEHIDERRICNAVSPDKDVDG
FHVINVGRMCLDQYSMLPATPWGVWEIIKRTGIPTLGKNVVVAGRSKNVGMPIAMLLHTDGAHERPGGDATVTIS
HRYTPKEQLKKHTILADIVISAAGIPNLITADMIKEGAVIDVGINRVHDPVTAKPKLVGDVDFEGVRQAGYIT
PVPGGVGPMTVAMLMKNTIIAAKKVLRLEEREVLKSKELGVATN

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FIGURE 13

GGCAGCTGCACGGCTCCTGGCCCCGGAGCATGCGCGAGAGCCGCCCGGAGCGCCCCGGAGCCCCCGCGTCCC
GCCCCGCGCGTCCCGCGCCCCGCGCCAGCGCACC CCGGACGCTATGGCCACCCCTCCGGCTGGCCCCCTCTG
TAGG**ATG**GTAGCACACAACCAGGTGGCAGCCGACAATGCAGTCTCCACAGCAGCAGAGCCCCGACGGCGGCCAGA
ACCTTCCTCCTCTTCCTCCTCCTCGCCCCGCGGCCCGCGCGCCCCGCGGCCGTGCCCCGCGGTCCCGGCCCGGC
CCCCGGCGACACGCACATTCCGCACATTCCGTTTCGCACGCCGATTACCGGCGCATCACGCGCGCCAGCGCGCTCCT
GGACGCCTGCGGATTCTACTGGGGGCCCCCTGAGCGTGCACGGGGCGCACGAGCGGCTGCGCGCCGAGCCCGTGGG
CACCTTCCTGGTGC GCGACAGCCGCCAGCGGAAGTCTTTTTCGCCCTTAGCGTGAAGATGGCCTCGGGACCCAC
GAGCATCCGCGTGCACTTTCAGGCCGGCCGCTTTACCTGGATGGCAGCCGCGAGAGCTTCGACTGCCTCTTCGA
GCTGCTGGAGCACTACGTGGCGGCGCCGCGCCGCATGCTGGGGGCCCCGCTGCGCCAGCGCCGCGTGC GCGCGCT
GCAGGAGCTGTGCCGCCAGCGCATCGTGGCCACCGTGGGCCGCGAGAACCTGGCTCGCATCCCCCTCAACCCCGT
CCTCCGCGACTACCTGAGCTCCTTCCCCCTCCAGATT**TGAC**CCGGCAGCGCCCGCCGTGCACGCAGCATTAACTGG
GATGCCGTGTTATTTTGTATTACTTGCCTGGAACCATGTGGGTACCCTCCCGGCCCTGGGTGGAGGGAGCGGA
TGGGTGTAGGGGCGAGGCGCCTCCCGCCCTCGGCTGGAGACGAGGCCGAGACCCCTTCTCACCTCTTGAGGGGG
TCCTCCCCCTCCTGGTGTCCCTCTGGGTCCCCCTGGTTGTTGTAGCAGCTTAACTGTATCTGGAGCCAGGACCT
GAACTCGCACCTCCTACCTCTTCATGTTTACATATACCCAGTATCTTTGCACAAACCAGGGGTGGGGGAGGGTC
TCTGGCTTTATTTTCTGCTGTGCAGAATCCTATTTTATATTTTTTAAAGTCAGTTTAGGTAATAAACTTTATTA
TGAAAGTTTTTTTTTT

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FIGURE 14

MVAHNQVAADNAVSTAAEPRRRPEPSSSSSSSPAAPARPRPCPAVPAPAPGDTHFRFRSHADYRRITRASALLD
ACGFYWGPLSVHGAHERLRAEPVGTFVLVRDSRQRNCFVALSVKMASGPTSI RVHFQAGRFHLDGSRESFDCLFEL
LEHYVAAPRRMLGAPLRQRRVRPLQELCRQIVATVGRENLARIFLNPVLRDYLSSFPFQI

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FIGURE 15

GGAAACTGAAAGTGAAATAGGGAGCTGGCTACCAGCGTTGAGTTGCCCTGTAAAGCCAAACCCCTAAAGGTCTC
CACACTGCTGTTTAAACGGCACACTTGACAATGGCTTCAGCAGCAGCGTTGACAATGATGTGGGAGGAGGTACAT
GCCCTATCTGCCTGGACCCCTTCGTGGAGCCTGTGAGCATCGAGTGTGGCCACAGCTTCTGCCAGGAATGCATCT
CTCAGGTTGGGAAAGGTGGGGGAGCGTCTGTCTGTGTGCCGGCAGCGCTTTCTGCTCAAGAATCTCCGGCCCCA
ATCGACAGCTAGCCAACATGGTGAACAACCTTAAAGAAATCAGCCAGGAGGCCAGAGAGGGGCACACAGGGGGAAC
GGTGTGCAGTGCATGGAGAGAGACTTCACCTGTTCTGTGAGAAAGATGGGAAGGCCCTTTGCTGGGTATGTGCCC
AGTCTCGGAAACACCGTGACCACGCCATGGTCCCTCTTGAGGAGGCTGCACAGGAGTACCAGGAGAAGCTCCAGG
TGGCATTAGGGGAACTGAGAAGAAAGCAGGAGTTGGCTGAGAAGTTGGAAGTGGAATTGCAATAAAGAGAGCAG
ACTGGAAGAAAACAGTGGAACACAGAAATCTAGGATTCACGCAGAGTTTGTGCAGCAAAAAACTTCCTGGTTG
AAGAAGAACAGAGGCAGCTGCAGGAGCTGGAGAAGGATGAGAGGGAGCAGCTGAGAATCCTGGGGGAGAAAGAGG
CCAAGCTGGCCCAGCAGAGCCAGGCCCTACAGGAGCTCATCTCAGAGCTAGATCGAAGGTGCCACAGCTCAGCAC
TGGAAGTGTGTCAGGAGGTGATAATTGTCTCTGGAAGGAGTGAGTCTGGAACCTGAAGGACCTGGATATTACCT
CTCCAGAACTCAGGAGTGTGTGCCATGTGCCAGGGCTGAAGAAGATGCTGAGGACATGTGCAGTCCACATCACTC
TGGATCCAGACACAGCCAATCCGTGGCTGATACTTCAGAAGATCGGAGACAAGTGAGGCTTGAGACACCCAGC
AGAGCATACCTGGAATGAAGAGAGATTTGATAGTTATCCTATGGTCTGGGTGCCAGCACTTTCACTCTGGAA
AACATTACTGGGAGGTAGATGTGACAGGAAAGGAGGCCCTGGGACCTGGGTGTCTGCAGAGACTCTGTGCGCAGGA
AGGGGCACTTTTTGTCTTAGTTCCAAGAGTGGCTTCTGGACAATTTGGTTGTGGAACAAACAAAAATATGAGGCTG
GCACCTACCCCCAGACTCCCTCCACCTTCAGGTGCCTCCATGCCAAGTTGGGATTTTCTGGACTATGAGGCTG
GCATGGTCTCCTTCTACAACATCACTGACCATGGCTCCCTCATCTACTCCTTCTCTGAATGTGCCCTTTACAGGAC
CTCTGCGGCCCTTCTTCAGTCTGGTTTCAATGATGGAGGAAAAACACAGCCCTCTAACCTCTGTCCACTGA
ATATTGGATCACAAGGATCCACTGACTATTGATGGCTTTCTCTGGACACTGCCACTCTCCCATTTGGCACCCTT
CTCAGCCACAAACCCTGCCTCTTTTCCCATGAACCTCTGAACCACCTTTGTCTCTGCAGAGGCATCCGGATCCCA
GCAAGCGAGCTTTAGCAGGGAAGTCACTTCACCATCAACATTCTGCCCCAGATGGCTTTGTGATTCCCTCCAGT
GAAGCAGCCTCCTTATATTTGGCCCAAACCTCATCTTGATCAACCAAAAACATGTTTCTGCCTTCTTTATGGGACT
TAAGTTTTTTTTTCTCCTCTCCATCTCTAGGATGTCTGCTTTGGTGAGATCTCTATTATATCTTGTATGGTTTG
CAAAAGGGCTTCCTAAAAATAAAAAATAAAATTTAAAAAAGTGTGAAAAAAAAAAAAAAAAA

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FIGURE 16

MASAA RL TMMWEEVTC PICLD P FVEPV SIECGHSF CQECISQVGKGGGSVCPVCRQRFLLKNLRPNRQLANMVNN
LKEISQEAREGTQGERCAVHGERLHLFCEKDGKALCWVCAQSRKHRDHAMVPLEEAAQEYQEKLOVALGELRRKQ
ELA EKLEVEIAIKRADWKKTVETQKSRIHAEFVQQKNFLVEEEQRQLQELEKDEREQLRILGEKEAKLAQQSQAL
QELISELDRRCHSSALELLQEVIIVLERSESWNLKDL DITSPELRSVCHVPG LKKMLRTCAVHITLDPDTANPWL
ILSEDRRQVRLGDTQQSIPGNEERFDSYPMVLGAQHFHSGKHYWEVDVTGKEAWDLGVCRDSVRRKGHFLSSKS
GFWTIWLWNKQKYEAGTYPQTPLHLQVPPCQVGIFLDYEAGMV SFYNITDHGSLIYSFSECAFTGPLRPFFSPGF
NDGGKNTAPLTLCPLNIGSQGSTDY

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FIGURE 17

CCTCGGTTCCGCGGCGCACCGGAGGGCAGC**ATGT**CGCGGCGGCGGCACAGCGACGAGAACGACGGTGCGCAGCCT
CACAAAAGGAGAAAGACCTCTGATGCAAATGAACTGAAGATCATTGGAACTCTTAATATGTAAAGTAGGAGAA
AAGAGTGCCTGCTCTTTGGAGAGCAACCTAGAAGGCTTGGCTGGTGTGTTTGAAGCTGATCTTCCTAACTACAAG
AGCAAGATCTTAAGGCTTCTTTGTACAGTTGCACGCTATTACCTGAGAAGCTGACAATTTATACAACATTAGTT
GGACTACTGAATGCCAGGAATTACAATTTTGGTGGAGAATTTGTAGAAGCCATGATTTCGTCAACTTAAAGATCA
TTGAAAGCAAACAATTATAATGAAGCCGTGATTGTTGGTCCGTTTTTATCTGATCTTGTGAATTGTCATGTGATT
GCCGCCCCATCAATGGTTGCTATGTTTGAATTTTGAAGCGTAACCTCAGGAAGAAGATGTACCTCAGGTGCGA
CGAGATTGGTATGTGTATGCAATTTCTGTCATCTTGGCCTGGGTTGGAAGGAGTTGTACGAAAAGAAAGATGCA
GAGATGGACCGCATCTTTGCCAACCTGAAAGCTATCTTAAAGACGCCAAAAGACTCATGTACCCATGTTACAG
GTATGGACTGCTGATAAACCACATCCACAAGAAGAGTATTAGATTGCCTGTGGGCCCAGATTAGAAAATTGAAA
AAGGATCGCTGGCAGGAACGGCACATCCTAAGACCTTATCTTGCCCTTTGACAGCATCCTGTGTGAAGCACTGCAG
CACAATCTGCCTCCTTTTACACCACCTCCTCACACTGAAGATTTCAGTGTACCCAATGCCAAGGGTCATCTTCAGA
ATGTTTGATTACACAGATGATCCCGAGGGTCTGTGATGCCAGGGAGTCATTTCAGTGGAAAGATTGTAAATAGAA
GAGAATCTTCACTGCATCATTAAAGTCCCACTGGAAGGAAAGGAAGACTTGTGCTGCACAGTTAGTGAGCTATCCA
GGGAAGAACAAGATCCCTTTGAACCTACCACATAGTTGAGGTGATCTTGCAGAGCTGTTTCAACTTCCAGCACCC
CCTCACATTGATGTGATGTACACAACCTCCTCATTGAACTGTGCAAACTTCAACCTGGCTCTTACCCCAAGTT
CTTGACAGGCAACTGAAATGCTATACATGCGTTTGGACACAATGAACACTACCTGTGTAGACAGGTTTATTAAT
TGGTTTTCTCATCATCTAAGTAACCTCCAGTTCCGTTGGAGCTGGGAAGATTGGTCAGATTGTCTTAGTCAAGAT
CCTGAAAGTCCCAAACCGAAGTTTGTAAAGAGAAGTTCTAGAAAAATGTATGAGGTTGTCTTACCATCAGCGTATA
TTAGATATTGTTCTCTACCTTCTCAGCTCTGTGTCCTGCAAACCCAACTGCATTTACAAGTATGGAGATGAA
AGTAGCAATTCTTCTCTGGACATTCTGTTGCCCTCTGTTTAGCTGTTGCCTTTAAAGTAAGGCAACCAATGAT
GAAATCTTCAGCATTCTGAAAGATGTACCAATCCTAACCAGGATGATGACGACGATGAAGGATTTCAGTTTAAAC
CCATTGAAAATAGAAGTCTTTGTACAGACTCTGCTACACTTGGCAGCCAAATCATTACGCCACTCCTTCAGTGCT
CTTGCAAAGTTTCATGAAGTCTTCAAACCCCTAGCTGAAAGTGATGAAGGAAAGTTACATGTGCTAAGAGTTATG
TTTGAGGTCTGGAGGAACCATCCACAGATGATTGCTGTACTAGTGGATAAGATGATTTCGTACACAAATAGTTGAT
TGTGCTGCCGTAGCAAATTGGATCTTCTCTTCAGAACTATCTCGTGACTTTTACCAGATTGTTTGTGTTGGGAAAT
TTGCACTCTACAATTCGTAAGATGAACAAACATGTCTGAAGATCCAGAAAGAGCTGGAAGAAGCTAAAGAGAAA
CTTGCTAGGCAACACAAACGGCGAAGTGATGATGACGACAGAAGCAGTGACAGGAAAGACGGGGTTCTTGAGGAA
CAAATAGAACGACTTCAGGAAAAAGTGAATCTGCTCAGAGTGAACAAAAGAATCTTTTCTCGTTATATTTTCAG
CGGTTTATCATGATCTTGACCGAGCACCTAGTACGATGCGAACTGATGGGACCAGTGATTAACACCATGGTAT
AAGAAGTGTATAGAGAGGCTGCAGCAGATCTTCTACAGCATCACCAATAATCCAGCAGTACATGGTGACCCCTG
GAGAACCTTCTCTTCACTGCTGAATTAGACCCTCATATCTTGGCCGTGTTCCAGCAGTTCTGTGCCCTGCAGGCC
TAAGGGTCATTTTTTCTCATGTCAAGGTTTTTTTTGATATCTTAAATAATTTGTCTTATTTTTTGATGGTTTG
AATGCTTGCTTCTTGTAGIATCCTTTCACCTCTTAAAGGAAACAAAGGGGAAGAGGACAGTGAATGAACATGGC
ATTACTTTTAATTGCCCTGAAAGCAAATACTTCTTAACGGCAGTAATGTGACTATGACCATGATATATTATATA
TGTGACAGATACAAATCTCTGTGATCAGTTTGTATTTTTTTCTCCTTAAGGCAACAAAATAATTGGTTTGAG
GTATGTGAAACACTAGAGGTCAACCTTACATAGTATATAGAAGTATGAGGTTTACCCAGCTACCCAGTAGCATAA
CTTTTCACAGCTCGGGGATGAATTAACATGGCTGAAATAAACTAAAAGTATG

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FIGURE 18

MSRRRHS DENDGGQPHKRRKTS DANETEDHLES LICKVGEKSACSLESNLEGLAGVLEADLPNYKSKILRLLCTV
ARLLPEKLTIIYTTLVGLLNARNYNFGGEFVEAMIRQLKESLKANNYNEAVYLVRFSLDLVNCHVIAAPSMVAMFE
NFVSVTQEEDVPQVRRDWYVYAF LSSLPWVGKELYEKKDAEMDRIFANTESYLKRRQKTHVPMLQVWTADKPHPO
EEYLDCLWAQIQKLKKDRWQERHILRPYLA FDSILCEALQHNLP PFTPPPHTEDSVYPMPRVIFRMFDYTDDPEG
PVMPGSHSVERFVIEENLH CIIKSHWKERKTCAAQLVSYPGKNKIPLNYHIVEVIFAELFQLPAPPHIDVMYTTL
LIELCKLQPGSLPQVLAQATEMLYMR LDTMNTTCVDRFINWFSHLSNFQFRWSWEDWSDCLSQDPESP KPFVR
EVLEKCMRLSYHQRILDIVPPTFSALCPANPTCIYKYGDESSNSLP GHSVALCLAVAFKSKATNDEIFSILKDVP
NPNQDDDDDEGFSFNPLKIEVFVQ TLLHLAAKSF SHFSALAKFHEVFKTLAESDEGKLHVLRVMFEVWRNHPQM
IAVLVDKMIRTQIVDCAAVANWIFSS ELSRDFTRLFVWEILHSTIRKM NKHVLKIQKELEEAKEKLARQH KRRSD
DDDRSSDRKDGVL EEQIERLQEKVES AQSEQKNLFLVIFQRFIMILTEHLVRCETDGT SVLTPWYKNCIERLQOI
FLQHHQIIQQYMTLENLLFTAELDPHILAVFQQFCALQA

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FIGURE 19

CACACCCTGACAAGCTGCCAGGCAGGTTCTCTTCTCTCACATACTGACCCACGGCTCCACCCTCTCTCCCCTGG
AAAGGACACCAATGAGCACTGAAAGCATGATCCGGGACGTGGAGCTGGCCGAGGAGGCGCTCCCCAAGAAGACAGG
GGGGCCCCAGGGCTCCAGGCGGTGCTTGTTCTCTCAGCCTCTTCTCTTCTGATCGTGCCAGGCGCCACCACGCT
CTTCTGCCTGCTGCACTTTGGAGTGATCGGCCCCCAGAGGGAAGAGTCCCCCAGGGACCTCTCTCTAATCAGCCC
TCTGGCCCCAGGCAGTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCTCA
AGCTGAGGGGCGAGCTCCAGTGCGTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGCGTGAGAGCTGAGAGATAA
CCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCCCAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTC
CACCCATGTGCTCCTCACCCACACCATCAGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGC
CATCAAGAGCCCCCTGCCAGAGGGAGACCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTGGG
AGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGACTATCTCGACTTTGCCGA
GTCTGGGCAGGTCTACTTTGGGATCATTGCCCTGTGAGGAGGACGAACATCCAACCTTCCCAAACGCCTCCCCTG
CCCCAATCCCTTTATTACCCCTCCTTCAGACACCTCAACCTCTTCTGGCTCAAAAAGAGAATTGGGGGCTTAG
GGTCGGAACCCAAGCTTAGAAGTTAAGCAACAAGACCACCTTCGAAACCTGGGATTCAGGAATGTGTGGCCT
GCACAGTGAAGTGCTGGCAACCACTAAGAATTCAAAGTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGAT
CCCTGACATCTGGAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGCAGGACTTGAGAAGACCTCA
CCTAGAAATTGACACAAGTGGACCTTAGGCCTTCTCTCTCCAGATGTTTCCAGACTTCCTTGAGACACGGAGCC
CAGCCCTCCCATGGAGCCAGCTCCCTCTATTTATGTTTGCCTTGATTTATTATTATTATTATTATTATTAT
TTATTACAGATGAATGTATTTATTTGGGAGACCGGGGTATCCTGGGGGACCCAATGTAGGAGCTGCCTTGGCTC
AGACATGTTTTCCGTGAAAACGGAGGCTGAACAATAGGCTGTTCCCATGTAGCCCCCTGGCCTCTGTGCCTTCTT
TTGATTATGTTTTTAAATATTATCTGATTAAGTTGTCTAAACAATGCTGATTGGTGACCAACTGTCACCTCAT
TGCTGAGGCCTCTGCTCCCCAGGGAGTTGTGTCTGTAATCGGCCTACTATTTCAGTGGCGAGAAATAAAGGTTGCT
TAGGAAAGAA

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FIGURE 20

MSTESMIRDVELAEEALPKKTGGPQGSRRCLFLSLFSFLIVAGATTLCLLHFGVIGPQREESPRDLSLISPLAQ
AVRSSRTPSDKPVAVHVVANPQAEGLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFKGQGCPSTHV
LLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPYIYLGGVFQLEKGDRLSAEINRPDYLDFAESGQ
VYFGIIAL

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FIGURE 21

GGTCCCAAGGCTTTCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGTGTGAGTTTCCGGCGTTCCGAAGGAC
TGAGCTCTTGTCGCGGATCCCGTCCGCCGTTTCCAGCCCCAGTCTCAGAGCGGAGCCCACAGAGCAGGGCACCG
GCATGGCCAAAGCCGCGGCGATCGGCATCGACCTGGGCACCACCTACTCCTGCGTGGGGGTGTTCCAACACGGCA
AGGTGGAGATCATCGCCAACGACCAGGGCAACCGCACCCAGCTACGTGGCCTTACGGACACCGAGCGGC
TCATCGGGGATGCGGCCAAGAACCAGGTGGCGCTGAACCCGCAGAACACCGTGTGTTGACGCGAAGCGGCTGATCG
GCCGCAAGTTCGGCGACCCGGTGGTGCAGTCGGACATGAAGCACTGGCCTTTCAGGTGATCAACGACGGAGACA
AGCCCAAGGTGCAGGTGAGCTACAAGGGGAGACCAAGGCATTCTACCCCGAGGAGATCTCGTCCATGGTGCTGA
CCAAGATGAAGGAGATCGCCGAGGCGTACCTGGGTACCCGGTGACCAACGCGGTGATCACCGTGCCGGCTACT
TCAACGACTCGCAGCGCCAGGCCACCAAGGATGCGGGTGTGATCGCGGGGCTCAACGTGCTGCGGATCATCAACG
AGCCACGCGCCGCCCATCGCCTACGGCCTGGACAGAACGGGCAAGGGGAGCGCAACGTGCTCATCTTTGACC
TGGGCGGGGGCACCTTCGACGTGCCATCCTGACGATCGACGACGGCATCTTCGAGGTGAAGGCCACGGCCGGGG
ACACCCACCTGGGTGGGGAGGACTTTGACAACAGGCTGGTGAACCACTTCGTGGAGGAGTTCAAGAGAAAACACA
AGAAGGACATCAGCCAGAACAAGCGAGCCGTGAGGCGGCTGCGCACCGCTGCGAGAGGGCCAAGAGGACCCTGT
CGTCCAGCACCCAGGCCAGCCTGGAGATCGACTCCCTGTTTGGGGCATCGACTTCTACACGTCCATCACCAGGG
CGAGGTTTCGAGGAGCTGTGCTCCGACCTGTTCCGAAGCACCCCTGGAGCCCGTGGAGAAGGCTCTGCGCGACGCCA
AGCTGGACAAGGCCCAGATTACGACCTGGTCTGTCGGGGGCTCCACCCGCATCCCCAAGGTGCAGAAGCTGC
TGCAGGACTTCTTCAACGGGCGCGACCTGAACAAGAGCATCAACCCCGACGAGGCTGTGGCCTACGGGGCGGCGG
TGCAGGCGGCCATCCTGATGGGGGACAAGTCCGAGAACGTGCAGGACCTGCTGCTGCTGGACGTGGCTCCCTGT
CGCTGGGGCTGGAGACGGCCGGAGGCGTGATGACTGCCCTGATCAAGCGCAACTCCACCATCCCCACCAAGCAGA
CGCAGATCTTCACCACCTACTCCGACAACCAACCCGGGTGCTGATCCAGGTGTACGAGGGCGAGAGGGCCATGA
CGAAAGACAACAATCTGTTGGGGCGCTTCGAGCTGAGCGGCATCCCTCCGGCCCCCAGGGGCGTGCCCCAGATCG
AGGTGACCTTCGACATCGATGCCAACGGCATCCTGAACGTACGGCCACGGACAAGAGCACCGGCAAGGCCAGCA
AGATCACCATCACCAACGACAAGGGCCGCCTGAGCAAGGAGGAGATCGAGCGCATGGTGCAGGAGGCGGAGAAGT
ACAAAGCGGAGGACGAGGTGCAGCGCGAGAGGGTGTGAGCCAAGAACGCCCTGGAGTCCTACGCCTTCAACATGA
AGAGCGCCGTGGAGGATGAGGGGCTCAAGGGCAAGATCAGCGAGGCGGACAAGAAGAAGGTTCTGGACAAGTGTC
AAGAGGTCTCTCGTGGCTGGACGCCAACACCTTGCCCGAGAAGGACGAGTTTGAGCACAAGAGGAAGGAGCTGG
AGCAGGTGTGTAACCCCATCATCAGCGGACTGTACCAGGGTGCCGGTGGTCCCGGGCCTGGGGGCTTCGGGGCTC
AGGGTCCCAAGGGAGGGTCTGGGTGAGGCCCTACCATGAGGAGGTGGATTAGGGGCTTTGTTCTTTAGTATGT
TTGTCTTTGAGGTGGACTGTTGGGACTCAAGGACTTGCTGCTGTTTTCTATGTCAATTTCTGCTTCAGCTCTTT
GCTGCTTCACTTCTTTGTAAAGTTAAGTTGTAACCTGATGGTAATTAGCTGGCTTCATTATTTTTGTAGTACAAC
CGATATGTTTCATTAGAATTCTTTGCATTTAATGTTGATACTGTAAGGGTGTTCGTTCCTTTAAATGAATCAAC
ACTGCCACCTTCTGTACGAGTTTGTTTTTTTTTTTTTTTTTTTTTTGTCTTGCGGAAAACACTACAAAGGC
TGGGAATGTATGTTTTATAATTTGTTTATTTAAATATGAAAAATAAATGTAAACTTT

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FIGURE 22

MAKAAAIGIDLGTITYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNPQNTVFDKRLIG
RKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEISSMVLTKMKEIAEAYLGYPVTNAVITVPAYF
NDSQRQATKDAGVIAGLNLRIINEPTAAAIAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGD
THLGGEDFDNRLVNHVFVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA
RFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLNKSINPDEAVAYGAAV
QAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVM TALIKRNSTIPTKQTQIFTTYSDNQPGVLIQVYEGERAMT
KDNLLGRFELSGIPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKASKITITNDKGRLSKEEIERMVQEAKEY
KADEVQRERVSAKNALESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELE
QVCNPIISGLYQGAGGPGPGGFGAQGPKGGSGSGPTIEEVD

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FIGURE 23

GTTCCGGTGGCCCATAGGGGAAGATGGCGGCTGCTCCTTTGGAGGAGCGGGATTGAGAGGATCGGGGTGGGGAGAC
CAAAACAAGAGAGACATTTCTGGCTCTGAAGGCGAACGCTTCGCTGGCCATTTAGGAGCTCTGCTCAAAGCCAGAC
GTATCCTAGAAGGAAAACATCACCATGGCTACAGAAATTGGTTCTCCTCCTCGTTTTTCCATATGCCAAGGTTTC
CAGCACCAGGCACCTCGACAGCTGTTTTATAAGCGACCTGATTTGCACAACAGCAAGCAATGCAACAGCTTACT
TTTGATGGAACGAATGAGAAAAGCTGTGAACCGAAAAACCATAGACTACAATCCATCTGTAATTAAGTATTTG
GAGAACAGAATATGGCAAAGAGACCAGAGAGATATGCGGGCAATTCAGCCTGATGCAGGTATTACAATGATCTG
GTCCCACCTATAGGAATGTTGAATAATCCTATGAATGCAGTAACAACAAAATTTGTTCCGACATCAACAAATAAA
GTAAAGTGTCCTGTATTTGTTGTTAGGTGGACTCCAGAAGGAAGACGCTTGGTCACTGGAGCTTCTAGTGGGGAG
TTTACCCTGTGGAATGGACTCACTTTCAATTTTGAACAATATTACAGGCTCACGACAGCCCAGTGAGGGCCATG
ACGTGGTCACATAATGACATGTGGATGTTGACAGCAGACCACGGAGGATATGTGAAATATTGGCAGTCGAACATG
AACAACGTCAGATGTTCCAGGCACATAAGGAGGCGATTAGAGAGGCCAGGTTTATACACAATATACCATTTTCT
GTAGTCCCTATTGTCTATGGTTAAATTATTCTCTAAGTGTATTCTGGGTGCAGAGATGCATGGGCTCTGTCTAGTTT
CTGGGAACTTTCTGCACCCTATAAACACAATATTTTCTTTGTTTTCACACATTCACCATTTTGCTGGCACCTT
TCTGAAGTAGTGTTGTCCCGGTATCAGCCTTTGCAATATGTTAGAGATGTACTGTCTGCCGCTTTTGCAGTGGT
TTTCTCTTTTCATTTATGATTAATAATGTGTATACGTTATTCTTTTTATTATCTACTGTGTAAGACAAGAATAT
TTCATTCCAAATAAAGAATTTCAGTCTTTTAATTATGCAACTGAATAAAATCTAAAGCCTACAGAAAACAACCTTCAG
AATTCACACAAAGTGGAAAAAGGCTTAAGTGAAGACCTGGTTGGCTTGGTTATGCCACGACTTCCAAAGGAAAGT
ATAGGACTAAACCCTCACAGATAACTGGATGTGGCAAACATTAAACGGAGTAATGAATGGGTTCTTCAAGCTTTG
CAGCTGTAAGCAGATCATTGTCAAGAAGACTCTAGGACTTTTCTTCTGATTCACTGTTGATAACATCACTTATGC
AAATGTATACAATAAGTGGAGTTTTAAATATTTTCACTGAGTTGTATATTTTACACATCAGTGAGGTATGTATA
GTAAACTGGGGGAAAAAGTTCCAAATACAAGCCTGAAGAATTGCTGCAGCCTCAGAATAAAGCTAAGCAGCATT
CTTTAAGGTTGTGCCACCCATGTGTGGGAGGAGGTTGACATCTTTATGGAAACATCATCCACTGTAGTCATTTGT
TCATACTTTTCAGAACTTAACAGAAATTGTTGGATGAACATGCTTCTGCTTTGTAGATTTTGCTTAGTGTCTAG
CCCATACATTGAGTTTACACAGCTGGTCCTTCATAGGATTCCAAAGTTCAAGGGAGTTTTTAGAGTTAGTTGAGA
AACTTGATGATCTTTCACTGCTGGGAAAACTGACTCCTTCTTGCAGCAGATTCTTTGGCTTTACACACAAGTCT
GAATGTCCTTATTTTAAAGTTTTCCTCAAAGGTGCAACATTTCATGGAATAGCTTGCCAGGAAGATGTGAACTTT
TCTACAGACCTTTGAAATGGATGAGAAACATTGTATGTAGGGATGTTTAGCAATCAGTCTTTTAAATAGACAGCCC
ACATTGTTTTCAGCTTATTTTCATGAAGTGCTGAGGCAGAAGCTGATGATAATTTTGGGAGCAGTATTTCGTGTGTG
ATTTAAAAGACTGCAGGAATACTGCAAAAATAGAATCCATTTATTTTACCACCTTAAGGCAGCTTCATGTGATT
CCTCGIATCATAGAAAATAGAGAAGGAACATGGATAGCATTAGCACTAATAATACACACTGAAGTTCTCAGAAT
ACTGATGATTGAAACTCAAACAAGTCTCTGTTGAAGTCTTCTTTTGATGAGATGCCTATGTTAGCTGACGACA
TTCATTTAAGGGCTTCTTCACTGGATTCTTCCCTCTCCTGTTTATAATGCAGCACAGTGTTTTTATTTTCCCT
GTCTGAGAAGCACAGATTATCTGTTAAATGCTGACTTCTTTCCCTGCTGTGTGTCTTCATGTAACAGTTTCTCA
CCCACGGATAATAAATTTGCTACATGCTCTG

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FIGURE 24

MATEIGSPPRFFHMPRFQHQAPRQLFYKRPDFAQQQAMQQLTFDGKMRKAVNRKTIDYNPSVIKYLENRIWORD
QRDMRAIQPDAGYYNDLVPPIGMLNNPMNAVTTKFVRTSTNKVKCPVFVVRWTPEGRRLVTGASSGEFTLWNGLT
FNFETILQAHDSPVRAMTWSHNDMWMLTADHGGYVKYWQSNMNNVKMFQAHKEAIREARFIHNIPFSVVPIVMVK
LFSKCILGAEMHGLCQFLGNFLHPINTIFFFVFTHSPFCWHLSEVLSRYQPLQYVRDVLAAAFCTGFLFSEMIN
NVYTLFLFIIYCVRQEYFIPNKEFSL

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FIGURE 25

CGGTGCCTGGTGC GGGAGCTACGGGGCCCCAGGGATTGTGTTTAAAGTAGTGCTTCTACCAACATGTCCCGTGGTT
CCAGCGCCGGTTTTGACCGCCACATTACCATTTTTTCACCCGAGGGTCGGCTCTACCAAGTAGAATATGCTTTTA
AGGCTATTAACCAGGGTGGCCTTACATCAGTAGCTGTCAGAGGGAAAGACTGTGCAGTAATTGTCACACAGAAGA
AAGTACCTGACAAATTATTGGATTCCAGCACAGTGA CTCACTTATTCAAGATAACTGAAAACATTGGTTGTGTGA
TGACCGGAATGACAGCTGACAGCAGATCCCAGGTACAGAGGGCACGCTATGAGGCAGCTAACTGGAAATACAAGT
ATGGCTATGAGATTCTGTGGACATGCTGTGTAAAAGAATTGCCGATATTTCTCAGGTCTACACACAGAATGCTG
AAATGAGGCCTCTTGGTTGTTGTATGATTTTAATTGGTATAGATGAAGAGCAAGGCCCTCAGGTATATAAGTGTG
ATCCTGCAGGTTACTACTGTGGGTTTTAAAGCCACTGCAGCGGGAGTTAAACAACTGAGTCAACCAGCTTCCTTG
AAAAAAAAGTGAAGAAGAAATTGATTGGACATTTGAACAGACAGTGGAACTGCAATTACATGCCTGTCTACTG
TTCTATCAATTGATTTCAAACCTTCAGAAATAGAAGTTGGAGTAGTGACAGTTGAAAATCCTAAATTCAGGATTC
TTACAGAAGCAGAGATTGATGCTCACCTTGTTGCTCTAGCAGAGAGAGACTAAACATTGTCGTTAGTTTACCAGA
TCCGTGATGCCACTTACCTGTGTGTTTGGTAACAACAAACAAACATCATGGAGGTCCCTGGATTGAAAAGGAGC
CTCTCCCACTCCTCCTACCACCGAAGTGGTTAGGACTCTATATAAATAAAAACAAGGCTTTTGGAAAAAAAAA
AAAA

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FIGURE 26

MSRGSSAGFDRHITIFSPEGRLYQVEYAFKAINQGGLTSVAVRGKDCAVIVTQKKVPDKLLDSSTVTHLFKITEN
IGCVMTGMTADSRSQVQRARYEAAWKKYKGYEIPVDMLCKRIADISQVYTQNAEMRPLGCCMILIGIDEEQGPQ
VYKCDPAGYYCGFKATAAGVKQTESTSFLEKKVKKKFDWTFEQTVETAITCLSTVLSIDFKPSEIEVGVTVENP
KFRILTEAEIDAHLVALAERD

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FIGURE 27

CAGGGGCGTG CAGCCCGCTTGCCAATCAGAGCGCGGCTGAGCGGCCCCGAGCCAACCCCCGAGGAGCGGCGGGC
TGGCGTCCGCGCGCCAGGAGTTGGGG~~ATG~~TCTACAAACCCATCGCCCCCTGCTCCCAGCAGCACCCCTGGCTC
CAGCACCCCTGGGCGGGCACCCCGGTCCCTACAGGAAGCGTCCCGTCGCCGTCGGGCTCAGTGCCAGGAGCCGG
CGCTCCTTTT CAGACCGCTGTTTAACTTTGGACCGCTTCCATGGGCTACGTGCAGGCGATGAAGCCACCCGG
CGCCAGGGCTCCCAGAGCACCTACACGGACCTGCTGTCAGTCATAGAGGAGATGGGCAAAGAGATCCGGCCTAC
CTATGCTGGCAGCAAGAGCGCCATGGAGCGCCTGAAGAGAGGTATCATCCATGCCCGGGCCCTAGTCAGAGAGTG
CCTGGCAGAGACAGAGCGGAACGCCCGCACG~~TAA~~CAGGAAGCGCCTCGGCCTCAGCGTCTGGACCTATCCGGCCA
CTGCAGAGCACCCGCTTCTCCCTGGCCTTCATCCCGAGTTGCACTAACCATCCTGGGCTTCCTGTCTGTGTCCC
TTGGTGGGTCCCCTCCAGGAACCAAGGAGTGGCCCTCCAGGTGGCAGCACTAAGGACACCCCCCACAACAAGAG
TTAGCAGCGAGGTCCCATGAGTCCCACCCATGACCTGCCGACAGTGTTGCCACCGGAACTTTTGTGGCCCCCTA
CCGCTCAGCCCTTCCCAGCACITCTCCCACTTTGTCCCGAGCCTCCTTCTCGCCCAGCAGGGGCACAGGCCTGGC
ACCTCCCTGCCTTGTGTCTGAGCCATAGTGACTCTTTTATCTGTGTGTCTTTTGCTAAATATGCCCTTTTATA
TTAATAAAAGATGATTTGGAGTTGTGCTCTC

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FIGURE 28

MSYKPIAPAPSSTPGSSTPGPGTPVPTGSPVSPSGSVPGAGAPFRPLFNDFGPPSMGYVQAMKPPGAQGSQSTYT
DILSVIEEMGKEIRPTYAGSKSAMERLKRGIIHARALVRECLAETERNART

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FIGURE 29

GCGCCTTTGTCTACGGCGGGCAGGTGGGCCGACGCGGAGGCGGCAGCGGCGGGCCTGAGGCGAAGGAGCGGCCG
GGAGCCCGCCGCGCTGGTAGCGATATTAATAAGGCAGCGGAAAGAAGAAATATGAATACGGCTCCATCAAGACCC
AGCCCCACACGAAGGGATCCATATGGCTTTGGAGACAGTCGAGATTCAAGGCGTGATCGATCCCCAATTCGAGGA
AGTCCAAGGAGAGAGCCCAGGGATGGCAGAAATGGCCGGGATGCCCGGGACAGCAGAGACATTCGAGACCCCCGA
GACTTGGCGGGACCACAGACATAGTAGAGATTTGCGGGATCACAGAGACAGCAGGAGTGTGCGCGACGTTCTGGGAC
GTGAGGGATCTTAGAGACTTTCGTGATCTAAGAGACTCTAGGGATTTTCGAGATCAGCGAGACCCCATGTACGAC
AGATACAGAGACATGAGAGACTCCCGAGATCCTATGTACAGGAGAGAAGGCTCTTATGACCGATACCTACGAATG
GATGACTATTGCAGGAGAAAGGATGACTCTTATTTTGACCGTTACAGAGATAGCTTTGATGGACGGGGCCCTCCA
GGCCCGAAGATCAGTCTCGTGCAAAAGAGCGTTTGAACGTGAGGAACGCGGTAGAGAAGAGCTTTATCGTCAA
TATTTTGAGGAAATCCAGAGACGCTTTGATGCCGAAAGGCCCGTTGATTGTTCTGTGATTGTGGTCAACAAACAG
ACAAAAGACTATGCTGAGTCTGTGGGGCGGAAGGTGCGAGACCTGGGCATGGTAGTGGACTTGATCTTCTTAAC
ACAGAAGTGCTACTGTCAACAGCCTTGGAGGATGTAGCAGGGGAGGTTCTCCTTTTGCTATTGTCATACCCAG
CAACACCAGATTACCGCTCCTGCACAGTCAACATCATGTTTGGAACCCCGCAAGAGCATCGCAACATGCCCCAA
GCAGATGCCATGGTGTCTGGTGGCCAGAAATTATGAGCGTTACAAGAATGAGTGCCGGGAGAAGGAACGTGAGGAG
ATTGCCAGACAGGCAGCCAAGATGGCCGATGAAGCCATCCTGCAGGAAAGAGAGAGAGGAGGCCCTGAGGAGGGA
GTGCGTGGGGGCCACCCTCCAGCCATCCAGAGCCTCATCAACCTGCTGGCAGACAACAGGTACCTCACTGCTGAA
GAGACTGACAAGATCATCAACTACCTGCGAGAGCGGAAGGAGCGGCTGATGAGGAGCAGCACCGACTCTCTGCCT
GGCCCGATTTCCCGCAACCACTCGGGGCGACCTCGGGTGCTCGCTGAAGACACAGCCAAGCTCCCAACCGCTC
CAGAGCGGCCAAGTGCTCCCCTCTGCTACACCCACTCCATCTGCACCCCCACCTCCCAGCAAGAGCTTCAGGCC
AAAATCCTCAGCCTCTTCAATAGTGGCACAGTGACGGCCAATAGCAGCTCTGCATCCCCCTCGGTTGCTGCCGGA
AACACCCCAAACCAAGATTTTCCACAGCAGCAAAACAGCCAGCCTCAACAAAGATCACAGGCTTCTGGCAATCAG
CCTCCAAGCATTTTGGGACAGGGAGGATCTGCTCAGAACATGGGCCCCAGACCTGGGGCTCCTTCCCAAGGGCTT
TTTGGCCAGCCTTCCAGTCGCCTGGCACCTGCTAGCAACATGACTAGCCAGAGGCCTGTGTCTTCCACAGGTATC
AACTTTGACAATCCAAGTGACAGAAGGCTCTGGATACCCTGATCCAGAGTGGCCCTGCTCTCTCCACCTGGTT
AGCCAGACCACAGCACAGATGGGGCAGCCACAGGCCCCCATGGGATCTTACCAGAGGCATTACTGAAGCTAAATC
TTTCAACTCTCCCCAGTCCCCTCTCCCCTGGCCTCCTCCCACTTACTTGTTCTAAATAGAGCTGTTGAGATGTT
CTCTGCGCTCCCAGGCCGGCATCGAGTGTCAATTTCTACCACCTGCTCTCTCTTCTGCCCAAGGCTGTGTTG
CTTATTCTTACAAAGTTTATACTGCATTTGGGGCTGTATCTTTTTTGTGTTTTTTTTTTTTTCTCTTTG
GAACTCTTGTTGTTAATAAAATGAAATGATTACTTTTTAATTAAATGTTCGAC

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FIGURE 30

APLSYGGQVGRGGGSGGPEAKERPGARRAGSDINKAAERRNMNTAPSRPSPTRRDYPYGFSDSRDSRRDRSPIRG
SPRREPRDGRNGRDARDSRDIRDPRDLRDHRHSRDLRDHRDSRSVRDVVDVRLRDFRDLRDSRDFRDQRDPMYD
RYRDMRDSRDPMYRREGSYDRYLRMDDYCRRKDDSYFDYRDSFDRGPPGPESQSRAKERLKKREERRREELYRQ
YFEEIQRRFDAERPVDCSVIVVNKQTKDYAESVGRKVRDLGMVVDLIFLNTTEVSLSQALEDVSRGGSPFAIVITQ
QHQIHRCTVNIMFGTPOEHRNMPQADAMVLVARNYERYKNECREKEREETARQAAMADEAILQERERGGPEEG
VRGGHPPAIQSLINLLADNRYLTAEETDKIINYLRERKERLMRSSTD SLPGPISRQPLGATSGASLKTQPSSQPL
QSGQVLP SATPTPSAPPTSQQELQAKILSLFNSGTVTANSSSASPVAAGNTPNQNFSTAANSQPQORSQASGNQ
PPSILGQGGSAQNMGPRPGAPSQGLFGQPSSRLAPASNMTSQRVVSSTGINFDNPSVQKALDTLIQSGPALSHLV
SQTTAQMGQPQAPMGSYQRHY

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FIGURE 31

AACAATAGGAAACGTCAAATTTGGGATAGTCGGCAGTTCTGGCCCCCTGCAGCTGGAGGTACCCTGAGTTCTGAGG
GTCGTAGTGCTGTTTTCTGGTATTCTCATCGCGGTACCTCTACCGGTGTGGACAAGTAAAGTTTGAATCAGCTTC
TCCATGGCCTGGGCACCAAGTTCCCGGCTGAGCCATTTTCCTTTTGGCTAAAAGTCCCCGCCAGAGGCCAATTCG
TCGCGGCGGCGGTGGAGATCGCAGGTGCTCAGGCTTGCAAGGGTTGTGGAGAGTGGTCAGAAACC
AGCAGCTGCAACAAGAAGGCTACAGTGAGCAAGGCTACCTCACCAGAGAGCAGAGCAGGAGAATGGCTGCGAGCA
ACATTTCTAACACCAATCATCGTAAACAAGTCCAAGGAGGCATTGACATATATCATCTTTTGAAGGCAAGGAAAT
CGAAAGAACAGGAAGGATTCATTAATTTGGAAATGTTGCCCTCCTGAGCTAAGCTTTACCATCTTGTCTACCTGA
ATGCAACTGACCTTTGCTTGGCTTCATGTGTTTGGCAGGACCTTGCGAATGATGAACCTTCTCTGGCAAGGGTTGT
GCAAATCCACTTGGGGTCACTGGTCCATATACAATAAGAACCACCTTTAGGATTTTCTTTTAGAAAAGTGTATA
TGCAGCTGGATGAAGGCAGCCTCACCTTTAATGCCAACCAGATGAGGGAGTGAACCTACTTTATGTCCAAGGGTA
TCCTGGATGATTGCGCAAAGGAAATAGCAAAGTTTATCTTCTGTACAAGAACAATAATTGGAAAAAACTGAGAA
TCTATCTTGATGAAAGGAGAGATGCTTGGATGACCTTGTAACATTGCATAATTTTAGAAATCAGTTCTTGCCAA
ATGCACTGAGAGAATTTTTTCGTATATCCATGCCCTGAAGAGCGTGGAGAGTATCTTGAAACTCTTATAACAA
AGTTCTCACATAGATTCTGTGCTTGCAACCCTGATTTAATGCGAGAACTTGGCCTTAGTCCTGATGCTGTCTATG
TACTGTGCTACTCTTTGATTCTACTTTCCATTGACCTCACTAGCCCTCATGTGAAGAATAAAATGTCAAAAAGGG
AATTTATTGAAATACCCGTCGCGCTGCTCAAAATATTAGTGAAGATTTGTAGGGCATCTTTATGACAATATCT
ACCTTATTGGCCATGTGGCTGCATAAAAAGCACAATTGCTAGGACTTCAGTTTTTACTTCAGACTAAAGCTACCC
AAGGACTTAGCAGATATGGGGGTTACATCAGTGCTGGTCATTGTAGCCTGAGTATACAATCAAGCTTCAGTGTGC
AACCTTTTTTTCTTTGCCATTTTCTATTTTAGTAATTTCTTGGGGAACATAATAATTTGCAAGATTTTCTCT
AATTTTGTATATCACGTTTGCACAAAGCAGAGCCACTGTCTAACACAGCTGTTAACGAATGATAAACTGACATT
ATACTCTAAAAGATGGTGTATTTGTGCATTAGATTGCCTGAAAACTTTATCCATTTCCATTCTTTATACAAAT
ACCATGTAATGTGTACATATTTAACTAAAGAGATTTATAGTCATAATTATTTATTGTAAAGATTTTAACTAAAG
TTTTCTCTTTCTCTCAAACCTGAGTTCTGAAATTTATTGATTCTGATCTGAACTATTGTCTTCGTAAAGTTA
GATCTGACTTCAGACAGAAACCAATACCAGCTTCCTTTTCTTTAACTTTGAAGAGTGTGATTGTTACTATA
TTACTATGCAAACTGGCAGTTATTTTATAATATAAATTTATAATTTGATTTTTTATTTTAAAACTGGGTAA
TCAAGTCTCGGTAAGTCCTTTAAACCATTTAGGATTTTAAACATCAAATTTATGATTTACATTATAGGAAT
AAAAATAAATATTATTAGAACTCTGGTAAAAA

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FIGURE 32

MGQGLWRVVRNQQLQQEGYSEQGYLTREQSRRMAASNISNTNHRKQVQGGIDYHLLKARKSKEQEGFINLEMLP
PELSFTILSYLNATDLCLASCWQDLANDELLWQGLCKSTWGHWSIYNKNPPLGFSFRKVYMQLDEGSLTFNANP
DEGVNYFMSKGILDDSPKEIAKFIFCTRTLNWKKLRIYLDERRDVLDDLVTLHNFRNQFLPNALREFFRHHIHAPE
ERGEYLETLITKFSHRFCACNPDLRELGLSPDAVYVLCYSLILLSIDLTSPHVKNKMSKREFIRNTRRAAQNIS
EDFVGHLVDNIYLIGHVAA

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FIGURE 33

AGCAGCTCCAACCAGGGCAGCCTTCCTGAGAAGATGCAACCAATCCTGCTTCTGCTGGCCTTCCTCCTGCTGCCC
AGGGCAGATGCAGGGGAGATCATCGGGGGACATGAGGCCAAGCCCCACTCCCGCCCCTACATGGCTTATCTTATG
ATCTGGGATCAGAAGTCTCTGAAGAGGTGCGGTGGCTTCCTGATACAAGACGACTTCGTGCTGACAGCTGCTCAC
TGTGGGGAAGCTCCATAAATGTCACCTTGGGGGCCACAATATCAAAGAACAGGAGCCGACCCAGCAGTTTATC
CCTGTGAAAAGACCCATCCCCATCCAGCCTATAATCCTAAGAACTTCTCCAACGACATCATGCTACTGCAGCTG
GAGAGAAAGGCCAAGCGGACCAGAGCTGTGCAGCCCCTCAGGCTACCTAGCAACAAGGCCCAGGTGAAGCCAGGG
CAGACATGCAGTGTGGCCGGCTGGGGGCAGACGGCCCCCTGGGAAAACACTCACACACACTACAAGAGGTGAAG
ATGACAGTGCAGGAAGATCGAAAGTGCGAATCTGACTTACGCCATTATTACGACAGTACCATTGAGTTGTGCGTG
GGGGACCCAGAGATTAAAAAGACTTCCTTTAAGGGGGACTCTGGAGGCCCTCTTGIGTGTAACAAGGTGGCCCAG
GGCATTGTCTCCTATGGACGAAACAATGGCATGCC TCCACGAGCCTGCACCAAAGTCTCAAGCTTTGTACACTGG
ATAAAGAAAACCATGAAACGCTACTAACTACAGGAAGCAAATAAGCCCCGCTGTAATGAAACACCTTCTCTGG
AGCCAAGTCCAGATTTACACTGGGAGAGGTGCCAGCAACTGAATAAATACCTCTCCCAGTGTAATCTGGAGCCA
AGTCCAGATTTACACTGGGAGAGGTGCCAGCAACTGAATAAATACCTCTTAGCTGAGTGG

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FIGURE 34

MQPILLLLAFLLLPRADAGEIIGGHEAKPHSRPYMAYLMIWDQKSLKRCGGFLIQDDFVLTAHHCWGSSINVTLG
AHNIKEQEPTQQFIPVKREIPHPAYNPKNFSNDIMLLQLERKAKRTRAVQPLRLPSNKAQVKPGQTCSVAGWGQT
APLGKHSHTLQEVKMTVQEDRKCESDLRHYYDSTIELCVGDPEIKKTSFKGDSGGPLVCNKVAQGIVSYGRNNGM
PPRACTKVSSFVHWIKKTMKRY

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FIGURE 35A

ATTTCCATCAACCATGATGAAAGTCTGCTGCCTGAGTCCTTAGAGAGCATGATGTATGGTAAGAAGGTGCTCAGC
CAAGAACCAAGCTCTTTTCAGGAGAGCCCAAGTACCAATACTGAATCTAGAAAAGATGTTATTACCATCTCAATA
AGCAAAGATGGGAAGTCCAGTCTGGTGGCCCTGAGGCAGAAATAGCTTCTGGCCCTACTTTTTATGGGTAGCTTA
GAAGCAGGAGGAGTAGCTCAAGCAAACATCAAAAATGGAACATTGTTGATGTCTATTTCAAAGGAAGGGGAG
CTCTGCTGCAGTGAGGCAGGACAGAGACCTGAAAAATTGGCCAGCTGGAAGCCAAGTGTAGCTTCCCTTCC
TTGAATCCAGGAAATGAAAGTGGGTTTGTAGATATGTGCAGTCTTAGTGTCTGTGACTCCAAAAGAAACCTGTCA
TCAGATCAGCAATTAATTGATTTATTGGAAAACAAAAGCTTAGAAAGTAAATTGATTTTGAGTCAGAACACAGT
GATGAGGAGGAAGAAGAGGAGGAAAACGAGGAGGAAAACCTTAGCCATGGCAGTAGGCATGGGGGAAAGGCCAGAG
GTATTGCATCTCACGGAGCCCACTACTAACATCTCAAGGGAAAAGAACCAAGGCTTCCAAGATGAAACCAAGAAA
GGAAGCTTAGAGGTGGCAAACAGACTCCTGGGCTACAGAGGGCTTTCCCGCTCCAGCAGCCTGTCTAGTGCCAC
TGCAAACACATGGAGAGGTGGATGCATGGCCTCGAGAATGATGAATTTGAAATCGAGAAACCCAAGGCTTATATC
CCAGATCTGTTCAAAGTAAACCAATACTATCGCCATGGAGGGTGAACCCACTGCTATTCCATCACAGCCGTTT
AAAGTGAAGCATGAGCTTTTAAAGAACCTTGAAAGAAAGTGCAGAGGGGCAAAACGTTTCCCCACATATCCT
CTTGAAGGAAGTGAGCTCAAATCAGAAGACATGGATTTTGAGAATAAAGATGATTATGATAGAGACGGAACTGC
CATAGTCAAGATTATCCAGGAAGTACTCTGAAGAGGAGAGCAAGAGCTCAACATCGGGCATCACAGGAGACATT
GGGGATGAGCTACAGGAGGCTCGAGCTCCCACTATTGCTCAGCTGCTACAGGAGAAAACCTCTCTATTCTTCTCT
GAGTGGCCAAAGGACCGCGTGATAATTAACCGCTAGATAATATCTGCCACGTGGTGTAAAGGGGAAGTGGCCC
TCTAGCCAGCAGTATGAGCCCTCAGGCACACTGCCACCCCGGTATTAACCAGCAGTGCTGGTTCTCGAACCCAGC
CTCTCAGAGCCGGAAGCAGCAGAACACAGCTTCAGCAACGGCGCAGCATTGGCGGCCAGATCCACAAGGAGAGC
TTCTTAGCTCCAGTATTACAAAGGATGAACAAAAGCACAGGCGTCCCTATGAGTTTGAGGTGGAGAGGGATGCA
AAGGCTCGGGGCTGGAGCAGTTCTCTGCCACCCACGGGCACACCCCTATCATCCTCAATGGCTGGCATGGGGAG
TCAGCTATGGACCTCTCCTGCTCATCAGAGGGTCCCAAGGAGCCACATCCCTTTCCAGTGAGCGCCAGCACC
CCTAAGATTGGGGCTATCAGTTCACTTCAGGGAGCCCTTGGCATGGACTTGTCTGGGATTCTGCAAGCTGGCCTG
ATCCATCCTGTGACTGGACAGATTGTCAATGGAAGCCTCAGAAGAGATGATGCAGCCACGAGGAGGCGGAGAGGG
AGGCGGAAACATGTTGAAGGAGGGATGGACCTCATTTTTGAAGGAGCAGACACTTCAGGCGGAATCTTGAA
GTCCATGAAGACCCAGGGCAGGCCACCTTGAGCACCACACCCCTGAGGGGCCAGGGCCTGCCACCTCGGCTCCT
GAGCCAGCTACGGCAGCCAGCAGCCAAGCCGAGAAATCCATTTCCAGCAAGAGTCTGCTTGACTGGCTAAGGCAG
CAGGCTGACTACTCCTTAGAAGTTCTGGCTTTGGGGCAAATTTTCAGACAAACCAAAGCAGAGGAGGCCACGC
TGTAAGAACCTGGAATAATTAGATGTCAGCTCCCTGAGCGGGGAAGAGAGATTCTGCCATCCCCAAGGAGCCA
GGACTGAGGGGGTTTCTTCCAGAAAACAAGTTCAATCACACTCTGGCTGAGCCTATTCTTCGAGATACGGGCCCC
CGCAGGAGGGGGAGGCGGCCCTCGGAGCGAACTCCTGAAGGCTCCTTCCATTGTGGCAGACTCTCCCTCTGGAATG
GGGCCACTGTTATGAATGGACTGATTGCTGGGATGGACCTGGTAGGACTTCAGAACATGAGAAATATGCCAGGC
ATCCCCCTCACCGGGCTGGTGGGGTTTCCAGCTGGCTTTGCCACGATGCCAACAGGTGAAGAGGTCAAAAGTACC
CTGAGCATGCTGCCCATGATGCTGCCAGGCATGGCTGCTGTGCCCCAGATGTTTGGTGTGGGGGACTCCTCAGT
CCACCCATGGCAACCACTGCACTTCCACTGCTCCGGCGTCTCTATCAAGCACAACGAAAAGTGGTACGGCAGTG
ACTGAAAAGACTGCGGAAGACAAGCCGAGTAGCCATGATGTGAAAACAGACACTTTAGCTGAGGACAAGCCTGGT
CCAGGTCCATTTTCTGATCAGTCTGAACCTGCAATAACTACTAGTAGTCTGTGGCTTTTAACCCATTCTCATC
CCAGGAGTATCTCCTGGACTCATTTACCCATCCATGTTCTCTCCCTGGTATGGGCATGGCTCTGCCAGCCATG
CAGCAGGCCAGACACTCGGAAATAGTAGGTCTGGAGAGCCAGAAGAGGAAGAAGAAGACAAAGGGGGACAAC
CCCAACTCCCACCCAGAGCCTGCTCCCAGCTGTGAAAGGGAGCCAGCGGTGATGAGAACTGTGCCGAACCCAGT
GCCCCCTTGCCCGCAGAGAGAGAATGGGGCACAGGCTGGGGAGGGGGCACTCAAAGACTCCAACAACGACACC
AATTAGAACTTTTTTCAITTAAGAAATTATTGTGACTTGTAAGTTTCTTATCCCATAAAGGTTTGTACTTCCCT
CACTTCACCTCCATAAGAACCTGTGTTTCCATAAGTAAGATTACGTACCTGATTTCTGTCTGAGAACTATGGTA
ACAGATGTTAATAGTTGCAGGGTCTCACCATTCAATAGATAAGTGTGTCTACCTAGTCTAGGAGGCACAGAAT
TCTCATTCTGTTATCCAGTTCATTCCAGCAATCATAGTTAATACAGTACTTGGTGACACGCCCTACCCCTTCTC
TTCCAAGTTTCCCACTCACTTGAGGAGGAAAAATGGCAAAGAAAGCTGTCTAGGGTTTTACCATTGAAGGGTGG
AAGAACAGAGACAAAGAGGAGCTCTTTTCTGTGAGCTGGGTTGCACAGGAAGAATGTCACAGGGAACCAAAAAG
CACAGAAAAGGAAGTGTGGTGCATATTTTTGAGTTAAATATTTCCCTATTTTATCATGATTACTAAGTGAGT

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FIGURE 35B

AGTATAGACAGAAGTATATAACTAATGGTTGAAAAATACATATATTCATTTCTTTATAAAAAACAAAAACCTTACC
GGTAGTAATATAATTTCCCCCTTGGTGGTTTTTCAGACACCTGCAGCAAGAAGAAATACTGACTGACTAGGCAIT
ATTTTCTATACATCCCTCTCACCAGTGAAAAGATTCTCTTGCTGCGAGAAAGCTTTACCCACCATGAGTTATTG
CTGTCGACGGGGGTGGGGCAAGGACCCGCGCTCCGTAGAGCTACACGCTGCTTCACAAGCACACGCCAGCGCTC
TGCTCTCACCTGGTTGCTTACAGATTTCTCTAGCCATTAATTTGCCTCTCTGTGTTTAAAGAGCACCAGGACCG
AATGGATTTTCACTTCAGGCTTTCCTTCACCAAGAATAAGGTTCTTTCTGGAGCCTGCAAGAAGACAGTTGCCCC
ACACTTTGACACTTGCTAGTAGGTCCTTTGATCAAGAGTGTCTGAGGCTGTCAAATGTGTGCCACCCTTTATAAT
ACAGCTATGAAAAGTTACTTCTCCATTAAATTTCTCCATTCTGTTTATATCTTACAGTTGGACCCAAATTCCAAAT
TATCAGTTAATCGAAACTACATTGCAAGTCAACATTATTTTCTCTTCTCCTCAGCTTCTCCATGTTTAGGAACT
GAGAAAGAACCTGCCTAAGCAGCACTTCCCCATGTCTTTACCTTCATGTTAACGTCCCTTCTGATGGTCTCAC
TCTTCACAGGTAGTTCACACTCTGAGACTTGAAGTAAGCTCATGGTTCAGTACTCTGGGGGCGCAGGGCTGCGCA
GGACCCTTGAAATGTTGCAAGTGTTACTAGTACCAGTTTCACTTTTTGTTGTCACAATTTACIGTATTTTTTAC
TTTTTCTGTTACAGTTTTGCTAATTTATCAGAAGGTCCAAAAGTCTGACATAACTATTTTCAATTTGCATTATTTA
TTTATGATGCTTTTTTTCATTGTCTTTTATACATTTGGGATTATAAATTATGTAAATGTTAAATGAGCATCTCAA
AGAAGTCTGTTAAATCATGACTGAAAAAATCAATCAGATGTATCTTCAAAAAGTGGAGTCCCAGTTTTATGAAT
CAGAGATATAAACCAGAAATTCTATACTGATCATAGAAGAAGATCCAGTAATTGAACAAATCCTATTTAATGA
CATCCTTGTAGCATAGATGGTCTATAATGCTGACCACAGATTTCTTAGAAATGCTGCTCTCTCTATTTAACTAAC
ATTTTGTTACAGTTTTGCCTCCAGTGGAAGCAGAAAGGGTTTTTTCAGCTGTTAAATCCTAAAAATCAATATAATT
TATTTATGTAAGAAAAATAACTCAATCAATATATTTTGAACCTTTTAAAGTACTAATTTTCTTTTATCACGTAG
AAAAAAAATGTATTTGCCCTAAATCCTTAAAAATACAAATGCTATAAAAATTCCTGTATCTTGAAAGCCTTACTG
CAAATGAGTATTATAGACATCCC

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FIGURE 36

ISINHDESLLPESLESMMYGKKVLSQEPSSFQESPSTNTESRKDVITISISKDGNCSGGPEAEIASGPTFMGSL
EAGGVAQANIKNGKHLMSISKEGELCCSEAGQRPENIGQLEAKCLASPSLNPNGESGFVDMCSLSVCDSKRNL
SDQQIDLLENKSLESKLILSQNHSDEEEEEEEENLAMA VGMGERPEVLHLTEPTTNISREKNQGFQDETKK
GSLEVANQTPGLQRAFPAPAAQCCHCKHMERWMHGLEND EFEIEKPKAYIPDLFKSKTNTIAMEGEPTAIP SQPF
KVKHELLKEPWKESAEGQNVFPTYPLEGSELKSEDMDFENKDDYDRDGNCHSQDYPGKYSEESKSSTSGITGDI
GDELQEARAPTIAQLLQEKTLYSFSEWPKDRVIINRLDNICHVVLKGWPSQQYEPSGTLPTPVLTSAGSRTS
LSEPEAAEHSFSNGAALAAQIHKESFLAPVFTKDEQKHRRPYEFEVERDAKARGLEQFSATHGHTPIILNGWHGE
SAMDLSCSSESGSPGATSPFPVSASTPKIGAISLQGALGMDLSGILQAGLIHPVTGQIVNGSLRRDDAATRRRG
RRKHVEGGMDLIFLKEQTLQAGILEVHEDPGQATLSTTHPEGPGPATSAPEPATAASSQAEKSIPSKSLLDWLRQ
QADYSLEVPGFGANFSDKPKQRRPRCKEPGLDVSLSGEERVPAIPKEPGLRGFLPENKFNHTLAEPILRDTGP
RRRGRRPRSELLKAPSI VADSPSGMGPLFMNGLIAGMDLVGLQNMNRNMPGIPLTGLVGFPAGFATMPTGEEVKST
LSMLPMMPLPGMAAVPQMFVGGLLSPPMATTCTSTAPASLSSTTKSGTAVTEKTAEDKPS SHDVKTDTLAEDKPG
PGPFSDQSEPAIT TSSPVAFNPFLIPGVSPGLIYPSMFLSPGMGMALPAMQARHSEIVGLESQKRKKKKTKGDN
PNSHPEPAPSCEREPSGDENCAEPSAPLPAEREHGAQAGEGALKDSNNDTN

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FIGURE 37

TAGCTAGGCAGGAAGTCGGCGCGGGCGGGCGGGACAGTATCTGTGGGTACCCGGAGCACGGAGATCTCGCCGGCT
TTACGTTACCTCGGTGTCTGCAGCACCTCCGCTTCCTCTCCTAGGCGACGAGACCCAGTGGCTAGAAGTTCAC
CATGTCTATTCTCAAGATCCATGCCAGGGAGATCTTTGACTCTCGCGGGAATCCCAGTGTGAGGTTGATCTCTT
CACCTCAAAGGTCTCTTCAGAGCTGCTGTGCCAGTGGTGTCTCAACTGGTATCTATGAGGCCCTAGAGCTCCG
GGACAATGATAAGACTCGCTATATGGGGAAGGGTGTCTCAAAGGCTGTTGAGCACATCAATAAACTATTGCGCC
TGCCCTGGTTAGCAAGAACTGAACGTCACAGAACAAGAGAAGATTGACAACTGATGATCGAGATGGATGGAAC
AGAAAATAAATCTAAGTTTGGTGCGAACGCCATTCTGGGGGTGTCCTTGCCGTCTGCAAAGCTGGTGCCGTGA
GAAGGGGGTCCCCCTGTACCGCCACATCGCTGACTTGGCTGGCAACTCTGAAGTCATCTGCCAGTCCCGGCGTT
CAATGTATCAATGGCGGTTCTCATGCTGGCAACAAGCTGGCCATGCAGGAGTTCATGATCCTCCAGTCGGTGC
AGCAAACCTTCAGGGAAGCCATGCGCATTGGAGCAGAGGTTTACCACAACCTGAAGAATGTCATCAAGGAGAAATA
TGGGAAAGATGCCACCAATGTGGGGGATGAAGGCGGGTTTGTCTCCCAACATCCTGGAGAATAAAGAAGGCCTGGA
GCTGCTGAAGACTGCTATTGGGAAAGCTGGCTACACTGATAAGGTGGTCATCGGCATGGACGTAGCGGCCTCCGA
GTTCTTCAGGTCTGGGAAGTATGACCTGGACTTCAAGTCTCCCGATGACCCAGCAGGTACATCTCGCCTGACCA
GCTGGCTGACCTGTACAAGTCCTTCATCAAGGACTACCCAGTGGTGTCTATCGAAGATCCCTTTGACCAGGATGA
CTGGGGAGCTTGGCAGAAGTTCACAGCCAGTGCAGGAATCCAGGTAGTGGGGGATGATCTCACAGTGACCAACCC
AAAGAGGATCGCCAAGGCCGTGAACGAGAAGTCCTGCAACTGCCTCCTGCTCAAAGTCAACCAGATTGGCTCCGT
GACCGAGTCTCTTCAGGCGTGAAGCTGGCCCAGGCCAATGGTTGGGGCGTCATGGTGTCTCATCGTTCGGGGGA
GACTGAAGATACCTTCATCGCTGACCTGGTTGTGGGGCTGTGCACTGGGCAGATCAAGACTGGTGCCCTTGCCG
ATCTGAGCGCTTGGCCAAGTACAACAGCTCCTCAGAATTGAAGAGGAGCTGGGCAGCAAGGCTAAGTTTGCCGG
CAGGAACTTCAGAAACCCCTTGGCCAAGTAAAGCTGTGGGCAGGCAAGCCCTTCGGTACCTGTTGGCTACACAGA
CCCCTCCCCTCGTGTACAGCTCAGGCAGCTCGAGGCCCCGACCAACACTTGCAGGGGTCCCTGCTAGTTAGCGCC
CCACCGCCGTGGAGTTCGTACCGCTTCCTTAGAATTCTACAGAAGCCAAGCTCCCTGGAGCCCTGTTGGCAGCT
CTAGCTTTGCAGTCGTGTAATTGGCCCAAGTCATTGTTTTCTCGCCTCACTTTCCACCAAGTGTCTAGAGTCAT
GTGAGCCTCGTGTATCTCCGGGTGGCCACAGGCTAGATCCCCGGTGGTTTTGTGCTCAAAATAAAAAGCCTCA
GTGACCCATGAG

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FIGURE 38

MSILKIHAREIFDSRCNPTVEVDLFTSKGLFRAAVPSGASTGIYEALERDNDKTRYMGKGVSKAVEHINKTIAP
ALVSKKLVNTEQEIKDKLMIEMDGTENKSKFGANA ILGVSLAVCKAGAVEKGVPLYRHIADLAGNSEVILPVP AF
NVIINGGSHAGNKLAMQEFMILPVGAANFREAMRIGAEVYHNLKNVIKEKYGKDATNVGDEGGFAPNILENKEGLE
LLKTAIGKAGYTDKVVIGMDVAASEFFRSGKYDLDFKSPDDPSRYISPDLADLYKSFIKDYPPVVSIEDPFDQDD
WGAWQKFTASAGIQVVGDDLTVTNPKRIAKAVNEKSCNCLLLKVNQIGSVTESLQACKLAQANGWGMVSHRSGE
TEDTFIADLVVGLCTGQIKTGAPCRSERLAKYNQLLRIEEEELGSKAKFAGRNFNPLAK

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FIGURE 39

GCCTGAGTGAGTCTCTGGCGTCCCAAATTGCCTGTTTTCTCGCAGGCTCTATTCCGTTTCGCTGGTTCGCCACCT
CAGGGGAACGATGGCCATGGAGTCCACAGCCACTGCCGCCGTCGCCGCGGACGTGGTTTTCTGCCGACAAAATTGA
AGATGTCCCTGCTCCTTCTACATCTGCAGATAAAGTGGAGAGTCTGGATGTGGATAGTGAAGCTAAGAACTATT
GGGTTTAGGACAGAAACATCTGGTGATGGGGGATATTCCAGCAGCTGTCAATGCATTCCAGGAAGCAGCTAGTCT
TTTAGGTAAGAAGTATGGAGAGACAGCTAATGAGTGTGGAGAAGCCTTCTTTTCTATGGGAAATCACTTCTGGA
GTTGGCAAGAATGGAGAATGGTGTGTGGGAAACGCCTTGGGAAGGTGTGCATGTGGAAGAGGAAGAAGGAGAAAA
AACAGAAGATGAATCTCTGGTAGAAAATAATGATAACATAGATGAGGAAGCAAGGGAAGAGTTGAGAGAACAGGT
TTATGACGCCATGGGAGAAAAAGAAAGCCAAAAAACAGAAGACAAGTCTTTGGCAAAGCCTGAAACTGATAA
AGAACAGGACAGTGAAATGGAGAAGGGTGGGAAGAGAAGATATGGATATAAGTAAATCTGCAGAGGAGCCACAGGA
AAAAGTTGACTTGA CTCTAGATTGGTTAACTGAAACCTCTGAAGAGGCAAAAGGAGGAGCAGCACCAGAAGGACC
GAATGAAGCTGAGGTCACTTCTGGGAAGCCAGAACAGGAAGTACCAGATGCTGAGGAAGAAAAATCAGTTTCTGG
AACTGATGTCCAAGAAGAGTGCAGAGAAAAAGGAGGTCAGGAGAAGCAGGGAGAGGTAATTGTGAGCATAGAGGA
GAAGCCAAAAGAAGTTTCAGAAGAGCAGCCTGTGGTGA CTCTAGAAAAGCAGGGCACTGCAGTGGAGGTAGAAGC
AGAGTCTTTAGACCCGACAGTCAAGCCAGTGGATGTGGGTGGGGACGAGCCAGAGGAGAAGGTAGTTACCTCTGA
AAACGAGGCAGGAAAGGCGGTTCTTGAACAACTGGTAGGTCAAGAAGTACCACCTGCTGAAGAGTCACCAGAGGT
GCAAACAGAGGCTGCAGAGGCCCTCAGCTGTAGAGGCTGGATCAGAAGTCTCTGAAAAGCCTGGGCAGGAGGCTCC
AGTTCTCCCTAAGGATGGTGCAGTCAATGGACCGTCAGTTGTAGGAGATCAGACTCCTATTGAACCACAGACTTC
TATAGAAAGACTGACAGAAAACAAAGATGGCTCAGGACTAGAGGAGAAGGTCAGGGCAAAGCTGGTTCCCTAGTCA
GGAGGAGACTAAGCTGTCTGTAGAAGAGTCTGAGGCAGCTGGAGATGGGGTTGATACCAAGGTAGCCCAGGGAGC
TACTGAGAAATCACCTGAAGACAAAGTTCAGATAGCTGCTAATGAAGAGACACAAGAGAGAGAAGAACAGATGAA
AGAGGGTGAAGAACTGAAGGCTCGGAAGAGGATGATAAAGAAAATGATAAGACTGAAGAAATGCCAAATGATTC
AGTCCTTGAAAACAAGTCTCTTCAAGAAAATGAGGAGGAGGAGATTGGGAACCTAGAGCTTGCCTGGGATATGCT
GGATTTAGCAAAGATCATTTTTTAAAGGCAAGAAACAAAGAAGCACAGCTTTATGCTGCCCAGGCACATCTTAA
ACTCGGAGAAGTTAGTGTGAATCTGAAAACATATGTGCAAGCTGTGGAGGAGTCCAGTCCCTGCCTTAACCTGCA
GGAACAGTACCTGGAAGCCCACGACCGTCTGCTTG CAGAGACCCACTACCAGCTGGGCTTGGCTTATGGGTACAA
CTCTCAGTATGATGAGGCAGTGGCACAGTTCAGCAAATCTATTGAAGTCATTGAGAACAGAATGGCTGTACTAAA
CGAGCAGGTGAAGGAGGCTGAAGGATCGTCTGAATACAAGAAAGAAATTGAGGAACTAAAGGAACTGCTACCCGA
AATTAGAGAGAAGATAGAAGATGCAAAGGAGTCTCAGCGTAGTGGGAATGTAGCTGAACTGGCTCTGAAAGCTAC
TCTGGTGGAGAGTTCTACTTCAGGTTTCACTCCTGGTGGAGGAGGCTCTTCAGTCTCCATGATTGCCAGTAGAAA
GCCAACAGACGGTGCTTCCCTCATCAAATTGTGTGACTGATATTTCCACCTTGTCAGAAAAGAAGAGGAAACCAGA
GGAAGAGAGTCCCCGGAAGATGATGCAAAGAAAGCCAAACAAGAGCCGGAGGTGAACGGAGGCAGTGGGGATGC
TGTCCTCGAGTGGAAATGAAGTTTCGGAACCATGGAGGAGGAGGCTGAGAATCAGCTGAAACGCGGAGCAGCAGT
GGAGGGGACACTGGAGGCTGGAGCTACAGTTGAAAGCACTGCATGTTAAGAGGGGGCACAGCCTCCTCCCAAGGG
AAAGTGTTTTTGTATATAATGTATTTTTTCACTTTTGGAGGATCTTTTGTATAACTTCAATAAAGATTGTAAG
CAAAAAAAAAA

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FIGURE 40

MAMESTATAA VAADVVSADKIEDVPAPSTSADKVESLDVDSEAKLLGLGQKHLVMGDIPAAVNAFQEAASLLGK
KYGETANECGEAFFFYGKSLLELARMENGVLGNALEGVHVEEEEGEKTEDESLVENNDNIDEEAREELREQVYDA
MGEKEEAKKTEDKSLAKPETDKEQDSEMEKGGREDMDISKSAEEPQEKVDLTLDWLTETSEEAKGGAPEGPNEA
EVTSGKPEQEVPDAAEEKSVSGTDVQEECREKGGQEKQGEVIVSIEEKPKVSEEQPVVTLKQGTAVEVEAESL
DPTVKPVDVGGDEPEEKVVTSENEAGKAVLEQLVGQEVPPAESPEVQTEAAEASAVEAGSEVSEKPGQEPVLP
KDGAVNGPSVVGDTPIEPQTSIERLTETKDGSGLEEKVRAKLVPSQEETKLSVEESEAAGDGVDTKVAQGATEK
SPEDKVQIAANEETQEREEQMKEGEETEGSEEDDKENDKTEEMPNDVLENKSLQENEEEEIGNLELAWDMLDLA
KIIFKRQETKEAQLYAAQHLKLGEVSVESENYVQAVEEFQSCNLQEQYLEAHDRLLAETHYQLGLAYGYNSQY
DEAVAQFSKSIEVIENRMAVLNEQVKEAGSSEYKKEIEELKELLPEIREKIEDAKESQRSGNVAELALKATLVE
SSTSGFTPGGGGSSVSMIASRKPTDGASSSNCVTDISHLVRRKKRKPEEESPRKDDAKKAKQEPEVNGGSGDAVPS
GNEVSENMEEEAENQLKRGAAVEGTLEAGATVESTAC

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FIGURE 41

TTTCTTCGCGGCTGCTCAAGATGAACCGACTCTTCGGGAAAGCGAAACCCAAGGCTCCGCCGCCAGCCTGACTG
ACTGCATTGGCACGGTGGACAGTAGAGCAGAATCCATTGACAAGAAGATTTCTCGATTGGATGCTGAGCTAGTGA
AGTATAAGGATCAGATCAAGAAGATGAGAGAGGGTCCTGCAAAGAATATGGTCAAGCAGAAAGCCTTGCGAGTTT
TAAAGCAAAAGAGGATGTATGAGCAGCAGCGGGACAATCTTGCCCAACAGTCATTCAACATGGAACAAGCCAATT
ATACCATCCAGTCTTTGAAGGACACCAAGACCACGGTTGATGCTATGAACTGGGAGTAAAGGAAATGAAGAAGG
CATACAAGCAAGTGAAGATCGACCAGATTGAGGATTTACAAGACCAGCTAGAGGATATGATGGAAGATGCAAATG
AAATCCAAGAAGCACTGAGTCGCAGTTATGGCACCACAGAACTGGATGAAGATGATTTAGAAGCAGAGTTGGATG
CACTAGGTGATGAGCTTCTGGCTGATGAAGACAGTTCTTATTTGGATGAGGCAGCATCTGCACCTGCAATTCCAG
AAGGTGTTCCCACTGATACAAAAACAAGGATGGAGTTCTGGTGGATGAATTTGGATTGCCACAGATCCCTGCTT
CATAGATTTGCATCATTCAAGCATATCTTGTAACAAACACATATTATGGGACTAGGAAATATTTATCTTTCCA
AATTTGCCATAACAGATTTAGGTTTCTTTCCTTCTTTGAAGGAAAGTTTAATTACATTGCTCTTTTATTTTTTC
CATTAAAGAGACTCATTGCTTGGGAAATGCTTCTTCGTACTAAATTTGATTCCTTTTTTCTTATGAAAAACGA
ACTCAGTTTAAAAGTATTTTTAGCTCGTATGACTTGTTTTATTCAATTAATAATAATTTGAAATAAACTAAGGA
AATGGAATCTTAAAAGTCTATGACAGTGTAACCTACAGTCCTCAAAATGACCCTGTAAATTTGGATAAGACCAA
AGATGAGATTATTGGGGCTGGTCATATTATGATTGAGAAATCCATTTCTATTGTGGGTATTATAGGGTTGGGTAA
AGGTGATGGCCCTTTTTGATGGGTTTTGTTGTGTCTTGTTGAACAAGTCGTTACTGTGTCCATTATTGGAATG

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FIGURE 42

MNRLF GKAKPKAPPSLTDCIGTVDSRAESIDKKI SRLDAELVKYKDQIKKMREGPAKNMVQKALRVLKQKRMV
EQQRDNLAQQSFNMEQANYTIQSLKDTKTVDAMKLGVKEMKKAYKQVKIDQIEDLQDQLEDMMEDANETQEALS
RSYGTPELDEDDLEAELDALGDELLADESSYLDEAASAPAIPEGVPTDTKNKDGVLVDEFGLPQIPAS

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FIGURE 43

GGAATCAGAGGGAGCATTCACTGAGTGCTTATTGGTTCTACGCACTGTTAGGTGTTCTTTGTGTCTTACCTCAT
CCACCTCTCGCATCCCCCTTGGAACAAGATAGCATCATTACCCTACATCTCTTGAAGGTTTCAGGTCCCTGGGCT
GCAAGGAGATAAGAGGCTCCCTCACACAGCCTCTGGAGGGCTAAATGAGATCCTACAGCAATGCCCTGGTGGGGC
TTCTCTCTCCCTCTTATGTCACTTGTACACCTGCTCTAGGTAATCATTTCCTCCAGATGAGAGGTGTAGGAAA
GGACCTGATGCCAGCAAGGAAAAAGGAATTGGTAACATGCTCTTTGTTTACCTAAAATCTGTCCCCACAACAAGA
ATGTAACCTTCCTTCGAGGCAGAAATTCAATTTCTTCTCCAGCCACCTACAAAGGCCCACTCAAGAGCAAGTT
CTGTGTAAAGGTGCTTAATAATACAGGTTCTTTGACAAAATGATAAAACATTTGTAACCTGAAAAAAA

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FIGURE 44

ESEGAFTECLLVLRRTVRCSEFVSYLIHLSHPPLEQDSIITLHLLKVQVPGLOGDKRLPHTASGGLNEILQQCPGGA
SLSLLCHLSHLL

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FIGURE 45

CGGCACGAGGCGACTTTGGTGGAGGTAGTTCTTTGGCAGCGGGCATGGCGGGTACCGTGGTGTGGACGATGTGG
AGCTGCGGGAGGCTCAGAGAGATTACCTGGACTTCCTGGACGACGAGGAAGACCAGGGAATTTATCAGAGCAAAG
TTCGGGAGCTGATCAGTGACAACCAATACCGGCTGATTGTCAATGTGAATGACCTGCGCAGGAAAAACGAGAAGA
GGGCTAACCGGCTTCTGAACAATGCCTTTGAGGAGCTGGTTGCCTTCAGCGGGCCTTAAAGGATTTTGTGGCCT
CCATTGATGCTACCTATGCCAAGCAGTATGAGGAGTTCTACGTAGGACTGGAAGGCAGCTTTGGCTCCAAGCAGC
TCTCCCGCGGACTCTTACCTCCTGCTTCCTCAGCTGTGTGGTCTGTGTGGAGGGCATTGTCACTAAATGTTCTC
TAGTTCGTCCCAAAGTCGTCCGAGTGTCCTACTGTCTGCTACTAAGAAGACCATAGAGCGACGTTATTCTG
ATCTCACCACCTGGTGGCCTTTCCCTCCAGCTGTGTCTATCTACCAAGGATGAGGAGAACAATCCCCTTGAGA
CAGAATATGGCCTTTCTGTCTACAAGGATCACCAGACCATCACCATCCAGGAGATGCCGGAAGGCCCCAGCCG
GCCAGTCCCCCGCTCTGTGGACGTCATTCTGGATGATGACTTGGTGGATAAAGCGAAGCCTGGTGACCGGGTTC
AGGTGGTGGGAACCTACCGTTGCCTTCCTGGAAAGAAGGGAGGCTACACCTCTGGGACCTTCAGGACTGTCTGA
TTGCCTGTAATGTTAAGCAGATGAGCAAGGATGCTCAGCCCTCTTTCTCTGCTGAGGATATAGCCAAGATCAAGA
AGTTCAGTAAACCCGATCCAAGGATATCTTTGACCAGCTGGCCAAGTCATTGGCCCCAAGTATCCATGGGCATG
ACTATGTCAAGAAAGCAATCCTCTGCTTGCTCTTGGGAGGGGTGGAACGAGACCTAGAAAATGGCAGCCACATCC
GTGGGGACATCAATATTCTTCTAATAGGAGACCCATCCGTGCCAAGTCTCAGCTTCTGCGGTATGTGCTTTGCA
CTGCACCCCGAGCTATCCCCACCACTGGCCGGGGCTCCTCTGGAGTGGGTCTGACGGCTGCTGTCAACACAGACC
AGGAAACAGGAGAGCGCCGTCTGGAAGCAGGGGCCATGGTCTGGCTGACCGAGGCGTGGTTTGCAATTGATGAAT
TTGACAAAATGTCTGACATGGATCGCACAGCCATCCATGAAGTGATGGAGCAGGGTCGAGTGACCATTGCCAAGG
CTGGCATCCATGCTCGGCTGAATGCCCGCTGCAGTGTTTTGGCAGCTGCCAACCCTGTCTACGGCAGGTATGACC
AGTATAAGACTCCAATGGAGAACATTGGGCTACAGGACTCACTGCTGTACGATTTGACTTGCTCTTCATCATGC
TGGATCAGATGGATCCTGAGCAGGATCGGGAGATCTCAGACCATGTCTTCGGATGCACCGTTACAGAGCACCTG
GGGAGCAGGATGGCGATGCTATGCCCTTGGGTAGTGCTGTGGATATCCTGGCCACAGATGATCCCACTTTAGCC
AGGAAGATCAGCAGGACACCCAGATTTATGAGAAGCATGACAACCTTCTACATGGGACCAAGAAGAAAAAGGAGA
AGATGGTGAGTGACGATTTCATGAAGAAGTACATCCATGTGGCCAAAATCATCAAGCCTGTCTGACACAGGAGT
CGGCCACCTACATTGCAGAAGAGTATTACGCCCTGCGCAGCCAGGATAGCATGAGCTCAGACACCGCCAGGACAT
CTCCAGTTACAGCCCGAACACTGGAACTCTGATTGACTGGCCACAGCCCATGCGAAGGCGCGCATGAGCAAGA
CTGTGGACCTGCAGGATGCAGAGGAAGCTGTGGAGTTGGTCCAGTATGCTTACTTTAAGAAGGTTCTGGAGAAGG
AGAAGAAACGTAAGAAGCGAAGTGAGGATGAATCAGAGACAGAAGATGAAGAGGAGAAAAGCCAAGAGGACCAGG
AGCAGAAGAGGAAGAGAAGGAAGACTCGCCAGCCAGATGCCAAAGATGGGGATTATACGACCCCTATGACTTCA
GTGACACAGAGGAGGAAATGCCTCAAGTACACACTCCAAAGACGGCAGACTCACAGGAGACCAAGGAATCCCAGA
AAGTGGAGTTGAGTGAATCCAGGTTGAAGGCATTCAAGGTGGCCCTCTTGATGTGTTCCGGAAGCTCATGCGC
AGTCAATCGGCATGAATCGCCTCACAGAATCCATCAACCGGGACAGCGAAGAGCCCTTCTCTCAGTTGAGATCC
AGGCTGCTCTGAGCAAGATGCAGGATGACAATCAGGTCATGGTGTCTGAGGGCATCATCTTCTCATCTGAGGAG
GCCTCGTCTCTGAACTTGGGTGTGCCGAGAGAGTTGTTCTGTGTTTTCCACCCTCTCCCTGACCCAAGTCTTT
GCCTCTACTCCCTTAACAGTGTTGAATTCAACTGAAGCGAGGAATGTTGGTGATGAAGCTGAGTTCAGGACTCG
GTGGACCCCTTTGGGAATGGGTGATGAAAGCTGCCATGGGGTGAGGAAAGAGGAGACAGTGGGAGAGGACAATGAC
TATTGCATCTTCATTGCAAAGCACTGGCTCATCCGCCCTACTTCCCATCCCACACAAACCAATTGTAAATAAC
ATATGACTTCTGAGTACTTTTGGGGGCACAACTGTTTCTGTTTGCTGTTTTTTTGTGTTTTTTTCTCCAG
AGCACTTTGGTCTAGACTAGGCTTTGGGTGGTTCCAATTGGTGGAGAGAAGCTCTGAGGCACGTCATGCAGGTCA
AGAAAGCTTTCTTTGAGTAGCACCAGTTAAGGTGAATATGTATTGTATCACAAAACAAACCAATATCCAGATG
AATATCCGAGATGTTGAATAAACTTAGCCATTTCTGTACAAAAAAGGGGGGCGCGTAAAC

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FIGURE 46

MAGTVVLDDVELREAQRDYLDFLDDEEDQGIIYQSKVRELISDNQYRLIVNVNDLRRKNEKRANRLLNNAFEELVA
FQALKDFVASIDATYAKQYEEFYVGLSGSGSKHVSPRILTSCLSCVVCVEGIVTKCSLVRPKVVRSVHYCPA
TKKTIERRYSDLTTLVAFPSVVYPTKDEENNPLETEYGLSVYKDHQTITIQEMPEKAPAGQLPRSVDVILDDDL
VDKAKPGDRVQVVGTYRCLPGKKGGYTSCTFRTVLIACNVKQMSKDAQPSFSAEDIAKIKKFSKTRSKDIFDQLA
KSLAPSIHGHDIYVKKAILCLLLGGVERDLENGSHIRGDINILLIGDPSVAKSOLLRYVLCTAPRAIPTTGRGSSG
VGLTAAVTTDQETGERRLEAGAMVLADRGVVCIDEFDKMSMDRTAIHEVMEQGRVTIAKAGIHARLNARCSVLA
AANPVYGRYDQYKTPMENIGLQDSLLSRFDLLFIMLDQMDPEQDREISDHVLRMHRYRAPGEQDGDAMPLGSAVD
ILATDDPNFSQEDQQDTQIYEKHDNLLHGTKKKKKEMVSAAFMKKYIHVAKI IKPVLTTQESATYIAEEYSRLRSQ
DSMSSDTARTSPVTARTLETILRLATAHAKARMSKTVDLQDAEEAVELVQYAYFKKVLEKEKKRKRSEDESETE
DEEEKSQEDQEQRKRKRKTRQPDAGDSYDPYDFSDTEEMPQVHTPKTADSQETKESQKVELSESRLKAFKVA
LLDVFREAHQAQSIGMNRLTESINRDSEEPFSSVEIQAALSKMQDDNQVMVSEGIIFLI

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FIGURE 47

AATGCCACCTGCTTGAAGGCTATATGTGACAAGTCACTAGAGGTTACCTGCAGGTTGACGCCATGTACACAAAT
GTCAAAGTAACTAATATTTGCTCTGATGGGACACTCTACTGCCAGGTGCCTTGTAAGGGTCTGAACAAGCTCAGT
GACCTTCTACGTAAGATAGAGGACTACTTCCATTGCAAGCACATGACCTCTGAGTGCTTTGTTTCATTACCCCTC
TGTGGGAAAATCTGCCTCTTCCATTGCAAAGGAAAATGGTTACGAGTAGAGATCACAAATGTTACAGCAGCCGG
GCTCTTGATGTTTCAGTTTCTGGACTCTGGCACTGTGACATCTGTAAAAGTGTGAGAGCTCAGGGAAAATCCACCT
CGGTTTCTACAAGAAATGATTGCAATACCACCTCAGGCCATTAAGTGCTGTTTAGCAGATCTTCCACAATCTATT
GGCATGTGGACACCAGATGCAGTGCTGTGGTTAAGAGATTCTGTTTTGAATTGCTCGGACTGTAGCATTAAAGGTT
ACAAAAGTGGATGAAACCAGAGGGATCGCACATGTTTTATTTATTTACCCCTAAGAACTTCCCTGACCCCTCATCGC
AGTATTAATCGCCAGATTACAAATGCAGACTTGTGGAAGCATCAGAAGGATGTGTTTTTGAGTGCCATATCCAGT
GGAGCTGACTCTCCCAACAGCAAAAATGGCAACATGCCCATGTGCGGCAACACTGGAGAGAATTTAGAAAGAAC
CTCACAGATGTCATCAAAAAGTCCATGGTGGACCATACGAGCGCTTTCTCCACAGAGGAAGTCCACCTCCTGTC
CACTTATCAAAGCCAGGGGAACACATGGATGTGTATGTGCCTGTGGCCTGTCAACCAGGCTACTTCGTCATCCAG
CCTTGGCAGGAGATACATAAGTTGGAAGTTCTGATGGAAGAGATGATTCTATATTACAGCGTGTCTGAAGAGCGC
CACATAGCAGTGGAGAAAGACCAAGTGTATGCTGCAAAAGTGGAAAATAAGTGGCACAGGGTGCTTTTAAAGGA
ATCCTGACCAATGGACTGGTATCTGTGTATGAGCTGGATTATGGCAAACACGAATTAGTCAACATAAGAAAAGTA
CAGCCCCTAGTGGACATGTTCCGAAAGCTGCCCTTCCAAGCAGTCACAGCTCAACTTGCAGGAGTGAAGTGCAAC
CAGTGGTCTGAGGAGGCTTCTATGGTGTTCGAAATCATGTGGAGAAGAAACCTCTGGTGGCACTGGTGCAGACA
GTCATTGAAAATGCTAACCTTGGGACCGGAAAGTAGTGGTCTACTTAGTGGACACATCGTTGCCAGACACCGAT
ACCTGGATTATGATTTTTATGTCAGAGTATCTGATAGAGCTTTCAAAAGTTAATTAATGACTGCTCTGAAACCT
TGACAACTAATTCAGATTTTTTAGCAATAACAAAATGTAGTAGGCTTAAAAAAATCTTAAGTCTGCTACATGGC
TCTGACTGCTGTGGGGGATTGAAAAGAATATGCTTATGTTTGATGAAAGATATTTAACAAGTTTGTTTTAACAG
AGTTGACTTTTCAAAGAAAATTGTACTTGAATTATTACTATAATATTAGAATAAAAATGTTTATC

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FIGURE 48

NATCLKAICDKSLEVHLQVDAMYTNVKVTNICS DGTLYCQVPCKGLNKLSDLLRKIEDYFHCKHMTSECFVSLPF
CGKICLFHCKGKWL RVEITNVHSSRALDVQFLDSGTVTSVKVSELREIPPRFLQEMIAIPPQAICKCLADLPQSI
GMWTPDAVLWL RDSVLNCSDCSIKVTKVDETRGIAHVYLFTPKNFPDPHRSINRQITNADLWKHQKDVFLSAISS
GADSPNSKNGNMPMSGNTGENFRKNLTDVIKKSMVDHTSAFSTEELPPPVHLSKPEGHMDVYVPVACHPGYFVIQ
PWQEIHKLEVLMEEMILYYSVSEERHIAVEKDQVYAAKVENKWHRVLLKGILTNGLVSVYELDYGKHELVNIRKV
QPLVDMFRKLFPQAVTAQLAGVKCNQWSEEASMVFRNHVEKKPLVALVQTVIENANPWDRKVVVYLVDTSLPDTD
TWIHD MFSEYLIELSKVN

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FIGURE 49

GCGGAAGGAACCGCCGGGGGCCATGGACGGAGCAGTGATGGAAGGCCGCTTTTTTGCAGAGTCAGCGCTTTGG
GACCAAGAGGTGGAGGAAGACCTGGGCCGTGCTCTACCCGGCCAGTCCCCACGGCGTAGCGCGGCTCGAGTTCTT
TGACCATAAGGGGTGAGCTCTGGGGGTGGCCGAGGGAGCTCGCGCCGCCTGGACTGCAAAGTGATCCGTCTGGC
TGAGTGTGTGAGTGTGGCCCCGTACCGTGGAGACCCCCCTGAGCCCGGCCACTGCCTTCCGCCTGGACAC
TGCTCAGCGCTCGACCTGCTGGCGGCCGACGCGCGTCCAGTGCAGCCTGGGTGCAGACGCTGTGCCGAAACGC
CTTTCCGAAAGGCAGCTGGACTCTGGCGCCTACCGATAACCCACCTAAGCTTTCTGCCCTGGAGATGCTGGAGAA
CTCCTTGACAGCCCTACCTGGGAAGGATCCCAATTCTGGGTAACGGTGCAGAGGACTGAGGCCGCCGAGCGCTG
TGGCCTGCATGGCTCCTACGTGCTGAGGGTGGAGGCTGAAAGGCTGACTCTCCTGACCGTGGGGGCCAGAGTCA
GATACTGGAGCCACTCCTGTCTGCTGGCCCTACACTCTGTTGCGTCGCTATGGCCGGGACAAGGTATGTTCTCTTT
CGAGGCCGGCCGCCGTGCCCTCAGGCCCTGGAACCTTACCTTCCAGACGGCACAGGGAAATGACATCTTCCA
GGCAGTTGAGACTGCCATCCACCGGCAGAAGGCCAGGGAAAGGCCGGACAGGGGCACGATGTTCTCAGAGCTGA
CTCCCATGAAGGGGAGGTGGCAGAGGGGAAGTTGCCTTCCCCACCTGGCCCCCAAGAGCTCCTCGACAGTCCCC
AGCCCTGTATGCTGAGCCCTTAGACTCCCTGCGCATTGCTCCATGCCCTTCCCAGGACTCCCTATACTCAGACCC
CTTGACAGCACGTCTGCTCAGGCAGGAGAGGGAGTACAACGGAAGAAACCTCTCTATTGGGACTTGTATGAGCA
TGCGCAGCAGCAGTTGCTGAAGGCCAAGCTGACAGACCCCAAAGAGGATCCCATCTATGATGAACCTGAGGGCCT
GGCCCCAGTCCCTCCCCAGGGCCTTTATGATCTGCCCTCGGGAGCCCAAGGATGCATGGTGGTGCCAAGCTCGGGT
GAAGGAGGAGGGCTATGAGCTCCCCTACAACCCTGCCACTGATGACTACGCTGTGCCACCCCTCGGAGCACAAA
GCCCCCTCCTTGCTCCCAAGCCCCAGGGCCCAGCCTTCCCTGAACCTGGTACTGCAACTGGCAGTGGCATCAAAAG
CCACAACCTCAGCCCTGTACAGCCAGGTCCAGAAGAGCGGGGCCCTCAGGGAGCTGGGACTGTGGGCTCTCTAGAGT
AGGGACTGACAAGACTGGGGTCAAGTCAGAGGGCTCTACCTTGAGAAGGACGGCAAGGCTGAGGTGGCTAAGGGGG
ACCATGGGGAGGTGGCACTAGGGATCAAAGAAGATGGTTAGAACCAGCAGAAGCCAGAGGGTGGGAGGGGCCATG
CTGTGTGAGACCAGGGGACCAGAGGGATGGGAGAGTCAAGGAAGGACAATCCAGGAAGTCCTAAGAAGTGGGG
CAGATGGCAGGGCTGAGGATGGGCTCTGCATCCCCCAAAGCCATCCCTTCCCTACTTCCCCAAATGAAGGGACGG
CTGTGGGACCAGGTCTGTGGAAGTGGTGCATGGTCAGAATGGGTGCAGTTTGAGGGGCCTGTGTGAGGCCTCA
GGGAGATGTTGGACTGTGCCTGGATCCTTACTCCTGCATTGTTCTTTGCCAGAGACCTATTTAAAAATTTAAAA
TTCTCATTAAGTCAAAAAAAAAAAAAAAAAAAAA

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FIGURE 50

MDGAVMEGPLFLQSQRFGTKRWKRTWAVLYPASPHGVARLEFFDHKGSSSGGGRGSSRRLDCKVIRLAECVSVAP
VTVETPPEPGATAFRDLTAQRSHLLAADAPSSAÄVQTLCRNAFPKGSWTLAPTNDNPPKLSALEMLENSLYSPTW
EGSQFWVTIVQRTAAERCGLHGSYVLRVEAERLTLLTVGAQSQILEPLLSWPYTLRLRYGRDKVMFSFEAGRRCF
SGPGTFTFQTAQGNDIFQAVETAIHRQKAQGKAGQGHDLRADSHGEVAEGKLPSPGPGQELLDSPPALYAEPL
DSLRIAPCPSQDSLYSDPLDSTSAQAGEGVQRKKFLYWDLYEHAQQQLLKAKLTDPKEDPIYDEPEGLAPVPPQG
LYDLPREPKDAWWCQARVKEEGYELPYNPATDDYAVPPPRSTKPLLAPKPQGPAPFEPGTATGSGIKSHNSALYS
QVQKSGASGSWDCGLSRVGTDKTGKSEGST

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FIGURE 51

AGTAAAAGTCCACAGTTACCGTGAGAGAAAAAAGAGGAGAAAGCAGTGCAGCCAACTCGGAAGAAAAGAGAGG
AGGAAAAGGACTCGACTTTTACACA*TGGAACAACCTTCTTTCCAGTGCTAAGGCTCTCTGATCTGGGGAACAACAC
CTGGACATGGCTCCAGAGATCAACTTGCCGGGCCCAATGAGCCTCATTGATAACACTAAAGGGCAGCTGGTGGTG
AATCCAGAAGCTCTGAAGATCCTATCTGCAATTACGCAGCCTGTGGTGGTGGTGGCGATTGTGGGCCTCTATCGC
ACAGGCAAATCCTACCTGATGAACAAGCTGGCTGGGAAGAAAAACGGCTTCTCTCTAGGCTCCACAGTGAAGTCT
CACACCAAGGGAATCTGGATGTGGTGTGTGCCTCATCCCAAGAAGCCAGAACACACCCCTAGTTCTGCTCGACACT
GAGGGCCTGGGAGATATAGAGAAGGGTGACAATGAGAATGACTCCTGGATCTTTGCCTTGGCCATCCTCCTGAGC
AGCACCTTCGTGTACAATAGCATGGGAACCATCAACCAGCAGGCCATGGACCAACTTCACTATGTGACAGAGCTG
ACAGATCGAATCAAGGCAAACCTCCTCACCTGGTAACAATTCTGTAGACGACTCAGCTGACTTTGTGAGCTTTTTT
CCAGCATTTGTGTGGACTCTCAGAGATTACCCCTGGAAGTGAAGTAGATGGAGAACCCATCACTGCTGATGAC
TACTTGGAGCTTTTCGCTAAAGCTAAGAAAAGGTACTGATAAGAAAAGTAAAAGCTTTAATGATCCTCGGTTGTGC
ATCCGAAAGTTCTTCCCAAGAGGAAGTGCTTCGTCTTCGATTGGCCCGCTCCTAAGAAGTACCTTGCTCACCTA
GAGCAGCTAAAGGAGGAAGAGCTGAACCTGATTTATAGAACAAGTTGCAGAATTTTGTTCCTACATCCTCAGC
CATTCCAATGTCAAGACTCTTTCAGGTGGCATTGCAGTCAATGGGCCTCGTCTAGAGAGCCTGGTGTGCTGACCTAC
GTCAATGCCATCAGCAGTGGGGATCTACCCTGCATGGAGAACGCAGTCCTGGCCTTGGCCAGATAGAGAACTCA
GCCGCAGTGGAAAAGGCTATTGCCCACTATGAACAGCAGATGGGCCAGAAGGTGCAGCTGCCACGGAAACCCCTC
CAGGAGCTGCTGGACCTGCACAGGGACAGTGAGAGAGAGGCCATTGAAGTCTTCATGAAGAACTCTTTCAAGGAT
GTGGACCAAATGTTCCAGAGGAAATTAGGGGCCAGTTGGAAGCAAGGCGAGATGACTTTTGTAAAGCAGAATTCC
AAAGCATCATCAGATTGTTGCATGGCTTTACTTCAGGATATATTTGGCCCTTTAGAAGAAGATGTCAAGCAGGGA
ACATTTTCTAAACCAGGAGGTTACCGTCTCTTTACTCAGAAGCTGCAGGAGCTGAAGAATAAGTACTACCAGGTG
CCAAGGAAGGGGATACAGGCCAAAGAGGTGCTGAAAAATATTTGGAGTCCAAGGAGGATGTGGCTGATGCACTT
CTACAGACTGATCAGTCACTCTCAGAAAAGGAAAAAGCGATTGAAGTGAACGTATAAAGGCTGAATCTGCAGAA
GCTGCAAAGAAAATGTTGGAGGAAATACAAAAGAAGATGAGGAGATGATGGAACAGAAAGAGAAGAGTTATCAG
GAACATGTGAAACAATTGACTGAGAAGATGGAGAGGGACAGGGCCAGTTAATGGCAGAGCAAGAGAAGACCCCTC
GCTCTTAAACTTCAGGAACAGGAACGCCTTCTCAAGGAGGGATTGAGAATGAGAGCAAGAGACTTCAAAAAGAC
ATATGGGATATCCAGATGAGAAGCAAATCATTGGAGCCAATATGTAACATACTCTAAAAGTCCAAGGAGCAAAAT
TTGCCTGTCCAGCTCCCTCTCCCAAGAAACAACATGAATGAGCAACTTCAGAGTGTCAAACAAGTCCATTAAA
CTTAACCTCAAAATCATGATGCATGCATTTTTTGTGAACCATAAAGTTTGCAAAGTAAAGTTAAGTATGAGGTCA
ATGTTTT

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FIGURE 52

MAPEINLPGPMSLIDNTKGQLVVNPEALKILSAITQPVVVVAIVGLYRTGKSYLMNKLAKKNGFSLGSTVKSH
KGIWMWCVPHPKPEHTLVLLDTEGLGDIEKGNENDSWIFALAILLSSTFVYNSMGTINQQAMDQLHYVTELT
RIKANSSPGNNSVDDSAFVSFFPAFVWTLRDFTLELEVDPITADDYLELSLKLKRGTDKKSFSFNDPRLCIR
KFFPKRKCFVFDWPAPKKYLAHLEQLKEEELNPDFIEQVAEFCSYILSHSNVKTLSGGIANGPRLESIVLTYVN
AISSGDLPCMENAVLALAQIENSAAVEKAIHAYEQQMGQKVQLPTETLQELLDLHRDSEREAIEVFMKNSFKDVD
QMFQRKLGAQLEARRDDFCKQNSKASSDCCMALLQDIFGPLEEDVKQGTFSKPGGYRLFTQKLQELKNKYYQVPR
KGIQAKEVLKKYLESKEDVADALLQTDQSLSEKEKAIEVERIKAESAEAAKKMLEEIQKKNEEMMEQKEKSYQEH
VKQLTEKMERDRAQLMAEQEKTALKLQEQRLLKEGFENESKRLQKDIWDIQMRKSLEPICNIL

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FIGURE 53

GCCCCGCCGCCGGCAGTGGACCGCTGTGCGCGAACCCTGAACCCTACGGTCCCGACCCGCGGGCGAGGCCGGGTA
CCTGGGCTGGGATCCGGAGCAAGCGGGCGAGGGCAGCGCCCTAAGCAGGCCCGGAGCGATGGCAGCCTTGATGAC
CCCCGGAACCGGGGCCCCACCCGCGCCTGGTGACTTCTCCGGGGAAGGGAGCCAGGGACTTCCCGACCCTTCGCC
AGAGCCCAAGCAGCTCCCGGAGCTGATCCGCATGAAGCGAGACGGAGGCCGCTGAGCGAAGCGGACATCAGGGG
CTTCGTGGCCGCTGTGGTGAATGGGAGCGCGCAGGGCGCACAGATCGGGGCCATGCTGATGGCCATCCGACTTCG
GGGCATGGATCTGGAGGAGACCTCGGTGCTGACCCAGGCCCTGGCTCAGTCGGGACAGCAGCTGGAGTGGCCAGA
GGCCTGGCGCCAGCAGCTTGTGGACAAGCATTCCAAGGGGGTGTGGGTGACAAGGTCAGCCTGGTCTCTGCACC
TGCCCTGGCGGCATGTGGCTGCAAGGTGCCAATGATCAGCGGACGTGGTCTGGGGCACACAGGAGGCACCTTGGA
TAAGCTGGAGTCTATTCTGGATTCAATGTCATCCAGAGCCCAGAGCAGATGCAAGTGCTGCTGGACCAGGCGGG
CTGCTGTATCGTGGGTCAGAGTGAGCAGCTGGTTCCTGCGGACGGAATCCTATATGCAGCCAGAGATGTGACAGC
CACCGTGGACAGCCTGCCACTCATCACAGCCTCCATTCTCAGTAAGAACTCGTGGAGGGGCTGTCCGCTCTGGT
GGTGGACGTTAAGTTTCGGAGGGGCGCCGCTCTCCCAACCAGGAGCAGGCCCGGGAGCTGGCAAAGACGCTGGT
TGGCGTGGGAGCCAGCCTAGGGCTTCGGGTCGCGGCAGCGCTGACCGCCATGGACAAGCCCCCTGGGTCTGCTGCGT
GGGCCACGCCCTGGAGGTGGAGGAGGCGCTGCTCTGCATGGACGGCGCAGGCCCGCCAGACTTAAGGGACCTGGT
CACCACGCTCGGGGGCGCCCTGCTCTGGCTCAGCGGACACGCGGGGACTCAGGCTCAGGGCGCTGCCCGGGTGGC
CGCGGCGCTGGACGACGGCTCGGCCCTTGGCCGCTTCGAGCGGATGCTGGCGGCGCAGGGCGTGGATCCCGGTCT
GGCCCGAGCCCTGTGCTCGGGAAGTCCCGCAGAACGCCGGCAGCTGCTGCCTCGCGCCCGGGAGCAGGAGGAGCT
GCTGGCGCCCCGAGATGGCACCGTGGAGCTGGTCCGGGCGCTGCCGCTGGCGCTGGTGTGACGAGCTCGGGGC
CGGGCGCAGCCGCGCTGGGGAGCCGCTCCGCCCTGGGGGTGGGCGCAGAGCTGCTGGTCTGACGTGGGTCTAGAGGCT
GCGCCGTGGGACCCCTGGCTCCGCGTGCACCGGGACGGCCCCGCGCTCAGCGGCCCGCAGAGCCGCGCCCTGCA
GGAGGCGCTCGTACTCTCCGACCGCGCGCCATTGCGCCCCCCCTCGCCCTTCGCAGAGCTCGTTCTGCCGCCGCA
GCAATTAAAGCTCCTTTGCCGCGAAA

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FIGURE 54

MAALMTPGTGAPPAPGDFSGEGSQGLPDPSPPEPKQLPELIRMKRDGGRLSEADIRGFVAAVVNGSAQGAQIGAML
MAIRLRGMDLEETSVLTQALAQSGQQLWPEAWRQQQLVDKHSTGGVGDKVSLVLAPALAACGCKVPMISGRGLGH
TGGTLDKLESIPGFNVIQSPEQMQLLDQAGCCIVGQSEQLVPADGILYAARDVTATVDSLPLITASILSKKLVE
GLSALVVDVKFGGAAVFPNQEQAARELAKTLVGVGASLGLRVAAALTAMDKPLGRCVGHAEVEEALLCMDGAGPP
DLRDLVTTLGGALLWLSGHAGTQAQGAARVAAALDDGSALGRFERMLAAQGVDFGLARALCSGSPAERRQLLPRA
REQEELLAPADGTVELVRALPLALVLHELGAAGRSRAGEPLRLGVGAELLVDVGQRLRRGTPWLRVHRDGPALSGP
QSRALQEALVLSDRAPFAAPSPFAELVLPPQQ

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FIGURE 55

AAGATGGCGGCGCGGGGCGCGCCGCGCTCCCAGGCTCTCCTCCCCAGCCTTCCTCCGGCTGGCAGCACGACT
CGCGTAGCCGTGCGCCGATTGCCTCTCGGCCTGGGCAATCGTCCCAGGCTGCCGGTCGACGACCGCCCCGCGTCAT
GCGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCGTCCGCGGCGTGGAGGTTGCAGAGGA
AAGTGGTCGCTTATGGTCAGAGGAGCTCCTGCATGACCCGATGGGCCGGGACAGGGCAGCAGAAGAGGCCAATGC
GGTGTGGGGCTGGACACCCAAGGCGATCACATGGTGATGCTGTCTGTGATTCTGGGGAAGCTGAGGACAAGGT
GAGTTCAGAGCCTAGCGGCGTCACCTGTGGTGCTGGAGGAGCGGAGGACTCAAGGTGCAACGTCCGAGAGAGCCT
TTTCTCTCTGGATGGCGCTGGAGCACACTTCCCTGACAGAGAGGAGGAGTATTACACAGAGCCAGAAGTGGCGGA
ATCTGACGCGACCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAGGAGAG
AAACATTACAGGATTAGAAAATTTCACTCTGAAAATTTTAAATATGTCACAGGACCTTATGGATTTTCTGAACCC
AAACGGTAGTACTGTACTCTAGTCCTGTTTTACACCCCGTGGTGCCGCTTTTCTGCCAGTTTGGCCCCCTCACTT
TAACTCTCTGCCCCGGGCATTTCCAGCTCTTCACTTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTAC
CAGGTTTGGCACCGTAGCTGTTCTAATATTTTATTATTTCAAGGAGCTAAACCAATGGCCAGATTTAATCATAC
AGATCGAACACTGGAAACACTGAAAATCTTCATTTTAAATCAGACAGGTATAGAAGCCAAGAAGAATGTGGTGGT
AACTCAAGCCGACCAATAGGCCCTCTTCCCAGCACTTTGATAAAAAGTGTGGACTGGTTGCTTGTATTTTCCTT
ATTCTTTTAAATTAGTTTTATTATGTATGCTACCATTCGAACTGAGAGTATTCCGGTGGCTAATTCAGGACAAGA
GCAGGAACATGTGGAGTAGTGATGGTCTGAAAGAAGTTGGAAAGAGGAACTTCAATCCTTCGTTTCAGAAATTAG
TGCTACAGTTTCATACATTTTCTCCAGTGACGTGTTGACTTGAAACTTCAGGCAGATTAAAAGAATCATTGTTG
AACAACTGAATGTATAAAAAAATTATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAATGCAAAAATATTCA
AAAAAAAAAAAAAAAAAAAA

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FIGURE 56

MVPAAGRRPPRVMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEELLHDPMGRDRAAEEANAVLGLDTQGDHNV
MLSVIPGEAEDKVSSEPSGVTCGAGGAEDSRCNVRESLFLDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNT
ESLKSPKVNCEERNITGLENFTLKILNMSQDLMDFLNPNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFFPALHF
LALDASQHSSLSTRFGTVAVPNILLFQGAKEPMARFNHIDRTLETLEKIFIFNQTGIEAKKNVVVTQADQIGPLPST
LIKSDWLLVFSLFFLISFIMYATIRTESIRWLIPGQEQUEHVE

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FIGURE 57

CCGTGGACATCTCAGGTCTTCAGGGTCTTCCATCTGGAAGTATATAAAGTTCAGAAAACATGTCTCGAAGATATG
ACTCCAGGACCACTATATTTTCTCCAGAAGGTCGCTTATACCAAGTTGAATATGCCATGGAAGCTATTGGACATG
CAGGCACCTGTTTGGGAATTTTAGCAAATGATGGTGTTTTGCTTGCAGCAGAGAGACGCAACATCCACAAGCTTC
TTGATGAAGTCTTTTTTCTGAAAAAATTTATAAACTCAATGAGGACATGGCTTGCAGTGTGGCAGGCATAACTT
CTGATGCTAATGTTCTGACTAATGAACCTAAGGCTCATTGCTCAAAGGTATTTATTACAGTATCAGGAGCCAATAC
CTTGTGAGCAGTTGGTTACAGCACTGTGTGATATCAAACAAGCTTATACACAATTTGGAGGAAAACGTCCCTTTG
GTGTTTCATTGCTGTACATTGGCTGGGATAAGCACTATGGCTTTTCTAGCTCTATCAGAGTGACCCCTAGTGGAAATT
ACGGGGGATGGAAGGCCACATGCATTGGAAATAATAGCGCTGCAGCTGTGTCAATGTTGAAACAAGACTATAAAG
AAGGAGAAATGACCTTGAAGTCAGCACTTGCTTTAGCTATCAAAGTACTAAATAAGACCATGGATGTTAGTAAAC
TCTCTGCTGAAAAAGTGGAAATTGCAACACTAACAAGAGAGAATGGAAAGACAGTAATCAGAGTTCTCAAACAAA
AAGAAGTGGAGCAGTTGATCAAAAAACATGAGGAAGAAGAAGCCAAAGCTGAGCGTGAGAAGAAAGAAAAAGAAC
AGAAAGAAAAGGATAAATAGAATCAGAGATTTATTACTCATTGGGGCACCATTTCAGTGTAAGCAGTCCTA
CTCTCCACACTAGGAAGGCTTTACTTTTTTTAACTGGTGCAGTGGGAAAATAGGACATTACATACTGAATTGGG
TCCTTGTCATTTCTGTCCAATTGAATACTTTATTGTAACGATGATGGTTACCCTTCATGGACGTCTTAATCTTCC
ACACACATCCCTTTTTTTTGGGAATAAAA

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FIGURE 58

MSRRYDSRTTIFSPGRLYQVEYAMEAIGHAGTCLGILANDGVLLAAERRNIHKLLDEVFFSEKIYKLNEDMACS
VAGITSDANVLTNELRLIAQRYLLQYQEPPIPCQLVTALCDIKQAYTQFGGKRPFVSVLLYIGWDKHYGFQLYQS
DPSGNYGGWKATCIGNNSAAAVSMLKQDYKEGEMTLKSALALAIKVLNKTMDVSKLSAEKVEIATLTRENGKTVI
RVLKQKEVEQLIKKHEEEEAKAEREKKEKEQKEKDK

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FIGURE 59

CTGAAGAACAAATCAGCCTGGTCACCAGCTTTTCGGAACAGCAGAGACACAGAGGGCAGTCAATGAGTGAGGTCAC
CAAGAATTCCTGGAGAAAATCCTTCCACAGCTGAAATGCCATTTACCTGGAACCTATTCAAGGAAGACAGTGT
CTCAAGGGATCTAGAAGATAGAGTGTGTAACCAGATTGAATTTTAAACACTGAGTTCAAAGCTACAATGTACAA
CTTGTTGGCTACATAAAACACCTAGATGGTAACAACGAGGCAGCCCTGGAATGCTTACGGCAAGCTGAAGAGTT
AATCCAGCAAGAACATGCTGACCAAGCAGAAATCAGAAGTCTAGTCACTTGGGGAAACTACGCCTGGGTCTACTA
TCACTTGGGCAGACTCTCAGATGCTCAGATTTATGTAGATAAGGTGAAACAAACCTGCAAGAAATTTTCAAATCC
ATACAGTATTGAGTATTCTGAACTTGACTGTGAGGAAGGGTGGACACAACCTGAAGTGTGGAAGAAATGAAAGGGC
GAAGGTGTGTTTTGAGAAGGCTCTGGAAGAAAAGCCCAACAACCCAGAATTCTCCTCTGGACTGGCAATTGCGAT
GTACCATCTGGATAATCACCCAGAGAAACAGTTCTCTACTGATGTTTTGAAGCAGGCCATTGAGCTGAGTCTGA
TAACCAATACGTCAAGGTTCTCTTGGGCCTGAAACTGCAGAAGATGAATAAAGAAGCTGAAGGAGAGCAGTTTGT
TGAAGAAGCCTTGGAAAAGTCTCCTTGCCAAACAGATGTCTCCGCAGTGCAGCCAAATTTTACAGAAGAAAAGG
TGACCTAGACAAAGCTATTGAACTGTTTTCAACGGGTGTTGGAATCCACACCAAACAATGGCTACCTCTATCACC
GATTGGGTGCTGCTACAAGGCAAAAGTAAGACAAATGCAGAATACAGGAGAATCTGAAGCTAGTGGAAATAAAGA
GATGATTGAAGCACTAAAGCAATATGCTATGGACTATTGGAATAAAGCTCTTGAGAAGGGACTGAATCCTCTGAA
TGCATACTCCGATCTCGCTGAGTTCTTGAGACGGAATGTTATCAGACACCATTCAATAAGGAAGTCCCTGATGC
TGAAAAGCAACAACAATCCCATCAGCGCTACTGCAACCTTCAGAAATATAATGGGAAGTCTGAAGACACTGCTGT
GCAACATGGTTTTAGAGGGTTTTGTCCATAAGCAAAAAATCAACTGACAAGGAAGAGATCAAAGACCAACCACAGAA
TGTATCTGAAAATCTGCTTCCACAAAATGCACCAAATTATTGGTATCTTCAAGGATTAATTCATAAGCAGAATGG
AGATCTGCTGCAAGCCAAATGTTATGAGAAGGAAC TGGGCCGCTGCTAAGGGATGCCCTTCAGGCATAGGCAG
TATTTTCTGTGTCAGCATCTGAGCTTGAGGATGGTAGTGAGGAAATGGGCCAGGGCGCAGTCAGTCCAGTCCAG
AGAGCTCCTCTCTAACTCAGAGCAACTGAAC TGAGACAGAGGAGGAAAACAGAGCATCAGAAGCCTGCAGTGGTG
GTTGTGACGGGTAGGAGGATAGGAAGACAGGGGGCCCAACCTGGGATTGCTGAGCAGGGAAGCTTGCATGTTGC
TCTAAGGTACATTTTTAAAGAGTTGTTTTTGGCCGGCGCAGTGCTCATGCCTGTAATCCAGAACTTTGGGAG
GCCGAGGTGGGCGGATCACGAGGTCTGGAGTTTGAGACCATCTGGCTAACACAGTGAAATCCCGTCTCTACTAA
AAATACAAAAAATTAGCCAGGCGTGGTGGCTGGCACCTGTAGTCCAGCTACTTGGGAGGCTGAGGCAGGAGAAT
GGCGTGAACCTGGAAGGAAGAGGTTGCAGAGAGCCAAGATTGCG

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FIGURE 60

MSEVTKNSLEKILPQLKCHFTWNLFKEDSVSRDLEDRCNQIEFLNTEFKATMYNLLAYIKHLDGNNEAALECLR
QAEELIQQEHADQAEIRSLVTWGN YAWVYYHLGRLSDAQIYVDKVKQTCKKFSNPYSIEYSELDCEEGWTQLKCG
RNERAKVCFEKALEEKPNNEPFSSGLAIAMYHLDNHPEKQFSTDVLKQAIELSPDNQYVKVLLGLKLQKMNKEAE
GEQFVEEALEKSPCQTDVLRSAAKFYRRKGDLDKAIELFQRVLESTPNNGYLYHQIGCCYKAKVRQMONTGESEA
SGNKEMIEALKQYAMDYSNKALEKGLNPLNAYSDLAEFLETECYQTPFNKEVPDAEKQQQSHQRYCNLQKYNGKS
EDTAVQHGLEGLSISKKSTDKEEIKDQPNVSENLLPQNAPNYWYLQGLIHKQNGDLLQAKCYEKELGRLLLRDAP
SGIGSIFLSASELEDGSEEMGQGA VSSSPRELLSNSEQLN

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FIGURE 61

CGGGATGCGGCGCGCCGCGCGTTGAACCTCCTTGGCCTGGGCGAAGCTGTGTGGACCAAGCAAGTCAGGAGTGTG
GCCATGTTTTTCTGAGCAGGCTGCCCAGAGGGCCACACTCTACTGTCCCCACCATCAGCCAACAATGCCACCTTT
GCCC GG GTGCCAGTGGCAACCTACACCAACTCCTCACAACCCTTCCGGCTAGGAGAGCGCAGCTTTAGCCGGCAG
TATGCCACATTTATGCCACCCGCCTCATCCAAATGAGACCCTTCCTGGAGAACC GG GCGCCAGCAGCACTGGGGC
AGTGGAGTGGGAGTGAAGAAGCTGTGTGAACTGCAGCCTGAGGAGAAGTGCTGTGTGGTGGGCACTCTGTTCAAG
GCCATGCCGCTGCAGCCCTCCATCCTGCGGGAGGT CAGCGAGGAGCACAACTGCTCCCCAGCCTCCTCGGAGT
AAATACATACACCCAGATGACGAGCTGGTCTTGGAAGATGAACTGCAGCGTATCAAATAAAAGGCACCATTGAC
GTGTCAAAGCTGGTTACGGGGACTGTCTGGCTGTGTTTGGCTCCGTGAGAGACGACGGGAAGTTTCTGGTGGAG
GACTATTGCTTTGCTGACCTTGCTCCCCAGAAGCCCGCACCCCCACTTGACACAGATAGGTTTGTGCTACTGGTG
TCCGGCCTGGGCTGGGTGGCGGTGGAGGCGAGAGCCTGCTGGGCACCCAGCTGCTGGTGGATGTGGTGACGGGG
CAGCTTGGGGACGAAGGGGAGCAGTGCAGCGCCGCCACGTCTCCGGGTTATCCTCGCTGGCAACCTCCTCAGC
CACAGCACCCAGAGCAGGATTCTATCAATAAGGCCAAATACCTACCAAGAAAACCCAGGCAGCCAGCGTGGAG
GCTGTTAAGATGCTGGATGAGATCCTCCTGCAGCTGAGCGCCTCAGTGCCCGTGGACGTGATGCCAGGCGAGTTT
GATCCCAACCAATTACACGCTCCCCAGCAGCCCTCCACCCCTGCATGTTCCCGCTGGCCACTGCCTACTCCACG
CTCCAGCTGGTCACCAACCCCTACCAGGCCACCATTGATGGAGTCAGATTTTGGGGACATCAGGACAGAACGTG
AGTGACATTTTCCGATACAGCAGCATGGAGGATCACTTGGAGATCCTGGAGTGGACCCTGCGGGTCCGTACATC
AGCCCCACAGCCCCGGACACTCTAGGTTGTTACCCCTTCTACAAAATGACCCGTTTCATCTTCCAGAGTGCCCG
CATGTCTACTTTTGTGGCAACACCCCCAGCTTTGGCTCCAAAATCATCCGAGGTCCTGAGGACCAGACAGTGCTG
TTGGTGACTGTCCCTGACTTCAGTGCCACGCAGACCGCCTGCCTTGTGAACCTGCGCAGCCTGGCCTGCCAGCCC
ATCAGCTTCTCGGGCTTCGGGGCAGAGGACGATGACCTGGGAGGCCTGGGGCTGGGCCCCTGACTCAAAAAAGTG
GTTTTGACCAGAGAGGCCCAGATGGAGGCTGTTTCAATTCCTGCAGTGTGCGCATTGTAAATAAAGCCTGGCACTT
GCTGATGCG

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FIGURE 62

MFSEQAAQRAHTLLSPPSANNATFARVPVATYTNS SQPFRLGERSFSRQYAHYATR LIQMRF FLENRAQQHWGS
GVGVKKLCELOPEEKCCVVGTLFKAMPLQPSILREVSEEHNLLPQPPRSKYIHPDDELVLEDELQRIKLGKTIDV
SKLVTGTVLAVFGSVRDDGKFLVEDYCFADLAPQKPAPPLDTRFVLLVSGLGGLGGGGESLLGTQLLV DVVTGQ
LGDEGEQCSAAHVSRVILAGNLLSHSTQSRDSINKAKYLTKKTQAASVEAVKMLDEILLQLSASVPVDVMPGEFD
PTNYTLPQQPLHPCMFPLATAYSTLQLVNTPYQATIDGVRFLGTSGQNVSDIFRYSSMEDHLEILEWTLRVRHIS
PTAPDTLGCYPFYKTDPFIFPECPHVYFCGNTPSFGSKIIRGPEDQTVLLVTVPDFSATQTACLVNLRSLACQPI
SFSGFGAEDDDLGGGLGLGP

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FIGURE 63

CGGGCGTCCGCGGTGGCTGCAGTCCCGTTCGGTCTCCCTGCTGTCCGGCGCGAGCTCTTCGAGTCTTGCTTGGGAT
GTTTCAGCAGCCCCCTGAGAAGGAAGAGGAGGAAGCTGAGGGCCCCGCTGAGGGCGCAGGACCTGAGGGAGTCTTAC
ATCCAGCTCGTCCAGGGTGTGCAGGAGTGGCAGGATGGTTGCATGTACCAGGGGGAGTTTGGGTTGAACATGAAG
CTTGATATGGCAAATTCTCTTGCCCCACAGGCGAGTCATACCATGGGCAGTTTTACCGGGACCACTGCCATGGC
CTGGGTACCTACATGTGGCCAGATGGCTCCAGTTTACGGGCACATTTTACCTCAGCCACCGAGAAGGCTACGGC
ACCATGTACATGAAGACACGGCTTTTCCAGGGGCTATACAAAGCGGACCAGCGTTTGGGCCAGGTGTCGAGACC
TACCCCGATGGCAGCCAGGACGTGGGGCTGTGGTTCCGAGAGCAGCTCATCAAGCTGTGCACCCAGATCCCCAGT
GGCTTCTCCCTCCTCAGATACCCTGAGTTCTCCAGCTTCATCACCCACAGCCCTGCCAGGATCAGCCTCTCAGAA
GAGGAGAAAACGGAGTGGGGACTGCAGGAGGGACAGGATCCCTTTTCTATGACTATAAGCGGTTTCTTCTGAAT
GACAACCTAACGCTGCCTCCAGAAATGTATGTCTACTCGACCAACAGTGACCACCTGCCCATGACAAGCTCTTTC
CGCAAAGAGCTGGACGCCCCGATCTTCTCAATGAAATTCTCCGTTTCGTTGAGGATGGAGAACCATGGTTCATA
ATCAATGAGACCCCTTGTGGTCAAAATCCAGAAGCAAACCTACAAGTTCAGGAACAAGCCAGCTCACACCAGC
TGGAACATGGGCGCCATCCTGGAGGGGAAGCGCAGTGGCTTTGCACCCTGTGGGCCCAAAGAGCAAACCTTCCATG
GAGATGATCCTAAAGGCTGAGGAAGGGAACACGAATGGATTGTAGGATCCTGAAGGACAACCTTTGCTAGTGCT
GACGTGGCGGACGCAAAGGGCTACACTGTGCTTGTGCGGCTGCTACTACTGCCACAACGACATTGTCAACCTT
CTCCTGGACTGTGGGGCCGACGTGAACAAGTGCTCAGATGAGGGTCTCACGGCACTCAGCATGTGTTTCTCCTC
CACTACCCCGCCAGTCTTCAAGCCCAATGTTGCTGAACGGACCATACTGAGCCCCAGGAACCTCCAAAATTC
CCAGTTGTTCCAATCCTTTTCATCATCATTTTATGGACACAAACCTGGAGTCTCTGTACTATGAGGTGAACGTGCCT
TCCCAGGGTAGCTATGAGCTGAGGCCACCGCCAGCACCCTGCTCCTGCCACGCGTCTCAGGCAGCCACGAGGGC
GGCCACTTCCAGGACACCGGGCAGTGTGGGGGGTTCATGGACCACAGGAGCAGCTCTCTGAAGGGGGACTCCCCG
TTGGTGAAGGGCAGCCTTGGCCATGTGGAAGCGGGCTTGAGGACGTGTTGGGAAACACAGACCGGGGCAGTCTG
TGCAGTGCTGAGACGAAATTTGAGTCCAACGTGTGTGTGTGCGACTTCTCCATCGAGCTCTCGCAGGCCATGCTG
GAGAGAAGCGCCAGTCCACAGCTTGTGTAAGATGGCCTCGCCCTACCGTGCACCAGCAGCTTCGACAAAGGG
ACCATGCGGAGGATGGCGCTGTCCATGATCGAGCGGAGGAAGCGCTGGCGGACCATCAAGCTGCTGCTGCGCCGG
GGCGCGGACCCCAACCTGTGCTGCGTGCCCATGCAGTCTGTTCCTTGCTGTGAAGGCCGGGGACGTGGATGGG
GTGAGGCTGCTGCTGGAGCACGGGGCGAGGACCGACATCTGCTTTCCGCCGAGCTGAGCACCTGACACCACCTC
CACATCGCTGCCGCCCTTCTGGGGAGGAGGGGTACAGATTGTGGAGCTGCTGTTGCATGCCATCACCGATGTG
GACGCCAAGGCATCCGACGAGGACGACACTTACAAGCCCGGAAGCTGGACCTGCTGCCCTCAAGTCTGAAGCTC
AGCAATGAGCCAGGCCCTCCCCAAGCCTACTACAGCACGGACACAGCCCTCCCGGAGGAGGGGGGAGGACGGCT
CTGCACATGGCCTGCGAGCGGGAGGATGACAACAAGTGTGCCAGGGACATAGTCCGGCTCCTTCTATCCCACGGA
GCAATCCTAACCTGCTGTGGAGTGGCCACTCCCCGCTCTCCCTGTCCATTGCCAGTGGGAATGAGCTGGTTGTG
AAGGAGCTCCTGACCCAGGGAGCTGACCCCAACCTGCCCTGACCAAAGGCTTGGGCAGTGCCCTGTGTGTTGCC
TGTGACCTGACCTACGAGCACAGAGGAACATGGACAGCAAGCTGGCCCTGATTGACCGACTCATCAGTCACGGG
GCCGACATCCTGAAGCCTGTAATGCTCAGGCAGGGAGAAAAGGAGGCAGTGGGCACAGCCGTGGACTATGGCTAC
TTCAGATTCTTCCAGGACCGGAGGATTGCCCCGTGCCCTTCCACACGCTGATGCCAGCAGAGCGGAGACGTTT
CTGGCGCGGAAGCGGCTCCTGGAGTACATGGGCTTGACGTACGGCAGGCTGTCTTTGCCAAGGAGAGCCAGTGG
GACCCACGTGGCTGTACCTGTGCAAGAGAGCGGAGCTGATCCCCAGCCACAGGATGAAGAAGAAGGGCCCCAGC
CTGCCCAGGGGCTGGATGTGAAGGAGCAGGGGCAAATTCCTTCTTCAAGTTCTGCTACCAGTGTGGCCGCTCC
ATCGGGGTCCGCTCTTGGCCCTGCCCTCGCTGCTACGGGATCCTGACCTGCAGCAAGTACTGCAAGACCAAGGCC
TGGACCGAGTTCCACAAGAAGGACTGCGGGGACCTGGTGGCCATCGTGACACAACCTGGAGCAAGTTTCCAGGAGG
AGAGAAGAATTCAGTGAAGCAGCAGCTGCACGTCCGAGGCTTGGGGAGGACCCAGGACTGTGTGGGTTTCTTAC
CTGCCTGAGCCACCTCAGGGAATCTTCCAGCCTAATGCAGGCATTCTGCACCTTTGGGGTCATGCTTTGTAGCA
GTGTCTCCCTTGCACCTCGCAATAAATTGGCCCCACGGGGTGATTTTGACAGTCAAAAAAAAAA

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FIGURE 64

MYQGEFGLNMKLGYGKFSWPTGESYHGQFYRDHCHGLGTYMWPDGSSFTGTFFYLSHREGYGTMYMKTRLFQGLYK
ADQRFPGPVETYPDGSQDVGLWFRQLIKLCTQIPSGFSLLRYPEFSSFITHSPARISLSEEEKTEWGLQEGQDP
FFYDYKRFLNDNLTLPPEMYVYSTNSDHLPMTSSFRKELDARIFLNEIPPFVEDGEPWFIINETPLLVKIQQT
YKFRNKPAHTSWNMGAILEGKRSGFAPCGPKEQLSMEMILKAEEGNHEWICRILKDNFASADVADAKGYTVLAAA
ATHCHNDIVNLLDDCGADVKNCSDEGLTALSMCFLHYPASFKPNVAERTIPEPQEPPKFPVVPILSSSFMDTN
LESLYYEVNVPSSQGSYELRPPAPLLLPRVSGSHEGGHFQDTGQCGGSMHRSSSLKGDSPILVKGSLGHVESGLE
DVLGNTDRGSLCSAETKFESNVCVCDFSIELSQAMLESAQSHSLLKMASPSPCTSSFDKGTMRMALSMIERRK
RWRTIKLLLRGADPNLCCVPMQVFLAVKAGDVGVRLLLEHGARTDICFPQLSTLPLHIAAALPGEEGVQI
VELLLHAITDVAKASDEDDTYKPGKLDLLPSSILKLSNEPGPPQAYYSTDTALPEEGGRTALHMACEREDDNKCA
RDIVRLLLSHGPNLLWSGHSPLSLSIASGNELVVKELLTQADPNLPLTKGLGSALCVACDLTYEHQRNMDSK
LALIDRLISHGADILKPVMLRQGEKEAVGTAVDYGFRFFQDRRIARCPFHTLMPAERETFLARKRLLEYMGLQL
RQAVFAKESQWDPTWLYLCKRAELIPSHRMKKKGP SLPRGLDVKEQGQIPFFKFCYQCGRSIGVRLLPCPRCYGI
LTCSKYCKTKAWTEFHKKDCGDLVAIVTQLEQVSRREEFQ

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FIGURE 65

GGAGCCCATGATTTCTGGAAGAGCCCTAGAGCTTTGCTTTTTCTCTCCTGCAGCACTTAACCGAAACCAGTTTT
GCAATCAATTCTGTTCAAAGGCSACCTACTCTTCTATCCGTCCTTTCTCCAGCCAGACACTCACAGCCCCCT
GCCAGACCAGGGGACCTCGGAGAGGCAAGGACAGAGGTTGAGGATCTTCTCTCCCTCGGGACCCAAGGSCACAA
AGGAGAGCTCCGTGGAGAGAAGAAAATCATTGACTCCTGGGGACACAGATTGCTGCCACAGAGGCTGATGGAC
AACCAGGCGGAGAGAGAAAGTGAGGCTGGTGTGGTTTGCAAAGGGATGAGGATGACGCTCCTCTGTGTGAAGAC
GTGGAGCTACAAGACGGAGATCTGTCCCCGAAGAAAAAATATTTTTGAGAGAATTCCCAGATTGAAAGAAGAT
CTGAAAGGGAACATTGACAAGCTCCGTGCCCTCGCAGACGATATTGACAAAACCCACAAGAAATTCACCAAGGCT
AACATGGTGGCCACCTCTACTGCTGTCATCTCTGGAGTGATGAGCCTCCTGGGTTTAGCCCTTGCCCCAGCAACA
GGAGGAGGAAGCCTGCTGCTCTCCACCGCTGGTCAAGGTTTGGCAACAGCAGCTGGGGTACCAGCATCGTGAGT
GGTACGTTGGAACGCTCCAAAAATAAGAAGCCCAAGCACGGGCGGAAGACATACTGCCACCTACGACCAAGAG
GACAGGGAGGATGAGGAAGAGAAGGCAGACTATGTACAGCTGCTGGAAAGATTATCTATAATCTTAGAAACACC
TTGAAGTATGCCAAGAAAAACGTCCGTGCATTTTGAAACTCAGAGCCAACCCACGCTTGCCCAATGCTACCAAG
CGTCTTCTGACCACTGGCCAAGTCTCCTCCCGAGCCGCTGCAGGTGCAAAAGGCCTTTGCGGGAACAACACTG
GCGATGACCAAAATGCTCGCGTGTGGGAGGTGTGATGTCCGCTTCTCCTTGCGTATGACTTGCCACTCTC
TCAAAGGAATGGAAGCACCTGAAGGAAGGAGCAAGGACAAAGTTTGCGGAAGAGTTGAGAGCCAAGGCCTTGAG
CTGGAGAGGAAACTCACAGAACTACCCAGCTCTACAAGAGCTTGACAGCAGAAAGTGAGGTCAAGGGCCAGAGGG
GTGGGGAAGGATTTAACTGGGACCTGCGAAACCGAGGCTTACTGGAAGGAGTTAAGGGAGCATGTGTGGATGTGG
CTGTGGCTGTGTGTGTGTCTGT
ATGGCCTTGAGAGGTCCAAATAATATCAAGTACATCTTGAGAGATGAGGGTGCCTGTCTGGACAGACCTCGGCATG
CCTTCTGTTTCTCCTTCAATGCTCCTTAAGGCCATGTGCTGGGAAAAGGCTCTCCCTGTTTGTGTGTGTGT
GTTTGT
AAAAGAAGAATAACAGTCATGTATCTTGTGTGACAGGGACGCATTCTGATAAATGTGTGATTAGGCAATTGC
ATTGTAGTGTGATTATCACAGATTGTACTTATACAAAACCTTAGATGGCATAGCCTACTGCATACCTAGGCTATAT
GGGAGAGCCTATTGCTCCAGGCTACGCACCTGTACAGCATGTGACTACTGAATACTATAGGCAATTGCAGCACA
ATGGGAAATATTTGTGTATCTAAACATATGTAAACAGAGAAAAAGGAAAGTAAAAATATGGCATAAAGATAAGA
ATTGGCTCTCCTGTACAGGGCACTTACTACGAATGGAGCTTGCAGGGCTGAGAGTTGCTCCAGATGAGTCAGTGA
GTGGTGAATGAATGTGAAGGCCTAGGGCATTACTGTATACTACTGTAGGCTTTATAAACACAGCACACTTAGGGT
ACACAAAATGCATATTAACATTTTCTTCTTCACTATATTAGGCAATAGGAATTTTCAAGTCCACTATAAAT
CTTATCAAACCATGGTTGTATATGCAGTTGACCGAAACATTGTTATTGGACACATAACTATAGTTGAAAGAATAA
GCAAAAAGTCTATCTAGGTGTGCTGTCTTGAGCAACTTTAATTATTCTCCTGTCTGCAATATGAGTTAATCTT
CTCTGATCGATGTAGATTCCAGGAAGGGGTGTCCAGGACAATTACCTTCTTCTGGAGAACTTCCCTTAATCAA
ATAAGAGAACTTCAAAGAAAATCCCTCCCTGTGCTTTGGAAGGGAAGGGAGGTGGGCAGCAGTGGGTCAGAGATA
GACCTTTGTTCTTATTTCTGAGGCCCTTCACTCTCCTTTATTCAAAGCACTCAGCATGCCAAAGCACCCCTATT
TTAGGGTATCTTTTCTGAGCCCTAAACACTGTGTGGGGATGTCAACTGTGACAGGAAAATATCTTGGGGCCCC
AGAATCACTAAGGAAAACCTCAAGCTTAGGGAACTTCTTAGGGCAAACCCACCTCCCACTCTATTCAAAGTTATC
TCTCTGCTCACTGAGATAGATACATATCTGATTGCCTCCTTGGAAAGGCTAATCAGAACTCAAAGAATGCAA
CTGTTTGTGTCTCACTATCTGTGACCTGGAAGCTCCCTCCCACTGAACCAATGTTCTTCTTACATATATTGAT
TAATGTCTTATGTCTCCCTAAAATGTATAAAACCAAGGTATGCCCCAACCATCTTGGCCACATGTCATCAGGACT
TCCTGAGTCTGTGTACAGTGTGTCTCAACCTTGGCAAAATAAATTTCTAAATTAAGTACAGACAAAAA
AAAAA

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FIGURE 66

MDNQAERESEAGVGLQRDEDDAPLCEDELQDGDLSPEEKIFLREFPRLKEDLKGNIDKLRLALADDIDKTHKKFT
KANMVATSTAVISGVMSLLGLALAPATGGGSLLS TAGQGLATAAGVTSIVSGTLERSKNKEAQAARAEDILPTYD
QEDREDEEEKADYVTAAGKIIYNLRNTLKYAKKNVRAFWKLRANPRLANATKRLTTGQVSSRSRVQVQKAFAGT
TLAMTKNARVLGGVMSAFSLGYDLATLSKEWKHLKEGARTKFAEELRAKALELERKLTCLTQLYKSLQQKVR SRA
RGVGKDLTGTCETEAYWKELREHVMMWLWLCVCLCVCVYVQFT

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FIGURE 67A

TGCAGAGAACAGAGAAAGGACATCTGCGAGGAAAGTTCCCTGATGGCTGTCAACAAAGTGCCACGTCTCTATGGC
TGTGTACGCTGAGCACACGATTTTATCGCGCCTATCATATCTTGGTGCATAAACGCACCTCACCTCGGTCAACCC
TTGCTCCGTCTTATGAGACAGGCTTTATTATCCGCATTTTATATGAGGGGAATCTGACGGTGGAGAGAGAATTAT
CTTGCTCAAGGCGACACAGCAGAGCCACAGGTGGCAGAATCCACCCGAGCCCGCTTCGACCCGCGGGGTGGAA
ACCACGGGCGCCCGCCCGGCTGCGCTTCCAGAGCTGAACTGAGAAGCGAGTCTCTCCGCCCTGCGGCCACCGCC
CAGCCCCGACCCCGCCCGGCGCCGATCTCACTCGCCGCCAGCTCCCCGCGCCACCCCGGAGTTGGTGGCGCA
GAGGCGGGAGGCGGAGGCGGGAGGGCGGGCGCTGGCACCGGGAACGCCCAGCGCCGGCAGAGAGCGCGGAGAGC
GCGACACGTGCGGCCAGAGCACCGGGGCCACCCGGTCCCCGAGGCCCGGGACCGCGCCCGCTGGCAGGCGACA
CGTGGAGAATACGGAGTTCTATACCAGAGTTGATTGTTGATGGCACATACTTTTAGAGGATGCTCATTGGCATT
TATGTTTATAATCACGTGGCTGTTGATTAAAGCAAAAATAGATGCGTGCAAGAGAGGCGATGTGACTGTGAAGCC
TTCCCATGTAATTTTACTTGGATCCACTGTCAATATTACATGCTCTTTGAAGCCAGACAAGGCTGCTTTCACTA
TTCCAGACGTAACAAGTTAATCCTGTACAAGTTTGACAGAAGAATCAATTTTACCATGGCCACTCCCTCAATTC
TCAAGTCACAGGTCTTCCCTTGGTACAACCTTGTGTTGCTGCAAACTGGCCTGTATCAATAGTGATGAAATTCA
AATATGTGGAGCAGAGATCTTCGTTGGTGTGCTCCAGAACAGCCTCAAAATTTATCCTGCATACAGAAGGGAGA
ACAGGGGACTGTGGCCTGCACCTGGGAAAGAGGACGAGACACCCACTTATACACTGAGTATACTCTACAGCTAAG
TGGACCAAAAAATTTAACCTGGCAGAAGCAATGTAAAGACATTTATTGTGACTATTTGGACTTTGGAATCAACCT
CACCCTGAATCACCTGAATCCAATTTACAGCCAAGGTTACTGCTGTCAATAGTCTTGGAAGCTCCTCTTCACT
TCCATCCACATTCACATTCTTGGACATAGTGAGGCCTCTTCCCTCCGTGGGACATTAGAATCAAATTTCAAAGGC
TTCCGTGAGCAGATGTACCCTTTATTGGAGAGATGAGGGACTGGTACTGCTTAATCGACTCAGATATCGGCCAG
TAACAGCAGGCTCTGGAATATGGTTAATGTTACAAAGGCCAAAGGAAGACATGATTTGCTGGATCTGAAACCATT
TACAGAATATGAATTTAGATTTCTCTAAGCTACATCTTTATAAGGGAAGTTGGAGTGATTGGAGTGAATCATT
GAGAGCACAACACCAGAAGAAGAGCCTACTGGGATGTTAGATGTCTGGTACATGAAACGGCACATTGACTACAG
TAGACAACAGATTTCTCTTTTCTGGAAGAATCTGAGTGTCTCAGAGGCAAGAGGAAAAATTTCTCACTATCAGGT
GACCTTGCAGGAGCTGACAGGAGGGAAGCCATGACACAGAACATCACAGGACACACCTCCTGGACCACAGTCAT
TCCTAGAACCAGAAATTGGGCTGTGGCTGTGCTGCGAGCAAAATCAAAGGCAGTTCTCTGCCCCTCGTATTAA
CATAATGAACCTGTGTGAGGCAGGGTTGCTGGCTCCTCGCCAGGTCTCTGCAAACTCAGAGGGCATGGACAACAT
TCTGGTGACTTGGCAGCCTCCCAGGAAAGATCCCTCTGCTGTTAGGAGTACGTGGTGGAAATGGAGAGAGCTCCA
TCCAGGGGGTGACACACAGGTCCCTCTAACTGGCTACGGAGTCGACCCTACAATGTGTCTGCTCTGATTTTACA
GAACATAAAATCCTACATCTGTTATGAAATCCGTGTGTATGCACTCTCAGGGGATCAAGGAGGATGCAGCTCCAT
CCTGGGTAACCTCTAAGCACAAAGCACCCTGAGTGGCCCCCACATTAATGCCATCACAGAGGAAAAGGGGAGCAT
TTTAATTTTCATGGAACAGCATTCCAGTCCAGGAGCAAATGGGCTGCCTCCTCCATTATAGGATATACTGGAAGGA
ACGGGACTCCAACTCCCAGCCTCAGCTCTGTGAAATTCCTTACAGAGTCTCCAAAATTCACATCCAATAAACAG
CCTGCAGCCCCGAGTGACATATGTCCTGTGGATGACAGCTCTGACAGCTGCTGGTGAAAGTTCCACGGAAATGA
GAGGGAATTTTGTCTGCAAGGTAAAGCCAATTGGATGGCGTTTGTGGCACCAAGCATTGCAATGCTATCATCAT
GGTGGGCATTTTCTCAACGCATTACTTCCAGCAAAAGGTGTTTGTCTCTTAGCAGCCCTCAGACCTCAGTGGTG
TAGCAGAGAAATTCAGATCCAGCAAATAGCACTTGCGCTAAGAAATATCCATTGCAGAGGAGAAGACACAGCT
GCCCTTGGACAGGCTCCTGATAGACTGGCCACGCCTGAAGATCCTGAACCGCTGGTCATCAGTGAAGTCCTTCA
TCAAGTGACCCCAAGTTTTCAGACATCCCCCTGCTCCAATGGCCACAAAGGGAAAAAGGAATCCAAGGTCAATCA
GGCCTCTGAGAAAGACATGATGCACAGTGCCCTCAAGCCCACCACCTCCAAGAGCTCTCCAAGCTGAGAGCAGACA
ACTGGTGGATCTGTACAAGGTGCTGGAGAGCAGGGGCTCCGACCCAAAGCCAGAAAACCCAGCCTGTCCCTGGAC
GGTGTCTCCAGCAGGTGACCTTCCACCCATGATGGCTACTTACCCTCCAACATAGATGACCTCCCTTCACATGA
GGCACCCTCTCGCTGACTCTCTGGAAGAACTGGAGCCTCAGCACATCTCCCTTTCTGTTTTCCCTCAAGTTCTCT
TCACCCACTCACCTTCTCCTGTGGTGATAAGCTGACTCTGGATCAGTTAAAGATGAGGTGTGACTCCCTCATGCT
CTGAGTGGTGAGGCTTCAAGCCTTAAAGTCAGTGTGCCCTCAACCAGCACAGCCTGCCCAATCCCCAGCCCC
TGCTCCAGCAGCTGTCTCTCTGGGTGCCACCATCGGTCTGGCTGCAGCTAGAGGACAGGCAAGCCAGCTCTGGG
GGAGTCTTAGGAATGGGAGTTGGTCTTCACTCAGATGCCTCATCTTGCCTTTCCAGGGCCTTAAATTTACATC
CTTCACTGTGTGGACCTAGAGACTCCAATTTGAATTCCTAGTAACTTTCTTGGTATGTGGCCAGAAAGGGAAAT
GAGGAGGAGAGTAGAAACCACAGCTCTTAGTAGTAATGGCATAACAGTCTAGAGGACCATTGATGCAATGACTATT

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FIGURE 67B

TCTAAAGCACCTGCTACACAGCAGGCTGTACACAGCAGATCAGTACTGTTCAACAGAACTTCCTGAGATGATGGA
AATGTTCTACCTCTGCACTCACTGTCCAGTACATTAGACACTAGGCACATTGGCTGTTAATCACTTGGAATGTGT
TTAGCTTGACTGAGGAATTAAATTTTGATTGTAAATTTAAATCGCCACACATGGCTAGTGGCTACTGTATTGGAG
TGCACAGCTCTAGATGGCTCCTAGATTATTGAGAGCCTCCAAAACAAATCAACCTAGTTCTATAGATGAAGACAT
AAAAGACACTGGTAAACACCAATGTAAAAGGGCCCCCAAGGTGGTCATGACTGGTCTCATTTCAGAAAGTCTAAG
AATGTACCTTTTTCTGGCCGGGCGTGGTAGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGA

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FIGURE 68

MAHTFRGCSLAFMFIITWLLIKAKIDACKRGDVTVKPSHVILLGSTVNITCSLKPRQGC FHYSRRNKLILYKFDR
RINFHHGHSLSNSQVTGLPLGTTLFVCKLACINSDEIQICGAEIFVGVAPEQPQNLSCIQKGEQGT VACTW ERGRD
THLYTEYTLQLSGPKNLTWQKQCKDIYCDYLD FGINLTPESPESNFTAKVTAVNSLGSSSSSLPSTF'TFLDIVRPL
PPWDIRIKFQKASVSRCTLYWRDEGLVLLNRLRYRPSNSRLWNMVNVT KAKGRHDLLDLKPFTEYEFQISSKLHL
YKGSWSDWSESLRAQTPEEEPTGMLDVWYMKRHIDYSRQQISLFWKNLSVSEARGKILHYQVTLQELTG GKAMTQ
NITGHTSWTTVIPRTGNWAVAVSAANSKGSSLPTRINIMNLCEAGLLAPRQVSANSEGMDNILVTWQPPRKDPSA
VQEYVVEWRELHPGGDTQVPLNWLRSRPYNVSALISENIKSYICYEIRVYALSGDQGGCSSILGNSKHKAPLSGP
HINAITEEKGSILISWNSIPVQEQMGCLLHYRIYWKERDSNSQPQLCEIPYRVSONSHPINSLQPRVTYVLWMTA
LTAAGESSSHGNEREFCLQGGKANWMAFVAPSICIAIIMVGIFSTHYFQQKFVLLAALRPQWCSREIPDPANSTCA
KKYP IAEKQTQLPLDRLLIDWPTPEDPEPLVISEVLHQVTPVFRHPPCSNWPQREKGIQGHQASEKDMMHSASSP
PPPRALQAESRQLVDLYKVLESRGSDPKPENPACPWTVLPAGDLPTHGYLPSNIDDLPSHEAPLADSLEELEPQ
HISLSVFPSSSLHPLTFSCGDKLTLDQLKMRCDSLML

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FIGURE 69

AAGACTGTAGGAGCATCTGGTGGGAGGTGGTGGAGGGAGAACTGTGGGTTTGGGAAGCTGCGCCCTCCCCCAGCC
ATGCGTTGGAACAGGAACAGTTACATGGAGAACAACCTTACCTTGTCGACACCCTCAGATCTTTGTCCCAGGCC
AAGAATCTTTTAATGACAGGATCCTCTGTGATTAGAGAGCAGATGTCAGTGTGAGAAGCAGGACAGGGTTTCCGT
GGGAGCAGCAGGGCAGGGAGGAGAAGTGTGCCTCCCGGGGGGAAGTCTCAGGATTGTGGCCGCGGGTGAGGTGGA
TGGGAGAGGGGAGAATGACTTTCACTGGGCAAGGGAGAGAGGCTCCTGCTCTGAGACTCCCCTGAGAAGAGGCCG
AAGGAGGCCCTGGGTGTGAGAATCTACAGGATGTAGAGCTGGGAATCAGCCAGGACCCCCCTCCAGCAGACACGGA
GGGACCACTGCAGAGTCATAAAGGAATTCCCATCATTTCTCATGAGACAGTCACATCAGGGTGTGACCATGGCC
TTGGTATCCCCCACTATGGATGGAGACACTTAGGTTTAGAAAAGTCAGTAAGAGACATTAAGTTTCAGAGGGCAC
AGCTGAAACCACTTCTTTGTTTATTGATTTTGTCTTTATTTGATTTTATTTT

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FIGURE 70

KTVGASGGRWWRENCGF GSCALPPAMRWNRNSYMNNTLSDTLRSL SQAKNLLMTGSSVIREQMSV

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FIGURE 71

ATGGCAGAGATTGGTGAGGATTTGGATAAATCTGATGTGTCCTCATTAAATTTTCCTCATGAAGGATTACATGGGC
CGAGGCAAGATAAGCAAGGAGAAGAGTTTCTTGGACCTTGTGGTTGAGTTGGAGAACTAAATCTGGTTGCCCCA
GATCAACTGGATTTATTAGAAAAATGCCTAAAGAACATCCACAGAATAGACCTGAAGACAAAAATCCAGAAGTAC
AAGCAGTCTGTTCAAGGAGCAGGGACAAGTTACAGGAATGTTCTCCAAGCAGCAATCCAAAAGAGTCTCAAGGAT
CCTTCAAATAACTTCAGGGAAGAACCAGTGAAGAAATCCATTGAGGAATCAGAAGCTTTTTTGCCTCAGAGCATA
CCTGAAGAGAGATACAAGATGAAGAGCAAGCCCCTAGGAATCTGCCTGATAATCGATTGCATTGGCAATGAGACA
GAGCTTCTTCGAGACACCTTCACTTCCCTGGGCTATGAAGTCCAGAAATTCTTGATCTCAGTATGCATGGTATA
TCCCAGATTCTTGGCCAATTTGCCTGTATGCCCCGAGCACCAGAGACTACGACAGCTTTGTGTGTGCTCCTGGTGAGC
CGAGGAGGCTCCAGAGTGTGTATGGTGTGGATCAGACTCACTCAGGGCTCCCCCTGCATCACATCAGGAGGATG
TTCAIGGGAGATTTCATGCCCTTATCTAGCAGGGAAGCCAAAGATGTTTTTTATTTCAGAACTATGTGGTGTGAGAC
GGCCAGCTGGAGGACAGCAGCCTCTTGGAGGTGGATGGGCCAGCGATGAAGAATGTGGAATTCAAGGCTCAGAAG
CGAGGGCTGTGCACAGTTCACCGAGAAGCTGACTTCTTCTGGAGCCTGTGTACTGCGGACATGTCCCTGCTGGAG
CAGTCTCACAGCTCACCGTCCCTGTACCTGCAGTGCCTCTCCCAGAACTGAGACAAGAAAGGGGGACAATTCCC
GGAAGTGAATTACAGAGTCAAAGGACATGCATTTTCAAGCCTCGGATGCATCTTACTAGATGTCCTATAG

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FIGURE 72

MAEIGEDLDKSDVSSLIFLMKDYMGRGKISKEKSF~~LDLV~~VELEKLN~~LVAPDQ~~LDLLEKCLKNIHRIDLKTKIQKY
KQSVQGAGTSYRNVLQAAIQSLKDPSNNFRE~~EPVK~~KSIQ~~SEAF~~LPQSIPEERYKMKSKPLGICLIIDCIGNET
ELLRDTFTSLGYEVQKFLHLSMHGISQILGQFACMPEHRDYDSFVCVLVSRGGSQSVYGVDQTHSGLPLHHIRM
FMGDSCPYLAGKPKMFFIQNYVSDGQLEDSSLLEV~~DGPAMKNVEFKAQ~~KRGLCTVHREADFFWSLCTADMSLLE
QSHSSPSLYLQCLSQKLRQERG~~TIPGSGITESKDMHFSS~~LGILLDVL

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FIGURE 73

TGAAGATCAGCTATTAGAAGAGAAAGATCAGTTAAGTCCTTTGGACCTGATCAGCTTGATACAAGAACTACTGAT
TTCAACTTCTTTGGCTTAATTCTCTCGGAAACGATGAAATATACAAGTTATATCTTGGCTTTTCAGCTCTGCATC
GTTTGGGTTCTCTTGGCTGTTACTGCCAGGACCCATATGTAAAGAAGCAGAAAACCTTAAGAAATATTTTAAT
GCAGGTCATTCAGATGTAGCGGATAATGGAACCTCTTTTCTTAGGCATTTTGAAGAATTGGAAGAGGAGAGTGAC
AGAAAAATAATGCAGAGCCAAATTGTCTCCTTTTACTTCAAACCTTTTAAAACTTTAAAGATGACCAGAGCATC
CAAAAGAGTGTGGAGACCATCAAGGAAGACATGAATGTCAAGTTTTTCAATAGCAACAAAAAGAAACGAGATGAC
TTCGAAAAGCTGACTAATTATTCGGTAACGACTTGAATGTCCAACGCAAAGCAATACATGAACATCCAAGTG
ATGGCTGAACGTGTCGCCAGCAGCTAAAACAGGGAAGCGAAAAAGGAGTCAGATGCTGTTTCAAGGTGGAAGAGCA
TCCCAGTAAATGGTTGTCTGCTGCAATATTTGAATTTTAAATCTAAATCTATTTATTAATATTTAACATTATTT
ATATGGGGAATATATTTTTAGACTCATCAATCAATAAGTATTTATAATAGCAACTTTTGTGTAATGAAATGAA
TATCTATTAATATATGTATTATTTATAATTCCTATATCCTGTGACTGTCTCACTTAATCCTTTGTTTTCTGACTA
ATTAGGCAAGGCTATGTGATTACAAGGCTTTATCTCAGGGGCCAACTAGGCAGCCAACTAAGCAAGATCCCATG
GGTTGTGTGTTTATTTCACTTGATGATACAATGAACACTTATAAGTGAAGTGATACTATCCAGTTACTGCCGGTT
TGAAAATATGCCTGCAATCTGAGCCAGTGCTTTAATGGCATGTCAGACAGAACTTGAATGTGTCAGGTGACCCTG
ATGAAAACATAGCATCTCAGGAGATTTTCATGCCTGGTGCTTCCAAATATTGTTGACAACTGTGACTGTACCCAAA
TGGAAAGTAACTCATTTGTTAAATTATCAATATCTAATATATATGAATAAAGTGTAAGTTCACAACT

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FIGURE 74

MKYTSYILAFQLCIVLGSLGCYCQDPYVKEAENLKKYFNAGHSDVADNGTLFLGILKNWKEESDRKIMQSQIVSF
YFKLFKNFKDDQSIQKSVETIKEDMNVKFFNSNKKRDDFEKLTNYSVTDLNVQRKAIHELIQVMAELSPAAGTG
KKKRSQMLFQGRRASQ

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FIGURE 75A

GAGTTGTGCTGGAGTGATGTTTAAGCCAATGTGAGGGCAAGGCAACAGTCCCTGGCCGTCTCCAGCACCTTTG
TAATGCATATGAGCTCGGGAGACCAGTACTTAAAGTTGGAGGCCCGGAGCCAGGAGCTGGCGGAGGGCGTTTCG
TCCTGGGAGCTGCACCTGCTCCGTGCGGTGCGCGGCTTACCGGACCGCAGGCTCCCGGGGAGGGCCGGGGCCA
GAGCTCGCGTGTGCGCGGGACATGCGCTGCGTGCCTCTAACCTCGGGCTGTGCTCTTTTTCCAGGTGGCCCGCC
GGTTTCTGAGCCTTCTGCCCTGCGGGGACACGGTCTGCACCTGCCCGCGGCCACGGACCATGACCATGACCCTC
CACACAAAGCATCTGGGATGGCCCTACTGCATCAGATCCAAGGGAACGAGCTGGAGCCCCGAACCGTCCGCAG
CTCAAGATCCCCCTGGAGCGGCCCTGGGCGAGGTGTACCTGGACAGCAGCAAGCCCGCGGTGTACAACACCCC
GAGGGCGCGCCCTACGAGTTCAACGCCGCGGCCCGCCGAACCGCAGGTCTACGGTCAGACCGGCTCCCTAC
GGCCCCGGGTCTGAGGCTGCGGCGTTCGGCTCCAACGGCCTGGGGGGTTTCCCCCACTCAACAGCGTGTCTCCG
AGCCCGCTGATGCTACTGCACCCGCGCCAGCTGTGCGCTTTCCTGCAGCCCCACGGCCAGCAGGTGCCCTAC
TACCTGGAGAACGAGCCCAGCGGCTACACGGTGCAGGAGGCCCGCCCGGCATTCTACAGGCCAAATTCAGAT
AATCGACGCCAGGGTGGCAGAGAAAGATTGGCCAGTACCAATGACAAGGGAAGTATGGCTATGGAATCTGCCAAG
GAGACTCGCTACTGTGCAGTGTGAATGACTATGCTTCAGGCTACCATATGGAGTCTGGTCTGTGAGGGCTGC
AAGGCTTCTTCAAGAGAAGTATTCAAGGACATAACGACTATATGTGTCCAGCCACCAACAGTGCAACATTGAT
AAAAACAGGAGGAAGAGCTGCCAGGCTGCCGGCTCCGCAATGCTACGAAGTGGGAATGATGAAAGGTGGGATA
CGAAAAGACCGAAGAGGAGGGAGAATGTTGAAACACAAGCGCCAGAGAGATGATGGGGAGGGCAGGGGTGAAGTG
GGGTCTGCTGGAGACATGAGAGCTGCCAACCTTTGGCCAAGCCCGCTCATGATCAAACGCTCTAAGAAGAACAGC
CTGGCCTTGTCCCTGACGGCCGACCAGATGGTCAGTGCCTTGTGGATGCTGAGCCCCCATACTCTATTCCGAG
TATGATCCTACCAGACCCCTTCAGTGAAGCTTCGATGATGGGCTTACTGACCAACCTGGCAGACAGGGAGCTGGTT
CACATGATCAACTGGGCGAAGAGGGTGCCAGGCTTTGTGGATTGACCCCTCCATGATCAGGTCCACCTTCTAGAA
TGTGCCTGGCTAGAGATCCTGATGATTGGTCTCGTCTGGCGCTCCATGGAGCACCCAGTGAAGCTACTGTTTGCT
CCTAACTTGCTCTTGACAGGAACAGGGAAATGTGTAGAGGGCATGGTGGAGATCTTCGACATGCTGCTGGCT
ACATCATCTCGGTTCCGCATGATGAATCTGCAGGGAGAGGAGTTTGTGTGCTCAAATCTATTATTTTGCTTAAT
TCTGGAGTGACACATTTCTGTCCAGCACCTGAAGTCTCTGGAAGAGAAGGACCATATCCACCGAGTCTTGAC
AAGATCACAGACACTTTGATCCACCTGATGGCCAAGGCAGGCCTGACCCTGCAGCAGCAGCACCAGCGGCTGGCC
CAGCTCCTCCTCATCTCTCCACATCAGGCACATGAGTAACAAAGGCATGGAGCATCTGTACAGCATGAAGTGC
AAGAACGTGGTGCCCTCTATGACCTGCTGTGGAGATGCTGGACGCCACCGCCTACATGCGCCCACTAGCCGT
GGAGGGGCATCCGTGGAGGAGACGGACCAAGCCACTTGCCACTGCGGGCTCTACTTCATCGCATTCTTGCAA
AAGTATTACATCACGGGGGAGGCAGAGGGTTTCCCTGCCACAGTCTGAGAGCTCCCTGGCTCCCACAGGTTTCAG
ATAATCCCTGCTGCATTTTACCCTCATATGCACCACTTTAGCCAAATCTGTCTCCTGCATACACTCCGGCATG
CATCCAACACCAATGGCTTTCTAGATGAGTGGCCATTCAATTTGCTTGCTCAGTTCTTAGTGGCACATCTTCTGTC
TTCTGTTGGGAACAGCCAAAGGGATTCCAAGGCTAAATCTTTGTAACAGCTCTCTTTCCCCCTTGCTATGTTACT
AAGCGTGAGGATTCCCGTAGCTCTTACAGCTGAACCTCAGTCTATGGGTTGGGGCTCAGATAACTCTGTGCATTT
AAGCTACTTGTAGAGACCCAGGCCTGGAGAGTAGACATTTTGCCTCTGATAAGCACTTTTTAAATGGCTCTAAGA
ATAAGCCACAGCAAAGAATTTAAAGTGGCTCCTTTAATTGGTGACTTGGAGAAAGCTAGGTCAAGGGTTTATTAT
AGCACCTCTTGTATTCCTATGGCAATGCATCCTTTTATGAAAGTGGTACACCTTAAAGCTTTTATATGACTGTA
GCAGAGTATCTGGTGATTGTCAATTCATTTCCCTTATAGGAATACAAGGGGCCACACAGGGAAGGCAGATCCCC
TAGTTGGCCAAGACTTATTTAACTTGATACACTGCAGATTCAGAGTGTCTGAAGCTCTGCCTCTGGCTTTCCG
GTCATGGGTTCCAGTTAATTCATGCCTCCCATGGACCTATGGAGAGCAACAAGTTGATCTTAGTTAAGTCTCCCT
ATATGAGGGATAAGTTCCCTGATTTTGTGTTTTATTTTGTGTTACAAAAGAAAGCCCTCCCTCCCTGAACTTGCA
GTAAGGTGAGCTTCAGGACCTGTTCCAGTGGGCACTGTAAGTGGATCTTCCCGCGTGTGTGTGCCTTACACAGG
GGTGAAGTGTTCAGTGTGGTGATGATGAGGGTAAATGGTAGTTGAAAGGAGCAGGGGCCCTGGTGTGTCAT
TTAGCCCTGGGGCATGGAGCTGAACAGTACTTGTGCAGGATTGTTGTGGCTACTAGAGAACAAAGAGGGAAAGTAG
GGCAGAAACTGGATACAGTTCTGAGCACAGCCAGACTTGCTCAGGTGGCCCTGCACAGGCTGCAGCTACCTAGGA
ACATTCTTGCAGACCCCGCATTGCCCTTTGGGGGTGCCCTGGGATCCCTGGGGTAGTCCAGCTCTTATTCAATTC
CCAGCGTGCCCTGGTTGGAAGAAGCAGCTGTCAAGTTGTAGACAGCTGTGTTCTACAATTGGCCAGCACCCCT
GGGGCACGGGAGAAGGGTGGGACCGTTGCTGTCACTACTCAGGCTGACTGGGGCCTGGTCAGATTACGTATGCC
CTTGGTGGTTTAGAGATAATCCAAATCAGGGTTTGGTTTGGGGAAGAAATCCTCCCCCTTCTCCCCCGCCCC

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FIGURE 75B

GTTCCCTACCGCCTCCACTCCTGCCAGCTCATTTCCTTCAATTTCTTTGACCTATAGGCTAAAAAGAAAGGCT
CATTCCAGCCACAGGGCAGCCTTCCCTGGGCCTTTGCTTCTCTAGCACAAATTATGGGTTACTTCCTTTTTCTTAA
CAAAAAAGAAATGTTTGATTTCTCTGGGTGACCTTATTGTCTGTAATTGAAACCCTATTGAGAGGTGATGTCTGT
GTTAGCCAATGACCCAGGTAGCTGCTCGGGCTTCTCTTGGTATGTCTTGTGTTGGAAAAGTGGATTTTCATTCATTT
CTGATTGTCCAGTTAAGTGATCACCAAAGGACTGAGAATCTGGGAGGGCAAAAAAAAAAAAAAAGTTTTATGT
GCACTTAAATTTGGGGACAATTTTATGTATCTGTGTTAAGGATATGCTTAAGAACATAATTCTTTTGTGTCTGTT
TGTTTAAGAAGCACCTTAGTTTGTGTTAAGAAGCACCTTATATAGTATAATATATATTTTTTTTGAATTACATTGC
TTGTTTATCAGACAATTGAATGTAGTAATCTGTTCTGGATTAAATTTGACTGGGTAAACATGCAAAAACCAAGG
AAAAATATTTAGTTTTTTTTTTTTTTTTTTTGTATACTTTTCAAGCTACCTTGTCTATGTATACAGTCATTTATGCCT
AAAGCCTGGTGATTATTCATTTAAATGAAGATCACATTTTCATATCAACTTTTGTATCCACAGTAGACAAAATAGC
ACTAATCCAGATGCCTATTGTTGGATATTGAATGACAGACAATCTTATGTAGCAAAGATTATGCCTGAAAAGGAA
AATTATTCAGGGCAGCTAATTTTGTCTTTTACCAAATATCAGTAGTAATATTTTTTGGACAGTAGCTAATGGGTCA
GTGGGTTCTTTTAAATGTTTATACTTAGATTTTCTTTTAAAAAATTAATAAAACAAAAAAATTTCTAGGAC
TAGACGATGTAATACCAGCTAAAGCCAAACAATTATACAGTGGAAGGTTTACATTATTCATCCAATGTGTTTCT
ATTCATGTTAAGATACTACTACATTTGAAGTGGGCAGAGAACATCAGATGATTGAAATGTTTCGCCAGGGGTCTC
CAGCAACTTTGGAATCTCTTTGTATTTTTACTTGAAGTGCCACTAATGGACAGCAGATATTTTCTGGCTGATGT
TGGTATTGGGTGTAGGAACATGATTTAAAAAAAACCTCTTGCCCTGCTTTCCCCACTCTGAGGCAAGTTAA
ATGTAAAGATGTGATTTATCTGGGGGGCTCAGGTATGGTGGGGAAGTGGATTCAGGAATCTGGGGAATGGCAA
TATATTAAGAAGAGTATTGAAAGTATTTGGAGGAAAATGGTTAATCTGGGTGTGCACCAAGGTTTCAGTAGAGTC
CACTTCTGCCCTGGAGACCACAAATCAACTAGCTCCATTTACAGCCATTTCTAAAAATGGCAGCTTCAGTTCTAGA
GAAGAAAGAACAACATCAGCAGTAAAGTCCATGGAATAGCTAGTGGTCTGTGTTTCTTTTCGCCATTGCCTAGCT
TGCCGTAATGATTCTATAATGCCATCATGCAGCAATTATGAGAGGCTAGGTCATCCAAAGAGAAGACCCTATCAA
TGTAGGTTGCAAAATCTAACCCTAAGGAAGTGCAGTCTTTGATTTGATTCCCTAGTAACCTTGCAGATAGTT
TAACCAAGCCATAGCCCATGCCTTTTGAGGGCTGAACAAATAAGGGACTTACTGATAATTTACTTTTGATCACAT
TAAGGTGTTCTCACCTTGAATCTTATACACTGAAATGGCCATTGATTTAGGCCACTGGCTTAGAGTACTCCTTC
CCCTGCATGACACTGATTACAAATACTTTCTATTCTACTTTCCAATTATGAGATGGACTGTGGGTACTGGGAG
TGATCACTAACACCATAGTAATGTCTAATATTCACAGGCAGATCTGCTTGGGGAAGCTAGTTATGTGAAAGGCAA
ATAAAGTCATACAGTAGCTCAAAAGGCAACCATAATCTCTTTGGTGCAAGTCTTGGGAGCGTGATCTAGATTAC
ACTGCACCATTCCCAAGTTAATCCCCTGAAAACCTACTCTCAACTGGAGCAAAATGAACTTTGGTCCCAATATCC
ATCTTTTTCAGTAGCGTTAATTATGCTCTGTTTCCAACCTGCAATTTCTTTCCAATTGAATTAAAGTGTGGCCTCGT
TTTTAGTCATTTAAATTTGTTTTCTAAGTAATTGCTGCCTCTATTATGGCACTTCAATTTGCACTGTCTTTTGA
GATTCAGAAAAATTTCTATTCAATTTTTTTGTCATCCAATTGTGCTGAACTTTTAAAAATATGTAAATGCTGCCAT
GTTCCAAACCCATCGTCAGTGTGTGTGTTTAGAGCTGTGCACCCTAGAAACAACATACTTGTCCCATGAGCAGGT
GCCTGAGACACAGACCCCTTTGCATTCACAGAGAGGTCATTGGTTATAGAGACTTGAATTAATAAGTGACATTAT
GCCAGTTTCTGTTCTCTACAGGTGATAAACAATGCTTTTTGTGCACTACATACTCTTCAGTGTAGAGCTCTTGT
TTTATGGGAAAAGGCTCAAATGCCAAATTGTGTTTGTGTTGATGGATTAATATGCCCTTTTGCCGATGCATACTATTACT
GATGTGACTCGGTTTTGTGCGAGCTTTGCTTTGTTTAAATGAAACACACTTGTAACCTCTTTTGCACCTTTGAAAA
AGAATCCAGCGGGATGCTCGAGCACCTGTAAACAAATTTCTCAACCTATTGATGTTCAAATAAAGAATTAACT

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FIGURE 76

MTMTLHTKASGMALLHQIQGNELEPLNRPQLKIPLERPLGEVYLDSSKPAVYNYPEGAAYEFNAAAAANAQVYGO
TGLPYGPGSEAAAFGSNGLGGFPPLNSVSPSPLMLLHPPPQLSPFLQPHGQQVPYYLENEPSGYTVREAGPPAFY
RPNSDNRRQGGRERLASTNDKGSMAKESAKETRYCAVCNDYASGYHYGVWSCEGCKAFFKRSIQGHNDYMCPATN
QCTIDKNRRKSCQACRLRKCYEVGMMKGGIRKDRRGGRMLKHKRQRDDGEGRGEVGSAGDMRAANLWPSPLMIKR
SKKNSLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRVPGFVDLTLHDQ
VHLLCAWLEILMIGLVWRSMHEHPVKLLFAPNLLLDNRNQGKCEGMVEIFDMLLATSSRFRMMNLQGEFVCLKS
IILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITDTLIHLMAKAGLTLOQQHQRLAQLLILSHIRHMSNKGMEHL
YSMKCKNVVPLYDLLEMLDAHRLHAPTSRGASVEETDQSHLATAGSTSSHSLQKYYITGEAEGFPATV

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FIGURE 77

CGTGCTGTAGCTGGTTCTTACGTCCAACCTGGGGGCAGTCTGCCCAGATCGCCTGCCTGGCCTCGCCTCTGCCCCA
TCAGACACTTGGTGCTGGAATCTCCGAGGCTGGGAGGGACTGGGAGCGCCCCAGTTCGTGTCTCTCCACACAG
CCCCTTTATGTAACCTGACTAAGATCAAGCAGTTAGTAAATGGTAGAAAGAATATTTGAATCTACCTAGTGAGT
CTCTAGTGCATGCTTTTGTCCGGTATCCTGGAAAGCCTCCACAAAAAGCTAATCTTTGCCCCATTCAAACATG
CACCTGAAGAAGCTGTTTGTACAGGATTGGGTTTATTCTGTTATTAAGACAAAGGCATCATGGCCTTTGGGTGA
GAGGCCCGTATGTGTTTGGGATTGGCAATCAGCAATCCATCTCTGTCATCACCATTATTGAGAAAATAGATGGA
TTGGTTCCCTCTCTGCAGTCCTGTGGAGCAGTTGGACTGCTCTCTGCTCTCAGGATGATACTGTGAGAACAAT
TTAAATATGCTAAGCACATGTCAGGAAACAGTTTGTGGTCTTTGGACACTCGCTGTAGCCATTCCGTTCCATT
CAGGTGATTTTATTCATTTTCAATTTGTAGAATAAAAAATAATCCATTNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNTATACACCACTAAAGCCTCCCATTAACCCATAGAAGACTTAAAGAGCTAAAAGAGGCTATTN
NN
ACGTGTTTGATCTTCACCTCTCTTAATATTGGTGTTTGATCTTCTCACAAGTGTTTTGCTTGC

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FIGURE 78

RAVAGSYVQPGGSLPRSPAWPRLCPSDTWCWNLRGWEGLGAPQFCVLPTQPLLCNLTKIKQLVNGRKNI

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FIGURE 79

ACAGGGGTGAAGGCCCAGAGACCAGCAGAACGGCATCCCAGCCACGACGGCCACTTTGCTCTGTCTGCTGTCCGC
CACGGCCCTGCTCTGTTCCCTGGGACACCCCCGCCCCACCTCCTCAGGCTGCCTGATCTGCCCAGCTTTCCAGC
TTTCCTCTGGATTCCGGCCTCTGGTCATCCCTCCCCACCTCTCTCCAAGGCCCTCTCCTGGTCTCCCTTCTTCT
AGAACCCCTTCTCCACCTCCCTCTCTGCAGAACTTCTCCTTTACCCCCACCCCCACCACTGCCCCCTTTCTT
TTTCTGACCTCCTTTTGGAGGGCTCAGCGCTGCCAGACCATAGGAGAGATGTTGGGAGGCTCAGTTCTTGGGCTT
GCTGTTTCTGCAGCCGCTTTGGGTGGCTCCAGTGAAGCCTCTCCAGCCAGGGGCTGAGGTCCCCTGGTGTGGGC
CCAGGAGGGGGCTCCTGCCAGCTCCCTGCAGCCCCACAATCCCCCTCCAGGATCTCAGCCTTCTGCGAAGAGC
AGGGGTCACTTGGCAGCATCAGCCAGACAGTGGCCCGCCGCTGCCGCCCCCGGCCATCCCCCTGGCCCCCGGCC
TCACCCGGCGGGCGCCCTCCTCCTGGGGGGCCAGGCCCGCCGCTACACGGTGTGAGCGTGGGTCCCAGAGCCCT
GCGCAGCGGGAGGCTGCCCCCTGCAGCCCCGCGTCCAGCTGGATGAGCGCGGCCGCGCAGCGCGGGGACTTCTCGCT
ATGGCTGCGCCCAGCCCGCGCGCGGACGCCGGGAGTACCGCGCCGCGGTGCACCTCAGGGACCGCGCCCTCTC
CTGCCGCTCCGCTCTGCGCCTGGGCCAGGCCCTCGATGACTGCCAGCCCCCAGGATCTCTCAGAGCCTCCGACTG
GGTCATTTTGAAGTGTCTCTTACGCCGCCCTGACCGCCAGCCTCTGTGCATTGGTTCCGGAACCGGGGCCAGGG
CCGAGTCCCTGTCCGGGAGTCCCCCATCACCACTTAGCGGAAAGCTTCTCTTCTGCCCCAAGTCAGCCCCAT
GGACTCTGGGGCCTGGGGCTGCATCCTCACCTACAGAGATGGCTTCAACGTCTCCATCATGTATAACCTCACTGT
TCTGGGTCTGGAGCCCCAACTCCCTTGACAGTGTACGCTGGAGCAGGTTCAGGGTGGGGCTGCCCTGCCGCT
GCCTGTGTTGTGGGGACCGGTCTTTCTCACTGCCAAGTGGACTCCTCCTGGGGGAGGCCCTGACCTCCTGGT
GACTGGAGACAATGGCGACTTTACCCTTCGACTAGAGGATGTGAGCCAGGCCAGGCTGGGACCTACACCTGCCA
TATCCATCTGCAGGAACAGCAGCTCAATGCCACTGTACATTGGCAATCATCACAGTGACTCCCAAATCCTTTGG
GTCACCTGGATCCCTGGGGAAGCTGCTTTGTGAGGTGACTCCAGTATCTGGACAAGAAGCCTTTGTGTGGAGCTC
TCTGGACACCCCATCCCAGAGGAGTTTCTCAGGACCTTGGCTGGAGGCACAGGAGGCCAGCTCCTTTCCAGCC
TTGGCAATGCCAGCTGTACCAGGGGAGAGGCTTCTTGGAGCAGCAGTGTACTTCACAGAGCTGTCTAGCCCAGG
TCCCCAACGCTCTGGGAGAGCCCCAGGTGCCCTCCAGCAGGCCACCTCCTGCTGTTTCTCACCTTGGTGTCTT
TTCTCTGCTCCTTTTGGTGAAGTGGAGCCTTTGGCTTTCACCTTTGGAGAAGACAGTGGCGACCAAGACGATTTTC
TGCCTTAGAGCAAGGGATTACCCCTCCGAGGCTCAGAGCAAGATAGAGGAGCTGGAGCAAGAACCGGAGCCGGA
GCCGGAGCCGGAACCGGAGCCCCGAGCCCGAGCCGAGCCGAGCAGCTCTGACCTGGAGCTGAGGCAGCCAGCAG
ATCTCAGCAGCCAGTCCAAATAAACGTCCTGTCTAGCAGC

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FIGURE 80

MWEAQFLGLLFLQPLWVAPVKPLQPGAEPVWVAQEGAPALPCSPITPLQDLSLLRRAGVTWQHQPDSGPPAAA
PGHPLAPGPHPAAPSSWGPRPRRYTVLSVGPGLRSGRLPLQPRVQLDERGRQRGDFSLWLRPARRADAGEYRAA
VHLRDRALESCRLRLRLGQASMTASPPGSLRASDWVILNCSFSRPDRPASVHWFRNRGQGRVPVRESPPHHLAESF
LFLPQVSPMDSGPWGCILTYRDGFNVSIMYNLTVLGLEPPTPLTVYAGAGSRVGLPCRLPAGVGTRSFLLAKWTP
PGGGPDLLVTGDNGDFTLRLEDVSAQAQAGTYTCHIHLQEQQLNATVILAIITVTPKSFSGPSLGKLLCEVTPVS
GQERFVWSSLDTPSQRSFSGPWLEAQEAQLLSQPWQCQLYQGERLLGAAYFTTELSSPGAQRSGRAPGALPAGHL
LLFLTGLVLSLLLLVTGAFGFHLWRRQWRPRRFSALEQGIHPRQAQTQDRGAGARTGAGAGAGTGARARARAGAA
LTWS

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FIGURE 81

GGCGTCCGCGCGCTGCACAATGGCGGCTCTGAAGAGTTGGCTGTCGCGCAGCGTAACTTCATTCTTCAGGTACAG
ACAGTGTGTTGTGTGTTCCGTGTGTGGCTAACTTTAAGAAGCGGTGTTTCTCAGAATTGATAAGACCATGGCACAA
AACTGTGACGATTGGCTTTGGAGTAACCCTGTGTGCGGTTCCATTGCACAGAAATCAGAGCCTCATTCCCTTAG
TAGTGAAGCATTGATGAGGAGAGCAGTGTCTTTGGTAACAGATAGCACCTCTACCTTTCTCTCTCAGACCACATA
TGCGTTGATTGAAGCTATTACTGAATATACTAAGGCTGTTTATACCTTAACTTCTCTTTACCGACAATATACAAG
TTTACTTGGGAAAATGAATTGAGAGGAGGAAGATGAAGTGTGGCAGGTGATCATAGGAGCCAGAGCTGAGATGAC
TTCAAAACACCAAGAGTACTTGAAGCTGGAAACCACTTGGATGACTGCAGTTGGTCTTTTCAGAGATGGCAGCAGA
AGCTGCATATCAAACCTGGCGCAGATCAGGCCTCTATAACCGCCAGGAATCACATTTCAGCTGGTGAAACTGCAGGT
GGAAGAGGTGCACCAGCTCTCCCGGAAAGCAGAAACCAAGCTGGCAGAAGCACAGATAGAAGAGCTCCGTCAGAA
AACACAGGAGGAAGGGGAGGAGCGGGCTGAGTCGGAGCAGGAGGCCTACCTGCGTGAGGATTGAGGGCGCTGAGCA
CACTGCCCTGTCTCCCCACTCAGTGGGGAAAGCAGGGGCAGATGCCACCCTGCCAGGGTTGGCATGACTGTCTG
TGCACCGAGAAGAGGCGGCAGGTCTGCCCTGGCCAATCAGGCGAGACGCCTTTGTGAGCTGTGAGTGCCTCCTG
TGGTCTCAGGCTTGCCTGGACCTGGTTCTTAGCCCTTGGGCACTGCACCCTGTTTAAACATTTACCCCACTCTG
TACAGCTGCTCTTACCCATTTTTTTTACCTCACACCCAAAGCATTTTGCCTACCTGGGTCAGAGAGAGGAGTCCT
TTTTGTCATGCCCTTAAGTTCAGCAACTGTTTAACTGTTTTCAGTCTTATTTACGTCGTCAAAAATGATTTAGT
ACTTGTTCCCTCTGTTGGGATGCCAGTTGTGGCAGGGGGAGGGGAACCTGTCCAGTTTGTACGATTTCTTTGTAT
GTATTTCTGATGTGTTCTCTGATCTGCCCCCACTGTCTGTGAGGACAGCTGAGGCCAAGGAGTAAAAACCTAT
TACTACTAAGAGAAGGGGTGCAGAGTGTTTACCTGGTGCTCTCAACAGGACTTAACATCAACAGGACTTAACACA
GAAAAAAA

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FIGURE 82

MAALKSWLSRSVTSFFRYRQCLCVPVVANFKKRCFSELIRPWHKTVTTIGFVTLCAVPIAQKSEPHSLSSSEALMR
RAVSLVTDSTSTFLSQTTYALIEAITEYTKAVYTLTSLYRQYTSLLGKMNSEEEDEVWQVIIGARAEMTSKHQY
LKLETTWMTAVGLSEMAAEAAYQTGADQASITARNHIQLVKLQVEEVHQLSRKAETKLAEAQIEELRQKTQEEGE
ERAESEQEAYLRED

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FIGURE 83

ACTTTCTGCCCTTCCCCGGCCAAGCCCAACTCCGGATCTCGCTCTCCACCGGATCTCACCCGCCACACCCGGA
CAGGCGGCTGGAGGAGGCGGGCGTCTAAAATTCTGGGAAGCAGAACCTGGCCGGAGCCACTAGACAGAGCCGGGC
CTAGCCCAGAGACATGGGAGAGTTGCTACAACCCAGGTCTGGATGGTATTATTGAATATGATGATTTCAAATTGAA
CTCCTCCATTGTGGAACCCAAGGAGCCAGCCCCAGAAACAGCTGATGGCCCCTACCTGGTGATCGTGGAACAGCC
TAAGCAGAGAGGCTTCCGATTTTGATATGGCTGTGAAGGCCCTCCCATGGAGGACTGCCCGGTGCCTCCAGTGA
GAAGGGCCGAAAGACCTATCCCACTGTCAAGATCTGTAACACGAGGGACCAGCCAAGATCGAGGTGGACCTGGT
AACACACAGTGACCCACCTCGTGCTCATGCCACAGTCTGGTGGGCAAGCAATGCTCGGAGCTGGGGATCTGCGC
CGTTTCTGTGGGGCCCCAAGGACATGACTGCCCAATTTAACAACCTGGGTGTCCTGCATGTGACTAAGAAGAACAT
GATGGGGACTATGATACAAAACTTCAGAGGCAGCGGCTCCGCTCTAGGCCCCAGGGCCTTACGGAGGCCGAGCA
GCGGGAGCTGGAGCAAGAGGCCAAAGAACTGAAGAAGGTGATGGATCTGAGTATAGTGCGGCTGCGCTTCTCTGC
CTTCCTTAGAGCCAGTGATGGCTCCTTCTCCCTGCCCTGAAGCCAGTCACCTCCCAGCCCATCCATGATAGCAA
ATCTCCGGGGGCATCAAACCTGAAGATTTCTCGAATGGACAAGACAGCAGGCTCTGTGCGGGGTGAGATGAAGT
TTATCTGCTTTGTGACAAGGTGCAGAAAGATGACATTGAGGTTTCGGTTCTATGAGGATGATGAGAATGGATGGCA
GGCCTTTGGGGACTTCTCTCCACAGATGTGCATAAACAGTATGCCATTGTGTTCCGGACACCCCCCTATCACAA
GATGAAGATTGAGCGGCCTGTAACAGTGTCTGCAACTGAAACGCAAGCGAGGAGGGGACGTGTCTGATTCCAA
ACAGTTCACCTATTACCCTCTGGTGGAAGACAAGGAAGAGGTGCAGCGGAAGCGGAGGAAGGCCCTTGCCACCTT
CTCCCAGCCCTTCGGGGGTGGCTCCACATGGGTGGAGGCTCTGGGGGTGCAGCCGGGGGCTACGGAGGAGCTGG
AGGAGGTGAGGGGTACTGATGGAGGGAGGGGTAAAGGTAAGAGAAGCTGTGGAGGAAAAAATCTGGGGGAGGC
CGGGCGTGCTTGCACGCCTGTAATCCAGCCTTTGGGAGGCCAAGGCAGGCAGTTACCTTGAGATCAGGAGTTCAA
GACCAGCTTGCCCAACAGCGTGAAACCTCGTCTCTACTAAAAATACAAACATTAGCTGGGCATGGTGGCAGGCGC
CTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGACAAGAGGTTGCAGTAAGC
TGAGATCACACCACTGCACTCCAGGCTGGGCAATAAGAGCGAAACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 84

MESCYNPGLDGIIEYDDFKLNSSIVEPKEPAPETADGPYLVIVEQPKQRGFRFRYGCEGFSHGGLPGASSEKGRK
TYPTVKICNYEGPAKIEVDLVTHSDPPRAHAHSLVGKQCSELGICAVSVGPKDMTAQFNNLGV LHVT KKNMMGT
IQKLQRQLRSRPQGLTEAEQRELEQEAKELKKVMDLSIVRLRFS AFLRASDGSFSLPLKPVTSQPIHDSKSPGA
SNLKISRMDKTAGSVRGGDEVYLLCDKVQKDDIEVRFYEDDENGWQAFGDFSPTDVHKQYAI VFRTPPYHKMKIE
RPVTVFLQLKRKRGGDVSDSKQFTYYPLVEDKEEVQRKRRKALPTFSQPFGGGSHMGGGSGGAAGGYGGAGGGEG
VLMEGGVKVREAVEEKNLGEAGRGLHACNPAFGRPRQAVT

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FIGURE 85A

[illegible]

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FIGURE 85B

AATTTCAAGTTTCCTTCGCTAGACTTGAATGTGTCTAGCCACTCTAATTTATGGGGGCTTTGGTTTTTTCCTA
TTGTACTTTGTATGTAGAATTGTTTTGAAATATCAAGCATATTTACTTTGAATTTGAACCTTTCTTAATTTTGT
ATTTATCCTTTGAATAAAATGTAAATCCAATATTTATTATT

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FIGURE 86

HCAFSLSDRVRS

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FIGURE 87

GGGGCAGACGTGGGACGGGAAGGACGGCTGCCGGGACTGGCGCGCGGGGACACTGGGCCGACGCGTGGAGTAGCG
GGGAGAGCGGGAAGCCTGAGGGGGCGGGGCCGGCGCGAGGCCGTGGGTGCGGCACGAGGATGCCGGCGGCGGGAC
AGCGCCCGTAGGCAGCCCCACGGGCAGGGCGCGCGGGCGGGGCGGGGCGGGCCAGAGGAGCTCCCGGCAT
GTCGCAAGGGCTCCCGGCCGCCGGCAGCGTCCTGCAGAGGAGCGTCGCGGCGCCCGGGAACCAGCCGACGCCGA
GCCGCAGCAGCAGAGCCCTGAGGATGATGACAGGAAGGTCCGAAGGAGAGAAAAAACCGAGTTGCTGCTCAGAG
AAGTCGGAAGAAGCAGACCCAGAAGGCTGACAAGCTCCATGAGGAATATGAGAGCCTGGAGCAAGAAAACACCAT
GCTGCGGAGAGAGATCGGGAAGCTGACAGAGGAGCTGAAGCACCTGACAGAGGCACTGAAGGAGCACGAGAAGAT
GTGCCCGCTGCTGCTCTGCCCTATGAACTTTGTGCCAGTGCCTCCCCGGCCGGACCCTGTGGCCGGCTGCTTGCC
CCGATGAAGCCGGGGACACTCCTCTGCCCAGCAAGGAGCCTTGGTCATTTTCATACCTGGGAGGAAGGCTTTTCC
TTCACAATTGTATACAGGGGGCACCTGTGGCCAGGCCTCCTCCTGGGAGCTCCAGGACCAGCCAGCTGTGTTCCC
TGCAGACTGGGCTCAGCCCGACATCCAACAGGCGCCAACTCACAGAGCCCTTGTGCAGATCCAGCATGGAGGCC
ACCCTCAGGAGTGACTTCTCATCCACCCTGGCAGCTAGTAGGTTCTGCTGTTATGCAGAGCCATTTCTCTAGAA
TTTGGATAATAAGATGCTTATTGTCTCTCCCTTCTCCAGTTCTGGGAATTTACAGGCACAATACACTTCCTTTT
CCTGG

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FIGURE 88

MSQGLPAAGSVLQRSVAAPGNQPQPQPQQSPEDDDRKVRRREKNRVAAQSRKKQTQKADKLHEEYESLEQENT
MLRREIGKLTEELKHLTEALKEHEKMCPLLLCPMNFVPVPPRPDPVAGCLPR

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FIGURE 89

GGGCGGGGTGCCGCATCCCCAGCCCGCCGCCATGCCGCCTACAACTGGTGCTGATCCGGCACGGCGAGAGCGC
ATGGAACCTGGAGAACCGCTTCAGCGGCTGGTACGACGCCGACCTGAGCCCGCGGGCCACGAGGAGGCGAAGCG
CGGCGGGCAGGCGCTACGAGATGCTGGCTATGAGTTTGACATCTGCTTCACCTCAGTGCGAGAAGAGAGCGATCCG
GACCTCTGGACAGTGCTAGATGCCATTGATCAGATGTGGCTGCCAGTGGTGAGGACTTGGCGCCTCAATGAGCG
GCACTATGGGGGTCTAACCGGTCTCAATAAAGCAGAACTGCTGCAAAGCATGGTGAGGCCAGGTGAAGATCTG
GAGGCGCTCCTATGATGTCCCACCACCTCCGATGGAGCCCGACCATCCTTTCTACAGCAACATCAGTAAGGATCG
CAGGTATGCAGACCTCACAGAAGATCAGCTACCCTCCTGTGAGAGTCTGAAGGATACTATTGCCAGAGCTCTGCC
CTTCTGGAATGAAGAAATAGTTCCCCAGATCAAGGAGGGGAAACGTGTACTGATTGCAGCCCATGGCAACAGCCT
CCGGGGCATTGTCAAGCATCTGGAGGGTCTCTCTGAAGAGGCTATCATGGAGCTGAACCTGCCGACTGGTATTCC
CATTGTCTATGAATTGGACAAGAACTTGAAGCCTATCAAGCCCATGCAGTTTCTGGGGGATGAAGAGACGGTGCG
CAAAGCCATGGAAGCTGTGGCTGCCCAGGGCAAGGCCAAGAAGTGAAGGCCGGCGGGGAGGATACTGTCCCCAGG
AGCACCTCCCTGCCCCGTCTGTGCCCTCTGCCCCCTCCACCTGCACATGTCACACTGACCACATCTGTAGACATC
TTGAGTTGTAGCTGCAGACGGGGACAGTGGCTCCCATTTTCATTTTAGCCATTTTGTGCGCTGCACCCACTCCC
TTCATACAATCTAGTCAGAAATAGCAGTTCTAGAGCACAGGTTCTCAGTCTAAGCTATGGAAAAGCTCCCTTATC
CAACAGAGTTTTAAAGTAGTGACTTGGGTTTTTTCGAGTGCTTTGTTTACTAAGGACTTTGGGGAGGAACCATGC
TAAGCCATGACCACTGAGGAGAAGCAACAGAGCCTGTCTGTCCCCATGAGCGGAGTCTGTCTCTGCTCTTCTGC
AGTCAGGTCACTGCCTACTGCCTGGGGGCTCTAGTCATTCCAGTGGAAGACGAATGTAACTGCGTGGTGATGTG
ACAACTGTTTCTCCTGACCCAGAGGATCTGGCTCTAGGTTGGGATCAATCCTGAATTTTCGTTATGTGTTAAT
TTACTTTTATTAATAAAGTATAGTATATATAATAACAAACAATAACCCTTCTGGGGTTTTCTGTGGCGGTTGAAA
TAGTCCCACATGTGGTCATCAGAAATAGCATTCTCATACCAATATAGGATCAGCTCCTTGACCTCTGAGGGGTC
AGGAGTGCTTCTGGTGTGTGATTAGAATCCCTTCTGCCTTGTTCATGGCAGTGAAATGCCTCTTGGTCCTG
TCCAGTGATCTTTCACTGATTTCTGAATCATGTTCTAGTTGCTTGACCCTGCCACATGGGTCCAGTGTTTATCT
GAGCATAACTGTACTAAATCCTTTTCCATATCAGTATAATAAAGGAGTGATGTGCAAT

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FIGURE 90

MAAYKLVLIRHGESAWNLENRFSGWYDADLSPAGHEEAKRGGQALRDAGYEFDICFTSVQKRAIRTLWTVLDAID
QMWLPVVRTWRLNERHYGGLTGLNKAETAAKHGAEQVKIWRRSYDVPPPPMEPDHFFYSNISKDRRYADLTEDQL
PSCESLKDTIARALPFWNEEIVPQIKEGKRVLIAAHGNSLRGIVKHLEGLSEEAIMELNLPTGIPIVYELDKNLK
PIKPMQFLGDEETVRKAMEAVAAQGKAKK

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FIGURE 91

GCGGCCGCTTTTCGATTTCGCTTTCCCTAAATGGCTGAGCTTCTCGCCAGCGCAGGATCAGCCTGTTCTCTGGGAC
TTTCCGAGAGCCCCGCCCTCGTTCCCTCCCCAGCCGCCAGTAGGGGAGGACTCGGCGGTACCCGGAGCTTCAGG
CCCCACCGGGGCGCGGAGAGTCCCAGACCCGGCCGGGACCGGGACGGCGTCCGAGTGCCAATGGCTAGCTCTAGG
TGTCCCGCTCCCCGCGGTGCCGCTGCCCTCCCCGAGCTTCTCTCGCATGGCTGGGGACAGTACTGCTACTTCTC
GCCGACTGGGTGCTGCTCCGGACCGCGCTGCCCGCATATTCTCCCTGCTGGTGCCACCGCGCTGCCACTGCTC
CGGTCTGGGCGGTGGGCCTGAGCCGCTGGGCCGTGCTCTGGCTGGGGGCTCGCGGGTCTCAGGGCAACGGTT
GGCTCCAAGAGCGAAAACGCAGGTGCCAGGGCTGGCTGGCTTTGAAGCCATTAGCTGCGGCACTGGGCTTG
GCCCTGCCGGGACTTGCCCTGTTCCGAGAGCTGATCTCATGGGGAGCCCCCGGTCCGCGGATAGCACCAGGCTA
CTGCACTGGGGAAGTCACCCTACCGCCTTCGTTGTCACTTATGCAGCGGCACTGCCCGCAGCAGCCCTGTGGCAC
AAACTCGGGAGCCTCTGGGTGCCCGCGGTGAGGGCGGCTCTGGAAACCTGTGCGTCGGCTTCTAGGCTGCCCTG
GGCTCGGAGACGCGCCGCTCTCGCTGTTCCCTGGTCTGGTGGTCTCTCTCTCTTGGGGAGATGGCCATTCCA
TTCTTTACGGGCGCCTCACTGACTGGATTCTACAAGATGGCTCAGCCGATACCTTCACTCGAACTTAACTCTC
ATGTCCATTCTCACCATAGCCAGTGAGTGCTGGAGTTCGTGGGTGACGGGATCTATAACAACACCATGGGCCAC
GTGCACAGCCACTTGACAGGGAGAGGTGTTTGGGGCTGTCTGCGCCAGGAGACGGAGTTTTTCCAACAGAACCAG
ACAGGTAACATCATGTCTCGGGTAACAGAGGACACGTCCACCCTGAGTGATTCTCTGAGTGAGAATCTGAGCTTA
TTTCTGTGGTACCTGGTGCGAGGCCTATGTCTCTTGGGGATCATGCTCTGGGGATCAGTGTCCTCACCATGGTC
ACCCTGATCACCCTGCCTCTGCTTTTCTTCTGCCCAAGAGGTGGGAAAATGGTACCAGTTGCTGGAAGTGCAG
GTGCGGGAATCTCTGGCAAAGTCCAGCCAGGTGGCCATTGAGGCTCTGTGCGCCATGCCCTACAGTTCTGAAGCTTT
GCCAACGAGGAGGGCGAAGCCAGAAGTTTAGGGAAAAGCTGCAAGAAATAAAGACACTCAACCAGAAGGAGGCT
GTGGCCTATGCAGTCAACTCCTGGACCACTAGTATTTCAAGTATGCTGCTGAAAGTGGGAATCCTCTACATTGGT
GGGCAGCTGGTGACAGTGGGGCTGTAAGCAGTGGGAACCTGTACATTTGTTCTCTACCAGATGCAGTTTACC
CAGGCTGTGGAGGTACTGCTCTCCATCTACCCAGAGTACAGAAGGCTGTGGGCTCCTCAGAGAAAATATTTGAG
TACCTGGACCGCACCCCTCGCTGCCACCCAGTGGTCTGTTGACTCCCTTACACTTGGAGGGCCTTGTCCAGTTC
CAAGATGTCTCCTTTGCCTACCCAAACCGCCAGATGCTTAGTGCTACAGGGGCTGACATTACCCCTACGCCCT
GGCGAGGTGACGGCGCTGGTGGGACCCAATGGGTCTGGGAAGAGCACAGTGGCTGCCCTGCTGCAGAATCTGTAC
CAGCCCACCGGGGACAGCTGCTGTTGGATGGGAAGCCCTTCCCCAATATGAGCACCGCTACCTGCACAGGCAG
GTGGCTGCAGTGGGACAAGAGCCACAGGTATTTGGAAGAAGTCTTCAAGAAAATATTGCCTATGGCCTGACCCAG
AAGCCAACTATGGAGGAAATCACAGCTGCTGCAGTAAAGTCTGGGGCCCATAGTTTCATCTCTGGACTCCCTCAG
GGCTATGACACAGAGGTAGACGAGGCTGGGAGCCAGCTGTGAGGGGTCAGCGACAGGCAGTGGCGTTGGCCGA
GCATTGATCCGGAACCGTGTGTACTTATCCTGGATGATGCCACCAGTGCCCTGGATGCAAACAGCCAGTTACAG
GTGGAGCAGCTCCTGTACGAAAGCCCTGAGCGGTACTCCCGCTCAGTGCTTCTCATCACCAGCACCTCAGCCTG
GTGGAGCAGGCTGACCACATCCTCTTCTGGAAGGAGGCGCTATCCGGGAGGGGGAACCCACCAGCAGCTCATG
GAGAAAAAGGGGTGCTACTGGGCCATGGTGCAGGCTCCTGCAGATGCTCCAGAATGAAAGCCTTCTCAGACCTGC
GCACTCCATCTCCCTCCCTTTTCTCTCTCTGTGGTGGAGAACCACAGCTGCAGAGTAGCAGCTGCCTCCAGGAT
GAGTTACTTGAAATTTGCCTTGAGTGTGTTACCTCCTTTCCAAGCTCCTCGTGATAATGCAGACTTCTGGAGTA
CAAACACAGGATTTGTAATTCCTACTGTAACGGAGTTTAGAGCCAGGGCTGATGCTTTGGTGTGGCCAGCACTCT
GAAACTGAGAAATGTTTCAAGATGTACGGAAAGATGATCAGCTATTTTCAACATAACTGAAGGCATATGCTGGCCC
ATAAACACCCTGTAGGTTCTTGATATTTATAATAAAATTGGTGTTTTGT

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FIGURE 92

MAELLASAGSACSWDFPRAPPSEPPPAASRGGLGGTRSFRRPHRGAESPRPGRDRDGVRVPMASSRCPAPRGCRCL
PGASLAWLGTVLLLLADWVLLRTALPRIFSLLVPTALPLLRVWAVGLSRWAVLWLGACGVLRAVGSKSENAGAQ
GWLAAALKPLAAALGLALPGLALFRELISWGAPGSADSTRLLHWGSHPTAFVVSAAAALPAAALWHKLSLWVPGG
QGGSGNPVRRLLGCLGSETRRLSLFLVLVVLSSLGEMAIFFFTGRLTDWILQDGSADTFTRNLTLMSILTIASAV
LEFVGDIYNNMTMGHVHSHLQGEVFGAVLRQETEFFQQNQTNIMSRVTEDTSTLSDSLSENLSLFLWYLVRGLC
LLGIMLWGSVSLTMVTLITLPLLFLLPKKVWKYQLLEVQVRESLAKSSQVAIEALSAMPTVRSFANEEGEAQKF
REKLQEIKTNLNQEAVAYAVNSWTTISGMLLKVGILYIGGQLVTSGAVSSGNLVTFLVLYQMFTQAVEVLLSIY
PRVQKAVGSSEKIFEYLDRTPRCPPSGLLTPLHLEGLVQFQDVSAFYPNRPDVLVLQGLTFTLRPGEVTALVGP
GSGKSTVAALLQONLYQPTGGQLLLDGKPLPQYEHRYLHRQVAAVGQEPQVFGRLQENIAYGLTQKPTMEEITAA
AVKSGAHSFISGLPQGYDTEVDEAGSQLSGGQRQAVALARALIRKPCVLILDDATSALDANSQEQVEQLLYESPE
RYSRSVLLITQHLSLVEQADHILFLEGGAIREGGTHQQLMEKKGCYWAMVQAPADAPE

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FIGURE 93

GGGATCCCGGGGCGCGCGTCGCTCGGGCCCCGCC**ATG**GCCGTCACCATCACGCTCAAAACGCTGCAGCAGCAG
ACCTTCAAGATCCGCATGGAGCCTGACGAGACGGTGAAGGTGCTAAAGGAGAAGATAGAAGCTGAGAAGGGTCGT
GATGCCCTTCCCCGTGGCTGGACAGAACTCATCTATGCCGGCAAGATCTTGAGTGACGATGTCCCTATCAGGGAC
TATCGCATCGATGAGAAGAACTTTGTGGTCGTCATGGTGACCAAGACCAAAGCCGGCCAGGGTACCTCAGCACCC
CCAGAGGCCCTCACCCACAGCTGCCCCAGAGTCCCTACATCCTTCCCGCCTGCCCCACCTCAGGCATGTCCCAT
CCCCACCTGCCGCCAGAGAGGACAAGAGCCCATCAGAGGAATCCGCCCCACGACGTCCCCAGAGTCTGTGTCA
GGCTCTGTTCCCTCTTCAGGTAGCAGCGGGCGAGAGGAAGACGCGGCCTCCACGCTAGTGACGGGCTCTGAGTAT
GAGACGATGCTGACGGAGATCATGTCCATGGGCTATGAGCGAGAGCGGGTCGTGGCCGCCCTGAGAGCCAGCTAC
AACAACCCCCACCGAGCCGTGGAGTATCTGCTCACGGGAATTCCTGGGAGCCCCGAGCCGGAACACGGTTCTGTC
CAGGAGAGCCAGGTATCGGAGCAGCCGGCCACGGAAGCAGCAGGAGAGAACCCCTGGAGTTCCTGCGGGACCAG
CCCCAGTTCCAGAACATGCGGCAGGTGATTCAGCAGAACCCTGCGCTGCTGCCCGCCCTGCTCCAGCAGCTGGGC
CAGGAGAACCCTCAGCTTTTACAGCAAATCAGCCGGCACCAGGAGCAGTTCATCCAGATGCTGAACGAGCCCCCT
GGGGAGCTGGCGGACATCTCAGATGTGGAGGGGGAGGTGGGCGCCATAGGAGAGGAGGCCCCGCAGATGAACCTAC
ATCCAGGTGACGCCGAGGAGAAAGAAGCTATAGAGAGGTTGAAGGCCCTGGGCTTCCCAGAGAGCCTGGTCATC
CAGGCCTATTTTCGCGTGTGAAAAAAATGAGAACTTGGCTGCCAACTTCCTCCTGAGTCAGAACTTTGATGACGAG
TGATGCCAGGAAGCCAGGCCACCGAAGCCCCCACCCTACCCCTTATTCATGAAAGTTTTATAAAAGAAAAATAT
ATATATATTCATGTTTATTTAAGAAATGAAAAAAATCAAAAATCTTAAAAAACAAGCAAACAGTCCAGCTT
CCTGTCTCTCTAAAGTGGCCCTGTTCCCATCTCCCGGGCCAGACAGCTGTCCCCCGTCTCTCTCCCCAGCCCA
GCCTGCTCAGAGAAGCTGGCAGGACTGGGAGGCGACAGATGGGCCCCCTTGGCCTCTGTCCCAGCTCTCTGCAG
CCAGACGGAAAGGCGGCTGCTTGCTCTCCATCCTCCGAAAAACCCCTGAGGACCCCCCCCCATCCTCTTCTAGG
ATGAGGGGAAGCTGGAGCCCCAATTTGATCCTCCATTGGAGTGGCCCAAATCTTTCCATCTAGGGCAAGTCCTG
AAAGGCCCAAGGCCCCCTCCCAGTCTGGCCTTGGCCTCCAGCCTGGAGAAGGGCTAACATCAGCTCATTGTCAAG
GCCACCCCCACCCAGAACAGAACCGTGTCTCTGATAAAGGTTTTGAAGTGAATAAAGTTTTAAAAACT

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FIGURE 94

MAVTITLKTLLQQQTFKIRMEPDETVKVLKEKIEAEKGRDAFPVAGQKLIYAGKILSDDVPIRDYRIDEKNFVVVM
VTKTKAGQGTSAPPEASPTAAPESSTSFPPAPTSGMSHPPPAAREDKSPSEESAPTTSPESVSGSVPSGSSGRE
EDAASTLVGTGSEYETMLTEIMSMGYERERVVAALRASYNPHRAVEYLLTGIPGSPEPEHGSVQESQVSEQPATE
AAGENPLEFLRDQPQFQNMQRQVIQQNPALLPALLQQLGQENPQLLQQISRHQEQFIQMLNEPPGELADISDVEGE
VGAIGEEAPQMNYIQVTPQEKEAIERLKALGFPESLVIQAYFACEKNENLAANFLLSQNFDDE

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FIGURE 95

GTCACTCGTATAAAAACCTATGCTTTGAAGTTCTCGTGTGTCTCGGCCTGCAGGTCTCGCTCAGAGCTGTGTCC
CTGAACATCCACCCTGCTGGGGTGGCTTGACGCACCTCTGTGCAAATCTGTTTCGCTCGCAACCCTACCTACCTCT
CTCCCGAACCGGAGAAAAACCTTCGGCGGGGTCCTTCGGGTTTTGTGTGCAATCTGCGGCGGCGACCCGGCGCCG
CGTCACGCGGTGGTGAATGTGCGGCAGTACGCGCGCCGCGTCGTTTTACGCGGCGATTTTCATCATGCTCCGAGCCG
GCGGCGCGCGCCGCTTCCGTCGCCACCCCTCTCTGGACAGCCAGGGCCGAGGCTCATGCCCTCTCCGCGTCCAG
TGCTGCTTAGAGGTGCTCGCGCCGCTCTGCTGCTGCTGCTGCCCCCCGGCTCTTAGCCCCGACCCCTCGCTCCTCC
TCCGCCGGTCCCTCAGCGCGGCTCCTGCGCCCCGATCTCCTTGCCCCGCGCCGCTCCCGGAGCAGCATGGACG
GCGCGGGGGCTGAGGAGGTGCTGGCACCTCTGAGGCTAGCAGTGCGCCAGCAGGGAGATCTTGTGCGAAACTCA
AAGAAGATAAAGCACCCCAAGTAGACGTAGACAAAGCAGTGCGTGAGCTCAAAGCCCGCAAGAGGGTTCTGGAAG
CAAAGGAGCTGGCGTTACAGCCCAAAGATGATATTGTAGACCGAGCAAAAATGGAAGATACCCTGAAGAGGAGGT
TTTTCTATGATCAAGCTTTTGTATTTATGGAGGTGTTAGTGGTCTGTATGACTTTGGGCCAGTTGGCTGTGCTT
TGAAGAACAATATTATTACAGACCTGGAGGCAGCACTTTATCCAAGAGGAACAGATCCTGGAGATCGATTGCACCA
TGCTCACCCCTGAGCCAGTTTTAAAGACCTCTGGCCATGTAGACAAAATTTGCTGACTTCATGGTGAAAGACGTAA
AAAATGGAGAATGTTTTCGTGTCTGACCATCTATTTAAAGCTCATTACAGAAATTGATGTCTGATAAGAAGTGTT
CTGTGCAAAAGAAATCAGAAATGGAAGTGTTTTGGCCAGCTTGATAACTATGGACAGCAAGAACTTGCGGATC
TTTTTGTGAACATAATGTAAATCTCCCATTAAGTGAATGATCTATCCCTCCAGTGTCTTTAACTTAATGT
TCAAGACTTTTCATTGGGCCTGGAGGAAACATGCCTGGGTACTTGAGACCAGAACTGCACAGGGGATTTTCTTGA
ATTTCAAACGACTTTTGGAGTTCAACCAAGGAAAGTTGCCTTTTGTCTGCTGCCAGATTGGAATTTCTTTTAGAA
ATGAGATCTCCCTCGATCTGGACTGATCAGAGTCAGAGAATTCACAATGGCAGAAATTGAGCATTGTGTAGATC
CCAGTGAGAAAGACCACCCCAAGTCCAGAATGTGGCAGACCTTCACCTTTATTTGTATTACAGCAAAAGCCCAGG
TCAGCGGACAGTCCGCTCGGAAAATGCGCCTGGGAGATGCTGTTGAACAGGGTGTGATTAATAACACAGTATTAG
GCTATTTTCATTGGCCGCATCTACCTCTACCTCACGAAGTTGGAATATCTCCAGATAAACTCCGCTTCCGGCAGC
ACATGGAGAATGAGATGGCCATTATGCCTGTGACTGTTGGGATGCAGAATCCAAAACATCCTACGTTGGATTG
AGATTGTTGGATGTGCTGATCGTTCCCTGTTATGACCTCTCCTGTGATGCACGAGCCACCAAAGTCCCCTGTAG
CTGAGAAACCTCTGAAAGAACCCAAAACAGTCAATGTTGTTTCAGTTTGAACCCAGTAAGGGAGCAATTGGTAAGG
CATATAAGAAGGATGCAAACTGGTGATGGAGTATCTTGCCATTTGTGATGAGTGCTACATTACAGAAATGGAGA
TGCTGCTGAATGAGAAAGGGGAATTCACAATTGAAACTGAAGGGAAAACATTTAGTTAACAAAAGACATGATCA
ATGTGAAGAGATTCCAGAAAACACTATATGTGGAAGAAGTTGTTCCGAATGTAATTGAACCTTCCTTCGGCCTGG
GTAGGATCATGTATACGGTATTTGAACATACATTCCATGTACGAGAAGGAGATGAACAGAGAACATTCTTCAGTT
TCCCTGCTGTAGTTGCTCCATTCAAATGTTCCGTCCTCCCACTGAGCCAAAACAGGAGTTTCATGCCATTTGTCA
AGGAATTATCGGAAGCCCTGACCAGGCATGGAGTATCTCACAAAGTAGACGATTCCCTCTGGGTCAATCGGAAGGC
GCTATGCCAGGACTGATGAGATTGGCGTGGCTTTTGGTGTACCATTGACTTTGACACAGTGAACAAGACCCCCC
ACACTGCAACTCTGAGGGACCGTGACTCAATGCGGCAGATAAGAGCAGAGATCTCTGAGCTGCCAGCATAGTCC
AAGACCTAGCCAATGGCAACATCACATGGGCTGATGTGGAGGCCAGGTATCCTCTGTTTGAAGGGCAAGAGACTG
GTAAAAAAGAGACAATCGAGGAATGAGGACAATTTTGACAACCTTTGACCACTTGCGCTAATAAAAAAAAAAAAA
CTACTCTTATGTCCACTTTACAAAAGAAAACAGCATTGTGATTACTCCCAGGGACCGTATTTTATCTTCAGTGGC
TGCCCTGATTTTACCCCCACAATTAAAGTTGAAGGAATCCTGA

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FIGURE 96

MDGAGAEVLAPLRLAVRQQGDLVRKLKEDKAPQVDVDKAVAEKARKRVLEAKELALQPKDDIVDRAKMEDTLK
RRFFYDQAFAIYGGVSGLYDFGPVGCALKNNIIQTWRQHF IQEEQILEIDCTMLTPEPVLKTSGHVDKFADFMVK
DVKNGECFRADHLLKAHLQKLMSDKKCSVEKKSEMESVLAQLDNYGQQELADLFVNYNVKSPITGNDLSPPVSFN
LMFKTFIGPGGNMPGYLRPETAQGIFLNFKRLLEFNQGLPFAAAQIGNSFRNEISPRSGLIRVREFTMAEIEHF
VDPSEKDHPKFQNVADLHLYLYSAKAQVSGQSARKMRLGDAVEQGVINNTVLGYFIGRIYLYLTKVGISPDKLRF
RQHMENEMAHYACDCWDAESKTSYGWIEIVGCADRSCYDLSCHARATKVPLVAEKPLKEPKTVNVVQFEPKSGAI
GKAYKKDAKLVMEYLAICDECYITEMEMLLNEKGEFTIETEGKTFQLTKDMINVKRFQKTLYVEEVVPNVIEPSF
GLGRIMYTVFEHTFHVREGDEQRTFFSFPVAVPFKCSVLPLSQNQEFMPFVKELSEALTRHGVSHKVDSSGSI
GRRYARTDEIGVAFGVTIDFDTVNKTPHTATLRDRDSMRQIRAEISELPSIVQDLANGNITWADVEARYPLFEGQ
ETGKKETIEE

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FIGURE 97

TCCCCGCCCTTCTCTTTTCTACAGTATCTGTTACCTCAGTCAGATTGAGGATGCACATATACTGGGAAAAATAATC
GACTTCCAGCGTCCCTCATGTAGTCTCTACCTGATTGAGGAATCTCTAACCCAGTATCGGAACGTTAAGCGGCTT
CTCCGCTTTTCTGCCGTGAGAACTCGAGGTGACCAACCTCCGTTTCCGGTTGGCTCCGGTTGCAGAGTTGAGTG
TCCTGAGAGGTCAGATTGCTGTCAGACATGGCCCCATGAACATGGACATGAGCATGGACATCATAAAATGGAACTT
CCAGATTATAGACAATGGAAGATAGAAGGGACACCATTAGAACTATCCAGAAGAAGCTGGCTGCAAAAGGGCTA
AGGGATCCATGGGGCCGCAATGAAGCTTGGAGATACATGGGTGGCTTTGCAAAGAGTGTTTCCTTTTCTGATGTA
TTCTTTAAAGGATTCAAATGGGGATTTGCTGCATTTGTGGTAGCTGTAGGAGCTGAATATTACCTGGAGTCCCTG
AATAAAGATAAGAAGCATCACTGAAGATAATACCTGGAAGCATCATAGTGTTTCTTAACTCTCCAAAATAAGAT
TTCTTCTCTGTAGCCTACTTGTCTGGTTTATCCCTTACAGAATATTAGTAAAGATTTAATCAATTAAAAATATATA
TAAAAAAAAAAAAAAAAA

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FIGURE 98

MAHEHGHEHGHKME L P D Y R Q W K I E G T P L E T I Q K K L A A K G L R D P W G R N E A W R Y M G G F A K S V S F S D V F F K G F K W G F
A A F V V A V G A E Y Y L E S L N K D K K H H

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FIGURE 99

GCTGCGCCCCACGCCAGCCCGCGCCCCGCATGGCTGCCGCGGGGCCAGGCCTGTGGAGCTGGGCTTCGCCGAGT
CGGCGCCGGCGTGGCGACTGCGCAGCGAGCAGTTCCCCAGCAAGGTGGGCGGGCGGCCGATGGCTGGGCGCGG
CCGGGCTGCCGGGGCCCCAGGCCCTGGCCTGCGAGCTGTGCGGCGCCCGCTCTCCTTCCTGCTGCAGGTGTATG
CGCCGCTGCCGTGGCCGCCCCGACGCCTTCCACCGCTGCATCTTCCTCTTCTGCTGCCGCGAGCAGCCGTGCTGTG
CCGGCTTGGAGTTTTTAGGAATCAACTACCCAGGAAAAACGATTTTTACTCATATGAGCCACCTTCTGAGAATC
CTCCCCAGAAACAGGAGAATCAGTGTGTCTCCAGCTTAAGTCTGGTGCTCATCTCTGCAGGGTTTGTGGCTGTT
TAGGCCCCAAAACGTGCTCCAGATGCCACAAAGCATATTACTGCAGCAAGGAGCATCAGACCCCTAGACTGGAGAT
TGGGACATAAGCAGGCTTGTGCACAACCAGATCATCTGGACCATATAATTCCAGACCACAACCTTCCTTTTTCCAG
AATTTGAAATTGTAATAGAAACAGAAGATGAGATTATGCCTGAGGTTGTGAAAAGGAAGATTACTCAGAGATTA
TAGGGAGCATGGGTGAAGCACTTGAGGAAGGACTGGATTCCATGGCAAAACATGAATCCAGGGAAGATAAAATTT
TTCAGAAGTTTAAACTCAGATAGCCCTTGAACCAGAACAGATTCTTAGATATGGCAGAGGTATTGCCCCATCT
GGATTTCTGGTGAAATATTCTCAAGAAAAGGATATTCCAGATTGCCCCCTGTGGTGCCAAGAGAATATTGGAAT
TCCAGGTCATGCCTCAGCTCTTAAACTACCTGAAGGCTGACAGACTGGGCAAGAGCATTGACTGGGGCATCCTGG
CTGCTTTCACCTGTGCTGAGAGCTGCAGCTTGGGTACTGGTTATACAGAAGAATTTGTGTGGAAGCAGGATGTAA
CAGATACACCGTAAAGGCATCTTAAAGCCTTGAAAAATGTTAATAATCTTTTATACCTTGCAATTCCATTTCTGG
GATTTTATCCTAAGGAAATACCTTATACCAAAAATAGAGGTGCAGAGATGTTGACGGATTGCTTACACAGTGTCTA
CTTATTAGTGAAACAAAAGTGTCCAGTGACAGGGAATTAATAAATTTTGGTACATCCACAAAAAAAAAAAAAAAA
AAAAAAA

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FIGURE 100

MAAAGARPVELGFAESAPAWRLRSEQFPSKVGGRPAWLGAAGLPGPQALACELCGRPLSFLLQVYAPLPGRPDAF
HRCIFLFCCREQPCCAGLRVFRNQLPRKNDFYSYEPPSENPPPETGESVCLQLKSGAHLCRVCGCLGPKTCSRCH
KAYYCSKEHQTLDWRLGHKQACAQPDHLDHIIPDHNFLFPEFEIVIETEDIMPEVVEKEDYSEIIGSMGEALEE
GLDSMAKHESREDKIFQKFKTQIALEPEQILRYGRGIAPIWISGENIPQEKDIPDCPCGAKRILEFQVMPQLLNY
LKADRLGKSIDWGILAAFTCAESCSLGTGYTEEFVWKQDVTDP

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FIGURE 101

TGGCGCAATTAAACCAAGCCATAGCCAAATGAATATGAAGTCCGGAGAAAGCTGCTAATAAAACGTTTGGAATGTCAC
GTACAATCCTTTGGCTGGTCTGACAGAGCTAAGAGCCAGACAGAAAAATTAGCCAAGGTTTACCAGCCGAAACGT
TCAGTCTTATCCCTAAAACCTACTATTTCTGTTGCCCATCTTTTGGCTGCAAGGCAGGACTTGTCAAAAGATTTTAA
AGGACAAGCAGCGGCTCTATAAGAGAAAAAGACTGCCTGTGCCATCAATAAGGTGTTGATGGGCAGGGTGCCTGAC
AGAGGTGGTAGACCCAATGAAATCGAACCTCCACCCAGAGATGCCACCGTGGCAGAAGAGGCAAGATGGCCCC
CAGCAGCAAACAGGAGGCCGAGTAGGAGGGAGAGGTGGCTATGAACATTCTCATACGGAGGACGAGGAGGTTCAT
GAACAAGGAGGCGGGAGAGGTGGACGTGGTGGCTATGACCATGGTGGCCGAGGGGGAGGAAGAGGAAATAAGCAT
CAAGGAGGCTGGACAGATGGAGGGAGTGGTGGAGGAGGTGGCTACCAAGATGGTGGTTATCGAGATTCAGGTTTC
CAGCCAGGTGGCTATCATGGTGGCCACAGCAGTGGTGGCTATCAAGGCGGAGGTTATGGTGGCTTCCAAACATCT
TCTTCATATACAGGAAGTGGATACCAGGGTGGTGGCTACCAGCAGGACAATAGATACCAAGATGGCGGGCACCAT
GGTGATCGTGGTGGTGGTGGTGGTGGCGAGGTGGTGGTGGAGGCCGAGGTGGTGGTGGCAGGCCAGGGAGGAGGC
TGGGGAGGAAGAGGGAGCCAGAATTATCACCAAGGGGGTCAATTTGAACAGCATTTCAGCATGGAGGTTATCAG
TATAATCATTCTGGATTTGGACAGGGAAGACATTACACTAGTTGAGGCTACCGAACTTTACATTTTGCTAGAGCT
CAAGTAATAGAACTTAGTTTCAGAATCCTGAATTCAGCACCTATTTTGAATTAATGTGAGACCACAGGTGGCAG
GCAGATTCCTGCTTGGCATAAGCATTGTAGGTCTTCATTCAATTCTGTTAGATTTTTTTATTGGACTTACATAA
TGCCGTTTATTTGAGAAACACATAACATCTCTCCTTCCTATGAAAAATTTTTTAAAAGGTGGTTAAAATTGCCTT
TAATTGCCAGTAGACTAATTCCACAGTCAGAACATGCAAACCTTTTTTGAAGAAATTACTTGAATAAGTAGTTTT
CATGTTTTCAATATGCAGTTTTGAAAATGAGGATTACCTAGACTTTTTTAGATTTACTACTAGGAAACCTTCCT
CATATGAATAACCATTTATATGTGTTTTGCTTAAAGTATTCCAATGCCTATTTTCCAAGCACAGTCTGCCCCCC
GGTTGACTTTTATGCCACGTGTGCTTCATGATGGAACTTTTAGGTCAGTTTCTATTAAATGAGCTCTTCTGCAGA
TAGCACATTCAGTAGCCTTATTTTGTGATGGAATACTGTATCATATGCTCAACTCTGAAAACCTTGAACACGGC
CAAATCCATAAAGATTATAAAAGCAAACCTAAGTTGTGAAGCTATAGTACATGTAGGCATTTAGTTAAGTATAGC
AATTCAAACCTGACCTGCATCCATCCAAAACAAATTCTCTCTCAACCTTATTTTTACTTGAAATTTGCTAGAAGA
AATAGCAAACCGAAATTTGTTTTATGCATGAGTTAATACCACTGGCTCAGCAAATACAAGTTAGTTTGCITTAAG
CAGGTAACTTTTTTTGTAAATGGAAGAAATGCACTACAAAGTTAAGACAGATTTTTGCTAAGTGCAGGAGGCCCTT
TATTATTGCTGCAGAAAAACAAAGCCTGGCTGAGTTGATGTTTTACATCTCCCTTACTGAAATCTACATGACAT
GATGCTTCTTGCTGGGTTTTTTGTACATGTAAACATTGTCAAGCTGTGAAAGAAAAATGGCTGGAGGTGTGCTTTGT
GTGAAAGGTGAGCAATAAAGTATCTGTTAAGTTCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 102

WAINQAIANEYEVRRKLLIKRLDVTVQSFQWSDRAKSQTEKLAKVYQPKRSVLSPKTTISVAHLLAARQDLSKIL
RTSSGSIREKTACAINKVLGRVPDRGGRPNEIEPPPEMPFPWQKRQDGPQQQTGGRVGGRRGGYEHSSYGGRRGGH
EQGGRRGGRRGGYDHGGRGGRRGNKHQGGWTDGGSGGGGGYQDGGYRDSGFQPGGYHGGHSSGGYQGGGYGGFQTS
SSYTGSYQGGGYQQDNRYQDGGHHGDRGGRRGGRRGGRRGGRRAGQGGGWGGRGSQNYHQGGQFEQHFQHGQYQ
YNHSGFGQGRHYTS

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FIGURE 103

GGGGGGGAGATGCAGTAGCCGAAAAC TGC GCGGAGGCACGAGAGGCCGGGAGAGCGTTCTGGGTCCGAGGGTC
CAGGTAGGGGTTGAGCCACCATCTGACCGCAAGCTGCGTCGTGTCGCCTTCTCTGCAGGCACCA**ATG**AGCCAGGAC
ACCGAGGTGGATATGAAGGAGGTGGAGCTGAATGAGTTAGAGCCCCGAGAAGCAGCCGATGAACGCGGCGTCTGGG
GCGGCCATGTCCCTGGCGGAAGCCGAGAAGAATGGTCTGGTGAAGATCAAGGTGGCGGAAGACGAGGCGGAGGCG
GCAGCCGCGGCTAAGTTCACGGGCTGTCCAAGGAGGAGCTGCTGAAGGTGGCAGGCAGCCCCGGCTGGGTACGC
ACCCGCTGGGCACTGCTGCTGCTCTTCTGGCTCGGCTGGCTCGGCATGCTTGCTGGTGCCGTGGTGATAATCGTG
CGAGCGCCGCGTTGTGCGGAGCTACCGGCGCAGAAGTGGTGGCACACGGGCCCCCTCTACCGCATCGGCGACCTT
CAGGCCTTCCAGGGCCACGGCGCGGGCAACCTGGCGGGTCTGAAGGGCGTCTCGATTACCTGAGCTCTCTGAAG
GTGAAGGGCCTTGCTGCTGGGTCCAATTCAAGAACCAGAAGGATGATGTCGCTCAGACTGACTGCTGCAGATC
GACCCCAATTTTGGCTCCAAGGAAGATTTTGACAGTCTCTTGCAATCGGCTAAAAAAGAGCATCCGTGTCATT
CTGGACCTTACTCCCAACTACCGGGGTGACAACTCGTGGTTCTCCACTCAGGTTGACACTGTGGCCACCAAGGTG
AAGGATGCTCTGGAGTTTTTGGCTGCAAGCTGGCGTGGATGGGTTCCAGGTTCCGGACATAGAGAATCTGAAGGAT
GCATCCTCATTCTTGGCTGAGTGGCAAAATATCACCAAGGGCTTCAGTGGAGACAGGCTCTTGATTGCGGGGACT
AACTCCTCCGACCTTCAGCAGATCCTGAGCCTACTCGAATCCAACAAAGACTTGCTGTTGACTAGCTCATACCTG
TCTGATTCTGGTTCTACTCCCCAGCATACAAATCCCTAGTCACACAGTATTTGAATGCCACTGGCAATCGCTGG
TGCAGCTGGAGTTTGTCTCAGGCAAGGCTCCTGACTTCCTTCTTGCCGGCTCAACTTCTCCGACTCTACCAGCTG
ATGCTCTTACCCTGCCAGGGACCCCTCTTTTCAGCTACGGGGATGAGATTGGCCTGGATGCAGCTGCCCTTCCT
CCACAGCCTATGGAGGCTCCAGTCATGCTGTGGGATGAGTCCAGCTTCCTGACATCCCAGGGGCTGTAAGTGCC
AACATGACTGTGAAGGGCCAGAGTGAAGACCCTGGCTCCCTCCTTTCTTGTTCGGCGGGCTGAGTGACCAGCGG
AGTAAGGAGCGCTCCCTACTGCATGGGGACTTCCACGCGTTCTCCGCTGGGCCTGGACTCTTCTCCTATATCCGC
CACTGGGACCAGAATGAGCGTTTTCTGGTAGTGCTTAACTTTGGGGATGTGGGCCTCTCGGCTGGACTGCAGGCC
TCCGACCTGCCTGCCAGCGCCAGCCTGCCAGCCAAGGCTGACCTCCTGCTCAGCACCCAGCCAGGCCGTGAGGAG
GGCTCCCCCTCTGAGCTGGGACGCCTGAACTGGAGCCTCACGAAGGGCTGCTGCTCCGCTTCCCTACGCGGCC
TGACCTCAGCCTGACATGGACCCACTACCCTTCTCCTTTCC TTCCAGGCCCTTTGGCTTCTGATTTTTTTTCTC
TTTTTTAAACAAACAAACAACTGTTGCAGATTATGAGTGAACCCCAAATAGGGTGT

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FIGURE 104

MSQDTEVDMKEVELNELEPEKQPMNAASGAAMSLAEAEKNGLVKIKVAEDEAEAAAAAKFTGLSKEELLKVAGSP
GWVTRWALLLLFWLGWLGMLAGAVVIVRAPRCRELPAQKWWHTGPLYRIGDLQAFQGHGAGNLAGLKGRLDYL
SSLKVKGLVLGPIHKNQKDDVAQTDLLQIDPNFGSKEDFDSLLQSAKKKSIRVILDLTTPNYRGDNSWFSSTQVDTV
ATKVKDALEFWLQAGVDGFGQVRDIENLKDASSFLAEWQNTKGFSGDRLLIAGTNSSDLQQILSLLESNKDLLLT
SSYLSDSGSTPQHTKSLVTQYLNATGNRWCSWSLSQARLLTSFLPAQLLRLYQLMLFTLPGTPLFSYGDEIGLDA
AALPPQPMAPVMLWDESSFPDIPGAVSANMTVKGQSEDPGSLLSLFRRLSDQRSKERSLLHGDHFHAFSAGPGLF
SYIRHWDQNERFLVVLNFGDVGLSAGLQASDLPASASLPAKADLLLSTQPGREEGSPPELGRLKLEPHEGLLLRF
PYAA

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FIGURE 105A

GATCAATACTGAGGCCGCGTCGACCCCTTGAGCCGAGACCCCCCAGCCAGCCCCACCCACCCCGCA
CACGCCCCACCCCCCCACGACCCAGCCTCATACCGCACCAGCTGAGGCACCCAAGAGGATTACCCCTGGGGCC
CTCTCCCGCCCCCAAAAAGAGAAGATCCCTCTCCTGGCCCATCCCTTCCCTTCTTCCCTCCCCCTCCCCC
GAACTTTCCCTCTCGCATGCTTTTCCCTGCACCAACGATCGCTCTCGGATGCCGCTTGCTGGAAGCTGCGTT
AGGAGCGAGCGGGCGGTGGCGGCGGTGGCGGCGGCGGCGGCGGCGGAGTCTATGACGGGCAAACCTCGCC
GAGAAGCTGCCGGTGACCATGAGCAGTTTGCTAAACCAACTGCCTGACAATCTGTACCCGAGGAGATCCCCAGC
GCGCTCAACCTCTTCTCCGGCAGCAGCGACTCGGTAGTCCATTACAATCAGATGGCTACAGAGAATGTAATGGAC
ATCGGTCTGACCAACGAGAAGCCCAACCCGGAACCTCTTTACTCCGGCTCCTTCCAGCCAGCCCCGGGAACAAG
ACCGTGACCTACTTGGGAAAGTTTCGCTTCGACTCCCTTCCAACCTGGTGCCAGGACAACATCATTAGCCTCATG
AGCGCCGGCATCTTGGGGGTGCCCCGGCTTCAGGGGCGCTAAGCACGCAGACGTCCACGGCCAGCATGGTGACG
CCACCGCAGGGTGACGTGGAGGCCATGTATCCCGCTACCCCTACTCCAACCTGCGGCGACCTCTACTCAGAG
CCCGTGTCTTTCCACGACCCCCAGGGCAATCCCGGGCTCGCTATTCCCCCAGGATTACCAATCGGCCAAGCCG
GCGTTGGACAGCAATCTTCTCCCATGATTCTGACTACAACCTCTACCACCACCCCAACGACATGGGCTCCATT
CCGGAGCACAAGCCCTTCCAGGGCATGGACCCCATCCGGGTCAACCCGCCCCCTACTACCCCTCTGGAGACCATC
AAGGCATTCAAAGACAAGCAGATCCACCCGGGCTTTGGCAGCCTGCCCCAGCCGCCGCTCACCTCAAGCCCATC
CGGCCCCGCAAGTACCCCAACCGGCTAGCAAGACACCGCTCCACGAACGGCCCCACGCGTGCCCGGCCGAGGGC
TGCGACCGCCGTTTTCAGCCGTTTCGGACGAGCTGACCCGGCACCTGCGCATCCACACGGGCCACAAGCCCTTCCAG
TGCCGGATCTGCATGCGGAGCTTCAGCCGAGCGACCACTCACCCTCACATCCGCACTCATACGGGCGAGAAG
CCCTTTGCGCTGCGAGTTCTGCGGGCGCAAGTTTGCGCGCAGCGACGAGCGCAAGCGCCACGCCAAGATCCACCTC
AAGCAAAAGGAGAAGAAGGCGGAGAAGGGCGGTGCACCTCTGCATCCTCGCGCCCCCGGTGTGCTGGCCCCC
GTGGTCAACACCTGCGCCCTGAGGATCGGGCCCCCAGATCCCCACTTTTCCCTCCAGTGCTTCCGGCTGCTAGC
CTGAAAGCAGCGGGAAAGCCAGCCACGAGGCGTAGGGGCGCGCCCTGGCTCTCCATGGACGTGCGGCCCTT
GCTTCCCTTTCGATGCCCCGTTTCCCAACCTTTCACGCGCGCCAGCGGTGAGGGCCAGGGCTGGAGGCGCCTT
CCCCTCGCGGTCCCCCACTTAGCCAAAGCGTGGGGGCGGAAAGGTGGCGTCTAGCCCGCTTTGTTTCAATTGCGAT
CGCCTTGATCCAGGGGCGCGGGGCGGCCAAGGACCTGCAAGGGACTGAAGGCGGAGCCCATCAACCTCGC
CCGACCCAAACACCTCATTGTTTCCCCACGTCTCCTCTATACCCCTCGAAGACTCGAGAGGGGAGGGGGTA
AGGAGCGCACCAAGCGCAGAGCTTGCTGCCCCCGCACGCGCGCGCTGCGTGCGGGGATGCGCGCGAGTGT
GTGCGTGTGCGGT
ACTCTTGAGCTGAACTGGGCTGTGTTTACCCCAAACTCTTCCCCACCTCGGGTCCCCAAGCCGCTGGGAGATGTC
CCATGCTGGGGGTCCGCACGTGGCTGGAGGAGGTGGTCTTCCATCCGCTCTGAAATCATGTTTCTTAGAGAAATG
CCTCGGATGCCGCCGACGCGGTGCTGCTGCCGCCGCTTCCGGTTTGGCCCCCTCAGAACCCCTCCTTTTCTGAGCG
CTTCCCTCTTAGGCCTCAGGGCAGTTTGATCTGTGGGGAGAAAGAGCAGCCATCGCTGAGCCTGCCTTTTAAAT
ATATGTGTATTTTCTTAGCCCCACTTAAGAAATCTATGTTCTGAGTTTGGCCCCCTGCCCTCCCACTCCTTCCC
CTTTTCCCTCTAAACCTTCTCCCATCTTTTCAAATCTTTTCCAGAAAGGCAGGCTTCAACCAGCCACTCCA
GCTTTGTGTCTTCTCTCAATTACATAGCAATTTCTCCTTCCACCATCATGGGGAAGCTGGCTCTGCTTTTGCCC
TTTGTATCACCAACACAACAGATAGAATTTAAATATAAGTATATGGTGTGCGTGTGTGTGTGTGTGTGTGTGT
TGCATGCATGTGTATAAAGATGCACATGCGTACATATACATAACATACACACAATATGTATTCCTAGCAAAATAA
AATCTCTAAGGTACTTGGTTATCCAGTGCACTGCAACCGGAATAAAGAGAATTTGTAGGCGTATACAGCTTTAAAT
GATTTATTTTTTATGAAAATGTTAACTGATGAGATATATCTACATACGTGTGTGTGTGTGTGTGTGTGTGTGT
ACACATATCTGTACATATACATGTGAGTGATACATATACACATATACACATCTATGTATGGATATGTGTGTATA
CACATATACACATCTCTGTCCAAATTTCTCAAAGATATGGGGATTTTTTCATGAATCCATGTGGATGAATGAG
GTGTCTCCTTTCCATACCCAGTCTCACCTTCTCCCCACCTACCTCACCTCTTCTCAGGCACCCCTCTTCCCCAG
CTGTCTGCCAGCCCTTCTCGTACAGGGTGCTCCTTTGAAGTGGAGTAATAGGGAAGGTTGCTCTCTGCCACAG
CTTGACGATGGTCTTGACTGAATGTACTGTTCTGTTAGCGTTACTTCTCCTGTGGTCAGTAAGTTGCCAGAG
AGAAGGAACAAAGGTCTGGAGTTTACAGAATGTCTGTTTTTAAAGTCACTTTATGCGTTTTCCACTTTTTTCTTT
TTTAAAGAAAAGAAGTACCATTTTTGTTTTGTTTTGTTTTGATTTTTTGGTGGTGGATAAATAATACTAAAGGAC
TCTAGTGGAAGGGGGGATATCGAAGAGCAGGGGGTGTGAATTTCCAGGTACTTGGACTTTTTGTAGAAGTAGA
GAGAAGAAGATGAAGTTTGCCAGGAGGGCCCATATTTTTTCAGCTGAAGGGTAAATCTTTCTTTGACAGACAG

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FIGURE 105B

TATTTTGCTGAATACTTTTTATAATGTGATGATTATTAAGCAAAAATTTGGTCACTTCCAAGCTAGAAGG
AGGAATCAGATACCCTTTAATATTTTTTCCTCGCTCCTTCTGGTATATGCATGTCACTGCATGATAATTGAGTTT
TCCTTTGTTTTAATAAACTGTTCTCAGACATTAAGCTAACTAAGAGAAAAATAACTTTGTGCCAAAAGGTTG
TGCTATCCAGATTTTTTATATGTCTGCATGTTTAAAAAAAAAAGCAACAAAAGAAAATGCACTCTAACTTATG
TGAACTGAGAGAAAAAATCAGGTTTTAAACAGGAAAACCTATGGGGAATGATATTTTTTGAAAGACTTTTGTAT
AAAGTTGAGTACTTAGAAAAAGACAAACCAGATGTAATATATTTGTGGATGTTTTTATTCTGGATTTATAG
TACCTTATACTAAGGTTAAAAAATATGCTTGATATTGTGAAAAGGTGAAATTCTTCACCAACATTTCAATTTGCT
CCTTTGTCATATTGTAATGCCAATATAATATAGTTAATGAAAACAGCATTTTTAAAAACCGAAATATTGAAATGG
TGTAATGTTGTACCATTTGCACTGTGAGCAAATGCTAATACAGTAAATATATTGTGTTTGCTGACAATCAAAAAA
AAAAAAAAAAAAAA

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FIGURE 106

MTGKLAEKLPVTMSLLNQLPDNLYPEEIPSA LNLFSGSSDSVVHYNQMATENVMDIGLTNEKPNPELSYSGSFQ
PAPGNKTVTYLGKFAFDSPSNWCQDNII SLMSAGILGVPPASGALSTQTSTASMVQPPQGDVEAMYPALFPYSNC
GDLYSEPVSFHDPPQGNPGLAYSPQDYQSAKPALDSNLFFMIPDYNLYHHPNDMGSIPEHKPFQGMDFIRVNPPT
TPLETIKAFKDKQIHPPGFGSLPQPPLTLKPIRPRKYPNRPSKTPLHERPHACPAEGCDRRFSRDELTRHLRIHT
GHKPFQCRICMRFSRSDHLTTHIRTHTGKPFACEFCGRKFARSDEKRRHAKIHLKQKEKKAEGGAPSASSAP
PVSLAPVVTTCA

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FIGURE 107

CTGACCCAATACACTGAGTGAAGGAAGAGAGACAGAGGATCAAGGGCTTTAGACAGCACTCCTTCAATATGCAAT
CACAGAGAAAAGATGCGCCTGATCCAAGTTAATATCTCTAAGGTGAGAGCCTTCTTAGAGTCAGTTTGTGCAAAT
TTCACCTACTCTGTTCTTTTTCCATCCATCCCCCTGAGTCAGTTGGTTGAAGGGAGTTATTTTTTCAAGTGGAATT
CAAACAAAGCTCAAACCAGAACTGTAAATAGTGATTGCAGGAATTATTTTTCTAAACTGCTTTGCCCTTTCTCTC
ACTGCCTTTTATAGCCAATATAAAATGTCTCTTTGCACACCTTTTGTGTGGTTTTATATTGTAACACCATTTTTTC
TTTGAAACTATTGTATTTAAAGTAAGGTTTCATATTATGTCAGCAAGTAATTAACCTATGTTTAAAGGTGGCCA
TATCATGTACCAAAAGTTGCTGAAGTTTCTCTTCTAGCTGGTAAAGTAGGAGTTTGCATGACTTCACACTTTTTTT
TGCGTAGTTTCTTCTGTTGTATGATGGCGTGAGTGTGTCTTGGGTACCGCTGTGTACTACTGTGTGCCTAGAT
TCCATGCACTCTCGTTGTGTTTGAAGTAAATATTGGAGACCGGAGGGTAACAGGTTGGCCTGTTGATTACAGCTA
GTAATCGCTGTGTCTTGTTCGCCCCCTCCCTGACACCCAGCTTCCCAGGATGTGGAAAGCCTGGATCTCAGCT
CCTTGCCCCATATCCCTTCTGTAAATTTGTACCTAAAGAGTGTGATTATCCTAATTCAAGAGTCACTAAAACTCAT
CACATTATCATTGCATATCAGCAAAGGGTAAAGTCCTAGCACCAATTGCTTCACATACCAGCATGTTCCATTTC
AATTTAGAATTAGCCACATAATAAAATCTTAGAATCTTCCTTGAGAAAGAGCTGCCTGAGATGTAGTTTTGTAT
ATGGTTCCCCACCGACCATTTTTGTGCTTTTTTCTTGTTTTGTTTTGTTTTGACTGCACTGTGAGTTTTGTAGTG
TCCTCTTCTTGCCAAAAACAAACGCGAGATGAACTGGACTTATGTAGACAAATCGTGATGCCAGTGATCCTTCCCT
TTCTTCAGTTCAGCAATAATGAATGGTCAACTTTTTTAAAAATCTAGATCTCTCTCATTTCATTTCAATGTATTTT
TACTTTAAGATGAACCAAAATTATTAGACTTATTTAAGATGTACAGGCATCAGAAAAAAGAAGCACATAATGCCTT
TTGGTGCATGGCACCTCACTGTGAACATGTGTAACCACATATTAATATGCAATATTGTTTCCAATACCTTTCTAAT
ACAGTTTTTTTATAATGTTGTGTGTGGTGATTGTTTCAGGTCGAATCTGTTGTATCCAGTACAGCTTTAGGTCTTCA
GCTGCCCTTCTGGCGAGTACATGCACAGGATTGTAAATGAGAAATGCAGTCATATTTCCAGTCTGCCTCTATGAT
GATGTTAAATTATTGCTGTTTAGCTGTGAACAAGGGATGTACCACTGGAGGAATAGAGTATCCTTTTGTACACAT
TTTGAAATGCTTCTTCTGTAGTGATAGAACAATAAATGCAACGAATACTCTGTCTGCCCTATCCCGTGAAGTCC
ACACTGGCGTAAGAGAAGGCCAGCAGAGCAGGAATCTGCCTAGACTTTCTCCAATGAGATCCCAATATGAGAG
GGAGAAGAGATGGGCCTCAGGACAGCTGCAATACCACTTGGGAACACATGTGGTGTCTTGATGTGGCCAGCGCAG
CAGTTCAGCACAAACGTACCTCCCATCTACAACAGTGTGGACGTGGGAATTCTAAGTCCCAGTCTTGAGGGTGGG
TGGAGATGGAGGGCAACAAGAGATACATTTCCAGTTCTCCACTGCAGCATGCTTCAGTCATTCTGTGAGTGGCCG
GGCCCAGGGCCCTCACAATTTCACTACCTTGCTTTTTACATAGTCATAAGAATTATCCTCAACATAGCCTTTTGA
CGCTGTAAATCTTGAGTATTCATTTACCCTTTTTCTGATCTCTGGAAACAGCTGCCTGCCTGCATTGCACTTCTC
TTCCCGAGGAGTGGGGTAAATTTAAAAGTCAAGTTATAGTTTGGATGTTAGTATAGAATTTTGAATTTGGGAATT
AAAAATCAGGACTGGGGACTGGGAGACCAAAAAATTTCTGATCCCATTTCTGATGGATGTGTACACCTTTTCTGT
CAAAATAAAATGTCTTGGAGGTTATGACTCCTTGGTGAAAAAAA

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FIGURE 108

MCHTFSVKIKCLGGYDSLK

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FIGURE 109

TGCTGCGAACCACGTGGGTCCCGGGCGCGTTTTTCGGGTGCTGGCGGCTGCAGCCGGAGTTCAAACCTAAGCAGCTG
GAAGGAACCAATGGCCAACTGTGAGCGTACCTTCATTGCGATCAAACCAGATGGGGTCCAGCGGGGTCTTGTGGGA
GAGATTATCAAGCGTTTTTGAGCAGAAAGGATTCCGCCTTGTGGTCTGAAATTCATGCAAGCTTCCGAAGATCTT
CTCAAGGAACACTACGTTGACCTGAAGGACCGTCCATTCTTTGCCGGCCTGGTGAAATACATGCACTCAGGGCCG
GTAGTTGCCATGGTCTGGGAGGGGCTGAATGTGGTGAAGACGGGCCGAGTCATGCTCGGGGAGACCAACCCTGCA
GACTCCAAGCCTGGGACCATCCGTGGAGACTTCTGCATACAAGTTGGCAGGAACATTATACATGGCAGTGATTCT
GTGGAGAGTGCAGAGAAGGAGATCGGCTTGTGGTTTTCACCCCTGAGGAACTGGTAGATTACACGAGCTGTGCTCAG
AACTGGATCTATGAATGACAGAGGAGGGCAGACCACATTGCTTTTACATCCATTTCCCCTCCTTCCCATGGGCAGA
GGACCAGGCTGTAGGAAAATCTAGTTATTTACAGGAACTTCATCATAATTTGGAGGGAAGCTCTTGGAGCTGTGAG
TTCTCCCTGTACAGTGTTACCATCCCCGACCATCTGATTAAATGCTTCCTCCCAGC

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FIGURE 110

MANCERTFIAIKPDGVQORGLVGEI I KRFEQKGFRLVGLKFMQASEDLLKEHYVDLKDRPFFAGLVKYMHS GPVVA
MVWEGLVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSDSVESAEKEIGLWFHPEELVDYTSCAQNWI
YE

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FIGURE 111A

CGAGCGCAGCGGAGCCTGGAGAGAAGGCGCTGGGCTGCGAGGGCGCGAGGGGCGAGGGGCGAGGGGCGAACCGGA
CCCCGCCCCGACCCATGCGCGCCGTCGCCGTCTGGGCCGCGCTGGCCGTCGGAAGCTCTGGGCTGCGGCGC
ACGCCCTTGCCCGCCAGGTGGCATTACACCCCTACGCCCGGAGCCCCGGGAGCACATGCCGGCTCAGAGAATACT
ATGACCAGACAGCTCAGATGTGCTGCAGCAAATGCTCGCCGGGCCAACATGCAAAAGTCTTCTGTACCAAGACCT
CGGACACCGTGTGTGACTCCTGTGAGGACAGCACAACACCCAGCTCTGGAAGTGGGTTCCTGAGTGCTTGAGCT
GTGGCTCCCGCTGTAGCTCTGACCAGGTGGAAGCTCAAGCCTGCACTCGGGAACAGAACCAGCATCTGCACCTGCA
GGCCCGGCTGCTACTGCGCGCTGAGCAAGCAGGAGGGGTGCCGGCTGTGCGCGCCGCTGCGCAAGTGCCGCCCGG
GCTTCGGCGTGGCCAGACCAGGAAGTGAACATCAGACGTGGTGTGCAAGCCCTGTGCCCCGGGGACGTTCTCCA
ACACGACTTCATCCACGGATATTTGCAGGCCCCACAGATCTGTAACGTGGTGGCCATCCCTGGGAATGCAAGCA
TGGATGCAGTCTGCACGTCCACGTCCCCACCCGGAGTATGGCCCCAGGGGCAGTAACTTACCCAGCCAGTGT
CCACACGATCCCAACACACGCAGCCAACTCCAGAACCCAGCACTGCTCCAAGCACCTCCTTCTGCTCCCAATGG
GCCCCAGCCCCCAGCTGAAGGGAGCACTGGCGACTTCGCTCTTCCAGTTGGACTGATTGTGGGTGTGACAGCCT
TGGGTCTACTAATAATAGGAGTGGTGAAGTGTGTCATCATGACCCAGGTGAAAAAGAAGCCCTTGTGCCTGCAGA
GAGAAGCCAAAGGTGCCTCACTTGCTGCTGCCGATAAGGCCCGGGGTACACAGGGCCCCGAGCAGCAGCACCTGTGA
TCACAGCGCCGAGCTCCAGCAGCAGCTCCCTGGAGAGCTCGGCCAGTGCGTTGGACAGAAGGGCGCCCACTCGGA
ACCAGCCACAGGCACCAGGCGTGGAGGCCAGTGGGGCCGGGGAGGCCCGGGCCAGCACCGGGAGCTCAGATTCTT
CCCCTGGTGGCCATGGGACCCAGGTCAATGTACCTGCATCGTGAACGTCTGTAGCAGCTCTGACCACAGCTCAC
AGTGCTCCTCCCAAGCCAGCTCCACAATGGGAGACACAGATTCAGCCCCCTCGGAGTCCCCGAAGGACGAGCAGG
TCCCCTTCTCCAAGGAGGAATGTGCCTTTTCGGTACAGCTGGAGACGCCAGAGACCCTGCTGGGGAGCACCGAAG
AGAAGCCCCCTGCCCTTGGAGTGCCTGATGCTGGGATGAAGCCAGTTAACCAGGCCGGTGTGGGCTGTGTCGTA
GCCAAGGTGGGCTGAGCCCTGGCAGGATGACCTGCGAAGGGGCCCTGGTCTTCCAGGGCCCCACCACTAGGAC
TCTGAGGCTCTTTCTGGGCCAAGTTCTCTAGTGCCCTCCACAGCCGAGCCTCCTCTGACCTGCAGGCCAAGA
GCAGAGGCAGCGAGTTGGGGAAAGCCTCTGCTGCCATGGTGTGTCCTCTCGGAAGGCTGGCTGGGCATGGACGT
TCGGGGCATGCTGGGGCAAGTCCCTGACTCTCTGTGACCTGCCCGCCAGCTGCACCTGCCAGCCTGGCTTCTG
GAGCCCTTGGGTTTTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTTCTCCCCCTGGGCTCTGCCAGCTCTGGCTT
CCAGAAAACCCCAGCATCCTTTTTCTGCAGAGGGGCTTTCTGGAGAGGAGGGATGCTGCCTGAGTCACCATGAAG
ACAGGACAGTGCTTCAGCCTGAGGCTGAGACTGCGGGATGTCCTGGGGCTCTGTGTAGGGAGGAGGTGGCAGCC
CTGTAGGGAACGGGGTCCCTTCAAGTTAGCTCAGGAGGCTTGGAAGCATCACCTCAGGCCAGGTGCAGTGGCTCA
CGCCTATGATCCAGCACTTTGGGAGGCTGAGGCGGGTGGATCACCTGAGGTTAGGAGTTCGAGACCAGCCTGGC
CAACATGGTAAAACCCCATCTCTACTAAAAATACAGAAATTAGCCGGGCGTGGTGGCGGGCACCTATAGTCCAG
CTACTCAGAAGCCTGAGGCTGGGAAATCGTTTGAACCCGGGAAGCGGAGGTTGCAGGGAGCCGAGATCACGCCAC
TGCACCTCCAGCCTGGGCGACAGAGCGAGAGTCTGTCTCAAAAGAAAAAAAAAAAAAGCACCGCCTCCAAATGCTAA
CTTGTCCTTTTGTACCATGGTGTGAAAGTCAGATGCCAGAGGGCCCAGGCAGGCCACCATATTAGTGCTGTGG
CCTGGGCAAGATAACGCACTTCTAACTAGAAATCTGCCAATTTTTTAAAAAAGTAAGTACCACTCAGGCCAACAA
GCCAACGACAAAGCCAAACTCTGCCAGCCACATCCAACCCCCACCTGCCATTGTCACCTCCGCCTTCACTCCG
GTGTGCCTGCAGCCCCGCGCCTCCTTCTTGTCTGTCTAGGCCACACCATCTCCTTTAGGGAATTTAGGAAT
AGAGATGACTGAGTCTCTGATGCCATCTCTCTACTCCTACCTCAGCCTAGACCCTCCTCCTCCCCAGAGGGGTG
GGTTCCTCTTCCCCACTCCCCACCTTCAATTCTGGGCCCAAACGGGCTGCCCTGCCACTTTGGTACATGGCCA
GTGTGATCCCAAGTGCCAGTCTTGTGTCTGCGTCTGTGTTGCGTGTGCTGGGTGTGTGTAGCCAAGGTTCGGTAAG
TTGAATGGCTGCCTTGAAGCCACTGAAGCTGGGATTCTTCCCCATTAGAGTCAGCCTTCCCCCTCCAGGGCCA
GGGCCCTGCAGAGGGGAAACCAGTGTAGCCTTGCCCGGATTCTGGGAGGAAGCAGGTTGAGGGGCTCCTGGAAAG
GCTCAGTCTCAGGAGCATGGGGATAAAGGAGAAGGCATGAAATGTCTAGCAGAGCAGGGGCAGGGTGATAAATT
GTTGATAAATTCCACTGGACTTGAGCTTGGCAGCTGAACATATTGGAGGGTGGGAGAGCCAGCCATTACCATGGA
GACAAGAAGGGTTTTTCCACCCTGGAATCAAGATGTGAGACTGGCTGGCTGCAGTGACGTGCACCTGTACTCAGGA
GGCTGAGGGGAGGATCACTGGAGCCCAGGAGTTTGGGCTGCAGCGAGCTATGATCGCGCCACTACACTCCAGCC
TGAGCAACAGAGTGAGACCCTGTCTCTTAAAGAAAAAAAAAAGTCAGACTGCTGGGACTGGCCAGGTTTCTGCCCA
CATTGGACCCACATGAGGACATGATGGAGCGCACCTGCCCCCTGGTGGACAGTCCTGGGAGAACCTCAGGCTTCC
TTGGCATCACAGGGCAGAGCCGGGAAGCGATGAATTTGGAGACTCTGTGGGGCCTTGGTTCCCTTGTGTGTGTGT

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FIGURE 111B

GTTGATCCCAAGACAATGAAAGTTTGCACTGTATGCTGGACGGCATTCTGCTTATCAATAAACCTGTTTGTTT
AAAAAAA

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FIGURE 112

MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTV
DSCEDSTYTQLWNWVPECLSCGSRCSDDQVETQACTREQNRICRPGWYCALSQEGCRLCAPLRKCRPGFGVA
RPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQ
HTQPTPEPSTAPSTSFLPMGPPSPAEGSTGDFALPVGLIVGTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV
PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQAPGVEASGAGEARASTGSSDSSPGGH
GTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDS SPSESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLP
LGVPDAGMKPS

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FIGURE 113A

GCCCTGCTTCCCCTTGACCTGCGCCGGGCGGCC**ATG**GACTTGTACAGCACCCCGGCCGCTGCGCTGGACAGGTT
CGTGGCCAGAAGGCTGCAGCCGCGGAAGGAGTTCGTAGAGAAGGCGCGCGCTCTGGGCGCCCTGGCCGCTGC
CCTGAGGGAGCGCGGGGGCCGCTCGGTGCTGCTGCCCCGCGGGTGTGAAACTGTCAAGGGAGGCTCCTCGGG
CCGGGGCACAGCTCTCAAGGGTGGCTGTGATTCTGAACCTGTTCATCTTCTCGACTGCTTCAAGAGCTATGTGGA
CCAGAGGGCCCCGCGTGCAGAGATCCTCAGTGAGATGCGGGCATCGCTGGAATCCTGGTGGCAGAACCAGTCCC
TGGTCTGAGACTCACGTTTCTGAGCAGAGCGTGCCTGGGGCCCTGCAGTTCGCGCTGACATCCGTAGATCTTGA
GGACTGGATGGATGTTAGCCTGGTGCCTGCCTTCAATGTCTGGGTGAGGCCGGCTCCGCGGTCAAACCCAAAGCC
ACAAGTCTACTCTACCCCTCTCAACAGTGGCTGCCAAGGGGGCGAGCATGCGGCCTGCTTCACAGAGCTGCGGAG
GAACCTTGTGAACATTCGCCCAGCCAAGTTGAAGAACCTAATCTTGCTGGTGAAGCACTGGTACCACCAGGTGTG
CCTACAGGGGTTGTGGAAGGAGACGCTGCCCCCGTCTATGCCCTGGAATTGCTGACCATCTTCGCTGGGAGCA
GGGCTGTAAGAAGGATGCTTTCAGCCTAGGCGAAGGCCCTCCGAACCTGTCTGGGCTGATCCAACAGCATCAGCA
CCTGTGTGTTTTCTGGACTGTCAACTATGGCTTCGAGGACCTGCAGTTGGGCAGTTCCTGACGCGGCAGGTTAA
GAGACCCAGGCCTGTGATCCTGGACCCAGCTGACCCACATGGGACCTGGGGAATGGGGCAGCCTGGCACTGGGA
TTTGCATGCCCAGGAGGCAGCATCCTGCTATGACCACCCATGCTTCTGAGGGGATGGGGACCCAGTGCAGTC
TTGGAAGGGGCCGGGCCCTTCCACGTGCTGGATGCTCAGGTTTGGGCCACCCATCCAGCTAGACCCTAACCAGAA
GACCCCTGAAAACAGCAAGAGCCTCAATGCTGTGTACCCAAGAGCAGGGAGCAAACCTCCCTCATGCCAGCTCC
TGGCCCCACTGCGGAGCCAGCATCGTACCCCTCTGTGCCGGGAATGGCCTTGGACCTGTCTCAGATCCCCACCA
GGAGCTGGACCGCTTCATCCAGGACCACCTGAAGCCGAGCCCCCAGTTCCAGGAGCAGGTGAAAAGGCCATCGA
CATCATCTTGCGCTGCCTCCATGAGAACTGTGTTACAAGGCCTCAAGAGTCAGTAAAGGGGGCTCATTGGCCG
GGGCACAGACCTAAGGGATGGCTGTGATGTTGAACATCATCTTCTCAACTGCTTCACGGACTACAAGGACCA
GGGGCCCCGCGCGCAGAGATCCTTGATGAGATGCGAGCGCACGTAGAATCCTGGTGGCAGGACCAGGTGCCAG
CCTGAGCCTTCAGTTTCTGAGCAGAATGTGCCTGAGGCTCTGCAGTTCCAGCTGGTGTCCACAGCCCTGAAGAG
CTGGACGGATGTTAGCCTGCTGCCTGCCTTCGATGCTGTGGGGCAGCTCAGTTCTGGCAGCAAACCAAATCCCCA
GGTCTACTCGAGGCTCCTCACCAGTGGCTGCCAGGAGGGCGAGCATAAGGCCTGCTTCGCAGAGCTGCGGAGGAA
CTTCATGAACATTTCGCCCTGTCAAGCTGAAGAACCTGATTCTGCTGGTGAAGCACTGGTACCGCCAGGTTGCGGC
TCAGAACAAAGGAAAAGGACCAGCCCTGCCTCTTGCCCCAGCCTATGCCCTGGAGCTCCTCACCATCTTTGC
CTGGGAGCAGGGCTGCAGGCAGGATTGTTTCAACATGGCCCAAGGCTTCCGGACGGTGTGGGGCTCGTGCAACA
GCATCAGCAGCTCTGTGTCTACTGGACGGTCAACTATAGCACTGAGGACCCAGCCATGAGAATGCACCTTCTTGG
CCAGCTTCGAAAACCCAGACCCCTGGTCTTGACCCCGCTGATCCCACCTGGAACGTGGGCCACGGTAGCTGGGA
GCTGTTGGCCCAGGAAGCAGCAGCGCTGGGGATGCAGGCCTGCTTCTGAGTAGAGACGGGACATCTGTGCAGCC
CTGGGATGTGATGCCAGCCCTCCTTTACCAAACCCAGCTGGGGACCTTGACAAGTTCATCAGTGAATTTCTCCA
GCCCCAACCGCCAGTTCTTGCCCAAGGTGAACAAGGCCGTTGATACCATCTGTTCATTTTTGAAGGAAAACCTGCTT
CCGGAATTCTCCCATCAAAGTGATCAAGGTGGTCAAGGGTGGCTCTTCAGCCAAAGGCACAGCTCTGCGAGGCCG
CTCAGATGCCGACCTCGTGGTGTTCCTCAGCTGCTTCAGCCAGTTCACTGAGCAGGGCAACAAGCGGGCCGAGAT
CATCTCCGAGATCCGAGCCAGCTGGAGGCATGTCAACAGGAGCGGCAGTTGAGGTCAAGTTTGAAGTCTCCAA
ATGGGAGAATCCCCGCGTGTGAGCTTCTCACTGACATCCAGACGATGCTGGACCAGAGTGTGGACTTTGATGT
GCTGCCAGCCTTTGACGCCCTAGGCCAGCTGGTCTCTGGCTCCAGGCCAGCTCTCAAGTCTACGTCGACCTCAT
CCACAGCTACAGCAATGCGGGCGAGTACTCCACCTGCTTCACAGAGCTACAACGGGACTTCATCATCTCTCGCCC
TACCAAGCTGAAGAGCCTGATCCGGCTGGTGAAGCACTGGTACCAGCAGTGTACCAAGATCTCCAAGGGGAGAGG
CTCCCTACCCCCACAGCACGGGCTGGAACCTCTGACTGTGTATGCCTGGGAGCAGGGCGGGAAGGACTCCCAGTT
CAACATGGCTGAGGGCTTCCGCACGGTCTTGAGCTGGTACCCAGTACCGCCAGCTCTGTATCTACTGGACCAT
CAACTACAACGCCAAGGACAAGACTGTTGGAGACTTCTGAAACAGCAGCTTCAGAAGCCCCAGGCCTATCATCCT
GGATCCGGCTGACCCGACAGGCAACCTGGGCCACAATGCCCGCTGGGACCTGCTGGCCAAGGAAGCTGCAGCCTG
CACATCTGCCCTGTGCTGCATGGGACGGAATGGCATCCCCATCCAGCCATGGCCAGTGAAGGCTGCTGTG**TGAAG**
TTGAGAAAATCAGCGGTCTACTGGATGAAGAGAAGATGGACACCAGCCCTCAGCATGAGGAAATTCAGGGTCCC
CTACCAGATGAGAGAGATTGTGTACATGTGTGTGTGAGCACATGTGTGCATGTGTGTGCACACGTGTGCATGTGT
GTGTTTTAGTGAATCTGCTCTCCAGCTCACACACTCCCTGCCTCCCATGGCTTACACACTAGGATCCAGACTC
CATGGTTTGACACCAGCCTGCGTTTGCAGCTTCTCTGTCACTTCCATGACTCTATCCTCATACCACCAGTGTGC

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FIGURE 113B

TTCCACCCAGCTGAGAATGCCCCCTCCTCCCTGACTCCTCTCTGCCCATGCAAATTAGCTCACATCTTTCCTCC
TGCTGCAATCCATCCCTTCTCCCATTTGGCCTCTCCTTGCCAAATCTAAATACTTTATATAGGGATGGCAGAGAG
TTCCCATCTCATCTGTCAGCCACAGTCATTTGGTACTGGCTACCTGGAGCCTTATCTTCTGAAGGGTTTTAAAGA
ATGGCCAATTAGCTGAGAAGAATTATCTAATCAATTAGTGATGTCTGCCATGGATGCAGTAGAGGAAAGTGGTGG
TACAAGTGCCATGATTGATTAGCAATGTCTGCACTGGATATGGAAAAAGAAGGTGCTTGCAGGTTTACAGTGTA
TATGTGGGCTATTGAAGAGCCCTCTGAGCTCGGTTGCTAGCAGGAGAGCATGCCCATATTGGCTTACTTTGTCTG
CCACAGACACAGACAGAGGGAGTTGGGACATGCATGCTATGGGGACCCTCTTGTTGGACACCTAATTGGATGCCT
CTTCATGAGAGGCCCTCCTTTTCTTCACCTTTTATGCTGCACTCCTCCCTTAGTTTACACATCTTGATGCTGTGGC
TCAGTTTGCCTTCCTGAATTTTTATTGGGTCCCTGTTTTCTCTCCTAACATGCTGAGATTCTGCATCCCCACAGC
CTAAACTGAGCCAGTGGCCAAACAACCGTGCTCAGCCTGTTTCTCTCTGCCCTCTAGAGCAAGGCCACCAGGTC
CATCCAGGAGGCTCTCCTGACCTCAAGTCCAACAACAGTGTCCACACTAGTCAAGGTTTCAGCCAGAAAAACAGAA
AGCACTCTAGGAATCTTAGGCAGAAAGGGATTTTATCTAAATCACTGGAAAGGCTGGAGGAGCAGAAGGCAGAGG
CCACCCTGGACTATTGGTTTCAATATTAGACCAC TGTAGCCGAATCAGAGGCCAGAGAGCAGCCACTGCTACTG
CTAATGCCACCCTACCCCTGCCATCACTGCCCCACATGGACAAAACCTGGAGTCGAGACCTAGGTTAGATTCTTG
CAACCACAAACATCCATCAGGGATGGCCAGCTGCCAGAGCTGCGGGAAGACGGATCCCACCTCCCTTTCTTAGCA
GAATCTAAATTACAGCCAGACCTCTGGCTGCAGAGGAGTCTGAGACATGTATGATTGAATGGGTGCCAAGTGCCA
GGGGGCGGAGTCCCCAGCAGATGCATCCTGGCCATCTGTTGCGTGGATGAGGGAGTGGGTCTATCTCAGAGGAAG
GAACAGGAAACAAAGAAAGGAAGCCACTGAACATCCCTTCTCTGCTCCACAGGAGTGTCTTAGACAGCCTGACTC
TCCACAAACCACTGTTAAACTTACCTGCTAGGAATGCTAGATTGAATGGGATGGGAAGAGCCTTCCCTCATTAT
TGTCATTCTTGGAGAGAGGTGAGCAACCAAGGGGAAGCTCCTCTGATTACCTAGAACCTGTTCTCTGCCGTCTTT
GGCTCAGCCTACAGAGACTAGAGTAGGTGAAGGGACAGAGGACAGGGCTTCTAATACCTGTGCCATATTGACAGC
CTCCATCCCTGTCCCCCATCTTGGTGCTGAACCAACGCTAAGGGCACCTTCTTAGACTCACCTCATCGATACTGC
CTGGTAATCCAAAGCTAGAACTCTCAGGACCCCAAACCTCCACCTCTTGGATTGGCCCTGGCTGCTGCCACACACA
TATCCAAGAGCTCAGGGCCAGTTCTGGTGGGCAGCAGAGACCTGCTCTGCCAAGTTGTCCAGCAGCAGAGTGGCC
CTGGCCTGGGCATCACAAGCCAGTGATGCTCCTGGGAAGACCAGGTGGCAGGTGCGAGTTGGGTACCTTCCATTCT
CCACCACACAGACTCTGGGCCTCCCCGCAAATGGCTCCAGAATTAGAGTAATTATGAGATGGTGGGAACCAGAG
CAACTCAGGTGCATGATACAAGGAGAGGTTGTCATCTGGGTAGGGCAGAGAGGAGGGCTTGCTCATCTGAACAGG
GGTGTATTTCAATCCAGGCCCTCAGTCTTTGGCAATGGCCACCCTGGTGTGGCATATTGGCCCCACTGTAACTT
TTGGGGGCTTCCCGGTCTAGCCACACCCTCGGATGGAAAGACTTGACTGCATAAAGATGTCAGTTCTCCCTGAGT
TGATTGATAGGCTTAATGGTCACCCTAAAAACCCACATATGCTTTTCGATGGAACCAGATAAGTTGACGCTAA
AGTTCTTATGGAAAAATACACACGCAATAGCTAGGAAAAACAGGGAAAGAAGAGTTCTGAGCAGGGCCTAGTCT
TAGCCAATATTAAACATACTATGAAGCCTCTGATACTTAAACAGCATGGCGCTGGTACGTAAATAGACCAATGC
AGTTAGGTGGCTCTTTCCAAGACTCTGGGGAAAAAAGTAGTAAAAAGCTAAATGCAATCAATCAGCAATTGAAAG
CTAAGTGAGAGAGCCAGAGGGCCTCCTTGGTGGTAAAAGAGGGTTGCATTTCTTGAGCCAGAGGCAGAGAAAG
TGAAGACCAAGTCCAGAATGAATCCTAAGAAATGCAGGACTGCAAAGAAATTGGTGTGTGTGTGTGTGTGTGTG
TGTGTGTGTGTTAATTTTTTAAAAAGTTTTTATTCGAATCCGCG

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FIGURE 114

MDLYSTPAAALDRFVARRLQPRKEFVEKARRALGALAAALRERGGRLGAAAPRVLKTVKGGSSGRGTALKGGCDS
ELVIFLDCFKSYVDQRARRAEILSEMRALESWWQNPVPGRLRTFPEQSVPGALQFRLTSVDLEDWMDVSLVPAF
NVLGQAGSAVKPKPQVYSTLLNSGCQGGEGAACFTELRRNFVNIRPAKLKNLILLVKHWYHQVCLQGLWKETLPP
VYALELLTIFAWEQGCKDAFSLGEGRLRTVLGLIQHQHLCVFWTVNYGFEDPAVGQFLQRHVKRPRPVILDPAD
PTWDLGNGAAWHWDLHAQEAAASYDHP CFLRGMGDFVQSWKGPGLPRAGCSGLGHP IQLDPNQKTPENSKSLNAV
YPRAGSKPPSCPAPGPTAEFASYPVPGMALDLSQIPTKELDRFIQDHLKPS PQFQEQVKAIDIILRCLHENCV
HKASRVSKGGSFGRGTDLRDGCDELIIIFLNCFTDYKDQGPRAEILDEMRAHVESWWQDQVPSLSLQFPEQNVP
EALQFQLVSTALKSWTDVSLPAPDAVQQLSSGTPNPQVYSRLTSGCQEGEHKACFAELRRNFMNIRPVKLKN
LILLVKHWYRQVAAQNKGGPAPASLPAYALELLTIFAWEQGCRQDCFNMAQGFRTVLGLVQQHQQLCVYWTVN
YSTEDPAMRMHLLGQLRKPRPLVLDPADPTWNVGHGSWELLAQEAALGMQACFLSRDGT SVQPWDVMPALLYQT
PAGDLDFI SEFLQPNRQFLAQVNKAVDTIC SFLKENCFRNSPIKVIKVVKGGSSAKGTALRGRSDADLVVFLSC
FSQFTEQGNKRAEII SEIRAQLEACQGERQFEVKFEVSKWENPRVLSFSLTSQTMLDQSVDFDVLPAFDALGQLV
SGSRPSSQVYVDLIHSYSNAGEYSTCFTELQDFII SRPTKLKSLIRLVKHWYQQCTKISKGRGSLPPQHGLELL
TVYAWEQGGKDSQFNMAEGFRTVLELVTQYRQLCIYWTINYNKDKTVGDFLKKQLQKPRPIILDPADPTGNLGH
NARWDLAKEAAACTSALCCMGRNGIP IQPWPVKA AV

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FIGURE 115A

GAAGTATAAGTGGGATTTTCACCAAAACCTATCCTTCCCCAGACTCCAGTGACAGTTTAAACGGTCAGCTGCATC
AAGGCTTGTGTACTGTGCAGTCTTAAAGGCCACCACTCCTGTCCATCTCGGTGAAATTGATGGTGGAGCAAAAGG
GAGTTTAGGTGGTTCCGGTCTGGGGAGAAGACGTGCAGGGTTTCAGATGCGAAAGTCGCACCCAACCGCTTCACT
CGGGCTCTAGGCCATCCGCAGGGGGCCCTGCTTCCTTCCACCTGCGAGCTTTTTCTGCAGAATGCGGGAAGCCGCC
GCCGCCGCCACAGAGGAGGGGGCGGAGGCAGAGGCGGAGGCGGCACCCAGGGGGCCGGGCGAGGGAGGCCGGGAC
CATCGCAGTGACAATTTATTTTCTGCAGCAGCGGCAGCAGGGACGGTTGCTGCAGGTTGCGGGTCCGCCGGCCT
GCGCGTGGGCTTGCAGGAGCGCTGTTCTGCTCCCTGCGCTGGGGTGTCCGACAGCGAGGAGGAGAACGACGCACGG
AGCCCCGCGGACTGGAACAGCAAAGCTCCATCTGTGCGCAGAGGAGAAGGGGGAGGAGGCACGCCGAGGCCAAA
CGAGCGGACGCCCTCGTCGCGGGGTGCCGGTATCACCCCGCTGCAACGCCTTCCAGCAAAAGCCACCGCGGCCCGG
GTTGCAGCAGCCGGACGGATGCCAAGGCCACACGGCAGCCACGGGGGCGAGCCGTGCGAGTCGCCGTCCACACGG
GCTGCGGACACCAAGGGTTGCTAATGAAGTGATTGAGAAGAAACAGTGAACATCCTCATTTCACAGATAAGACAA
CATGGATCAGCCTTTTACTGTGAATTCTCTGAAAAAGTTAGCTGCTATGCCTGACCATACAGATGTTTCCCTAAG
CCCAGAAGAGCGAGTCCGTGCCCTAAGCAAGCTTGTTGTAATATCACCATCAGTGAAGACATCACTCCACGACG
TTACTTTAGGTCTGGAGTAGAGATGGAGAGGATGGCGTCTGTGATTTGGAAGAAGGAAATTTGGAATATGCCTT
TGTTCTTTATAATAAATTTATAACCTTATTTGTAGAAAAGCTTCCTAACCATCGAGATTACCAGCAATGTGCAGT
ACCTGAAAAGCAGGATATTATGAAGAACTGAAGGAGATTGCATTCCTAAGGACAGATGAATTGAAAAACGACCT
TTTAAAGAAATATAACGTAGAAATACCAAGAATATTGCAAAAGCAAAAACAAATATAAGCTGAAATTTCTCAAAAA
ATTGGAGCATCAGAGATTGATAGAGGCAGAAAGGAAGCGGATTGCTCAGATGCGCCAGCAGCAGCTAGAATCGGA
GCAGTTTCTGTTTTTCGAAGATCAACTCAAGAAGCAAGAGTTAGCCCCGAGGTCAAATGCGAAGTCAGCAAAACCTC
AGGGCTGTGACAGCAGATTGATGGGAGCGCTTTGTCTGCTTTTCCACACACCAGAACAATTCCTTGCTGAATGT
ATTTGCAGATCAACCTAATAAAAGTGATGCAACCAATTATGCTAGCCACTCTCCTCCTGTAAACAGGGCCTTAAC
GCCAGCTGCTACTCTAAGTGCTGTTTCTGAGATTTAGTGGTTGAAGGACTGCGATGTGTAGTTTGGCAGAAGATCT
TTGCCACAAATTTCTGCAACTGGCAGAATCTAATACAGTGAGAGGAATAGAAACCTGTGGAATACTCTGTGGAAA
ACTGACACATAATGAATTTACTATTACCCATGTAATTGTGCCAAAGCAGTCTGCGGGACCAGACTATTGTGACAT
GGAGAATGTAGAGGAATTATTCAATGTTTCTGAGTCAACATGATCTCCTCACTCTAGGATGGATCCATACACATCC
CACTCAAACTGCATTTTTATCCAGCGTTGATCTTCACACTCACTGTTCTATCAACTCATGTTGCCAGAGGCCAT
TGCCATTGTTTGCTCACCAAAGCATAAAGACACTGGCATCTTCAGGCTCACCAATGCTGGCATGCTTGAGGTTTC
TGCTTGTAAGAAAAAGGGCTTTTATCCACACACCAAGGAGCCAGGCTGTTTCTGATTTAGAAATTCCTTTCTGG
GATAATTTCTGGCACTGCTTTGGAGATGGAGCCCCGAAAATTGGCTATGGACCAATGGATTCCCCTCTTGGG
GATCTCTAGGTATCATCACCATCTGAACAGCTCTGAGAGAGACAAGAAGTGGAATGGAGAAGGTGATTAGGTAA
TCCAAGAATTGCCAGGCGAACAATTGTGAAAATCTTTCATAGAGTTCCCGATGAAAACAACCTCTTTCTTGTAGC
CATTATCTCTGCCTTTTCTTTCTAAAGAAAAACACGTCATTTTCTGATTATCAGTTTCTCAAGTACTCATGG
ATGTGAGGCCAGGTACCTGTACCTTGGCTCTGTTTGGGATGCAATGTTGTGTTTGTACCACTTCCCATTTCCC
CAAAAGCATCTTTAACATAGACCATTCATTCTTCAAGTTCAAAATGCTTAAGCTGAACTAACCTCAAAGGGCCCT
CATTAAATTTACAGACATTTGAATAACACCCATATTCAATTTCTGCTACTGAACCAAGCCTTTTCCAAAAAATCA
TCTAGCAAACTGTTTTTGGCAGGCCAAATATTAACAGGTATATATATTTGCATACATAAATATTTACCTCTATGT
CTGTGTGTTTTTGTATGAGACAGAGTCTCACTCTGTCGCCAGGCTGGAGTGCAGTGGCACAGTCTCAGCTCA
CTGCAACCTCCACCTCCCAGGTTCAAGCGATTCTCATGCCTCAGCCTCCCGAGTAGCGAGGACTACAGGCGTGCA
CCACCACGCCCAGCTAATTTTGTATTTTGTAGAGATGGGGTTTTACCCTGTTGGCCAGGGTGGTCTCGAATT
CCTGACCTCTGATGATCTGCCCGCCTGGACCTCTCAAAGTGCTGGGATTACAGACATGAGCCACTGTGCCCTGCC
TCTGTTTTGTGTATTTACATAAATACATGCTCCAGAGCTTTAAATTTCTTCTTAAATTTTAAACTAGAACTAAA
CCAGACATTGAGAGGACCCAGAAATATACCTGACTAACGTGGGTGGAATTTTCAATTGGCTTGACTCTTTGGTGA
AAAAAATAAATCAGGCTCTCAAGGACTCAATTTGGTGAACCAATGCCAAATAGAAAAATGTTCTTGACATTTT
CCCCAAATAGATGTCTAAAGATTTTGCATTTCAAATTGGTACTTTATGTATTTAAAGTGATATTGAACTAAAT
TCCTACCCAATTAGTTGAAAAATATGAAAAAGCAATTGCTAGAGAATGCAATTTATTAATGTTGGTGGTCTTT
TAAAAAATGAATTCCTCTTGTAGCCAGTGAGATCAGTTATTTATTTATTTTAAATAGTAACAAGGTCTCACT
ATATTGTCCAGGCTGATCTTGAACCTCTGGCCTCAAGCTGTCTCCCATCTCAGCTTCCCAAAGTGCTGAGATTA
TAGGCATGAGCCACCATGCTGGCTAGTTAATGGTATTAAGTAATACAAACATTTCTGTGAATTCACCAGATC

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FIGURE 115B

ATTGACTTTGGCATAGTTCACTTAAGACTTTGTTTGATAAAATAAATCTCTTTCACTCTAATTAGGAAGCATTTT
TGGGATCCTGATTAATGCTCTAATATTGTGGGGCCAAAAATATGTGGAACGTGGCCCTGCAGTTAGATGAGCTG
AGATCACTATAGTACTATATAGCGCTCTAAATCCTAAATGCTAGATCACTGTAATACTGTACAGATCAGCCACTT
GCTGGCTTGTGACTCTGGGCCATTTACTTCACCTCTCAAAAGGCATATTTAAAGTGAGGAAAATAATAAGTTTAT
TTTGAAATTCAGTTAGATGATGCAAATTGTTTACTGTAATTTCTAGCATGTAGTTCGTGCTCCATGCATTTAAC
TGTTATTACAGTTGTATTAGTATCACATTAAATTACCCACTGAAGTGAAAGTGAAACCAGAATGCTGTCAACGA
TT

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FIGURE 116

DNMDQPFTVNSLKKLAAMPDHTDVSLSPEERVRLSKLGCNITISEDITPRRYFRSGVEMERMAVYLEEGNLEN
AFVLYNKFITLFVEKLPNHRDYQQCAVPEKQDIMKKLKEIAFPRTDELKNDLLKKYNVEYQEYLQSKNKYKAEIL
KKLEHQRLIEAERKRIAQMRQQLESEQFLFFEDQLKKQELARGQMRSQQTSGLSEQIDGSALSCFSTHQNNSL
NVFADQPNKSDATNYASHSPVNRALTPAATLSAVQNLVVEGLRCVVLPELCHKFLQLAESNTVRGIETCGILC
GKLTHNEFTITHVIVPKQSAGPDYCDMENVEELFNVQDQHDLLTLGWITHPTQTAFSSVDLHHCYQLMLPE
AIAIVCSPKHKDTGIFRLTNAGMLEVSACKKKGFHPHTKEPRLFSIQKFLSGIISGTALEMEPLKIGYGPNGFPL
LGISRSSSPSEQL

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FIGURE 117

ATCCCCTCCGGTTTTCTCAGTCTCCACGTACGTCCTCAAAGCGCGTCCTAAAACCCGGATAACCGGAGCGCTC
CCCATGGACCACACGGAGGGCTTGCCCGCGGAGGAGCCGCCTGCGCATGCTCCATCGCCTGGGAAATTTGGTGAG
CGGCCTCCACCTAAACGACTTACTAGGGAAGCTATGCGAAATTATTTAAAAGAGCGAGGGGATCAAACAGTACTT
ATTCTTCATGCAAAAGTTGCACAGAAGTCATATGGAAATGAAAAAGGTTTTTTTGCCACCTCCTTGTTATAT
CTTATGGGCAGCGGATGGAAGAAAAAAGAACAATGGAACGCGATGGTTGTTCTGAACAAGAGTCTCAACCG
TGTGCATTTATTGGGATAGGAAATAGTGACCAAGAAATGCAGCAGCTAAACTTGGAAGGAAAGAACTATTGCACA
GCCAAAACATTGTATATACTGACTCAGACAAGCGAAAGCACTTCATTTTTCTGTAAAGATGTTCTATGGCAAC
AGTGATGACATTGGTGTGTTCTCAGCAAGCGGATAAAAGTCATCTCCAAACCTTCCAAAAGAAGCAGTCATTG
AAAAATGCTGACTTATGCATTGCCCTCAGGAACAAAGGTGGCTCTGTTTAATCGACTACGATCCCAGACAGTTAGT
ACCAGATACTTGTCATGTAGAAGGAGTAATTTTCATGCCAGTTCACAGCAGTGGGGAGCCTTTTTTATTCATCTC
TTGGATGATGATGAATCAGAAGGAGAAGAATTCACAGTCCGAGATGTCTACATCCATTATGGACAAACATGCAAA
CTTGTGTGCTCAGTTACTGGCATGGCACTCCCAAGATTGATAATTATGAAAGTTGATAAGCATAACCGCATTATTG
GATGCAGATGATCCTGTGTCACAACTCCATAAATGTGCATTTTACCTTAAGGATACAGAAAGAATGTATTGTGC
CTTCTCAAGAAAGAATAATTCAATTTCAAGGCCACTCCATGTCCAAAAGAACCAATAAAGAGATGATAAATGAT
GGCGCTTCCTGGACAATCATTAGCACAGATAAGGCAGAGTATACATTTTATGAGGGAATGGGCCCTGTCCTTGCC
CCAGTCACTCCTGTGCCTGTGGTAGAGAGCCTTCAGTTGAATGGCGGTGGGGACGTAGCAATGCTTGAACCTTACA
GGACAGAATTTCACTCCAAATTTACGAGTGTGGTTTGGGGATGTAGAAGCTGAAACTATGTACAGGTGTGGAGAG
AGTATGCTCTGTGTCGTCCAGACATTTCTGCATTCCGAGAAGGTTGGAGATGGGTCCGGCAACCAGTCCAGGTT
CCAGTAACTTTGGTCCGAAATGATGGAATCATTTATTTCCACCAGCCTTACCTTTACCTACACACCAGAACCAGGG
CCACGGCCACATTGCAGTGTAGCAGGAGCAATCCTTCCAGCCAATTCAAGCCAGGTGCCCCCTAACGAATCAAAC
ACAAACAGCGAGGGAAGTTACACAAACGCCAGCACAAATTCACCAGTGTACATCATCTACAGCCACAGTGGTA
TCCTA

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FIGURE 118

MDHTEGLPAEPPAHAPSPGKFGERPPPKRLTREAMRNYLKERGDQTVLILHAKVAQKSYGNEKRFFCPCPPCVYL
MSGWKKKKKEQMERDGCSEQESQPCAFIGIGNSDQEMQQLNLEGKNYCTAKTLYISDSDKRKHFIFSVKMFYGNS
DDIGVFLSKRIKVISKPSKKKQSLKNADLCIASGTKVALFNRLRSQTVSTRYLHVEGGNFHASSQQWGAFFIHLL
DDDESEGEETFVRDVYIHYGQTCKLVCSVTGMALPRLIIMKVDKHTALLDADDPVSQ LHKCAFYLK DTERMYLCL
SQERIIQFQATPCPKENKEMINDGASWTIIISTDKAETTFYEGMGFVLAPVTPVPVVESLQLNGGGDVAMLELTG
QNFTPNLRVWFGDVEAETMYRCGESMLCVVPDISAFREGWRWVRQP VQVPVTLVRNDGIIYSTSLTFTYTPEPGP
RPHCSVAGAILPANSSQVPPNESNTNSEGSYTNASTNSTSVTSSTATVVS

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FIGURE 119

GGTAAAGAGACAACCTTACAGATTGGGAGAATATATTTCCAAACTATTGTTGGGGCTCAGAAACGGATACCCTAAC
ATATAGTGATTTGACAGGTGGAACCTAAAGAAGACTCGAGGTCTCTCTGACCTCCTCCTCAACCTCTGTTTCTTAA
TCCTCTGTTTTTCCAGAGCACAGGAGGAAGTTCTCTGAAGTTCCTTTATCTGCTTTAAGTTCAGACTCACCAAAT
AAGAAAACAGTTAATTCTGGTGCCTTCCATGGGTTTTCTAATACTGAAGTCATATTGTAGGAAAAAGAATGAAGT
CTCTTAACCCACCTGGATAGATTTTTCTCACAACCATTTGTCTTCTCIGCAAGCCCAGTAGACTTTGTCCCAGGC
CATTTATGTGATCTTCACCCCATTAAGTTCTCCCCAAATTATTTACTCTTCCCCCAAATCACCCACACTTCCCC
ATCTCCCTCTCCCCTAAGGACAAGGGTATATCACCATCTATACCCCATTTGCTTGGTGGGGTGATCACTCTGATTC
TCTGCATGCATTTTTATAGATTTGTTTGCCATTTATCCTATTAATCTGCATTCTGTCAATTGTGGCAAGTTATCA
GCATATTTTTTAACTTTTAATTATTATTAATGGAAAGACACTTCTGTATACACTGGAAATCTCAGGAAATTTCTT
TTTTCTTAAGCTTAATTGAAATGTTTACTTTTCAGTAAATTTCAAGCTTGAGTAATGTTTCATGCCTGCTTTTC
ATTGAAATAGAATGAAAAGGTTGCACAATATTATTTTCATGAAATTACTTCTAGTATAATTCTGAATAAACACTT
TGAAAGGCAGTGAACGTAAATATATTACAGCTATCTCTTATTTCTTCAGGGCGGGTCTCAATTATGTAAAAGATG
ATTGGCTTTCTGTTTTAAGTAATAGTCATTTTGAAAACACTTTAAACTGTCAAGTGAAG

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FIGURE 120

VKRQLTDWENIFPNYCWGSETDILTYSDLTGGTKEDSRSL

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FIGURE 121

CGGCAGCCAGCTGAGAGCAATGGGAAATGGGGAGTCCCAGCTGTCTCGGTGCCTGCTCAGAAGCTGGGTTGGTT
TATCCAGGAATACCTGAAGCCCTACGAAGAATGTCAGACACTGATCGACGAGATGGTGAACACCATCTGTGACGT
CTGCAGGAACCCCGAACAGTTCCTCCCTGGTGCAGGGAGTGGCCATAGGTGGCTCCTATGGACGGAAAACAGTCTT
AAGAGGCCAACTCCGATGGTACCCTTGTCCTTTTCTTCAGTGACTTAAACAATTCCAGGATCAGAAGAGAAGCCA
ACGTGACATCCTCGATAAACTGGGGATAAGCTGAAGTTCTGTCTGTTACGAAGTGGTTGAAAAACAATTTGCA
GATCCAGAAGTCCCTTGATGGGTCCACCATCCAGGTGTTACAAAAAATCAGAGAATCTCTTTTCAGAGTGCTGGC
CGCCTTCAACGCTCTGAGCTTAAATGATAATCCCAGCCCTGGATCTATCGAGAGCTCAAAGATCCTTGGATAA
GACAAATGCCAGTCTGTGAGTTTGAGTCTGCTTCACTGAACTCCAGCAGAAGTTTTTTGACAACCGTCCTGG
AAAATAAGGATTTGATCCTCTTGATAAAGCACTGGCATCAACAGTGCCAGAAAAAATCAAGGATTTACCCTC
GCTGTCTCCGTATGCCCTGGAGCTGCTTACGGTGTATGCCTGGGAACAGGGGTGCAGAAAAGACAACCTTTGACAT
TGCTGAAGGCGTCAGAACGGTTCTGGAGCTGATCAAATGCCAGGAGAAGCTGTGTATCTATTGGATGGTCAACTA
CAACTTTGAAGATGAGACCATCAGGAACATCCTGCTGCACCACTCCAATCAGCGAGGCCAGTAATCTTGGATCC
AGTTGACCCAAACCAATAATGTGAGTGAGATAAAATATGCTGGCAATGGCTGAAAAAAGAAGCTCAAACCTGGTT
GACTTCTCCCAACCTGGATAATGAGTTACCTGCACCATCTTGGAAATGTCTGCCTGCACCACTCTTCACGACCCC
AGGCCACCTTCTGGATAAGTTCATCAAGGAGTTTCTCCAGCCCAACAAATGCTTCCTAGAGCAGATTGACAGTGC
TGTTAACATCATCCGTACATTCTTAAAGAAAACTGCTTCCGACAATCAACAGCCAAGATCCAGATTGTCCGGGG
AGGATCAACCGCCAAAGGCACAGCTCTGAAGACTGGCTCTGATGCCGATCTCGTCTGTGTTCCATAACTCACTTAA
AAGCTACACCTCCCAAAAAACGAGCGGCACAAAAATCGTCAAGGAAATCCATGAACAGCTGAAAGCCTTTTGGAG
GGAGAAGGAGGAGGAGCTTGAAGTCAGCTTTGAGCCTCCCAAGTGGAAGGCTCCCAGGGTGCTGAGCTTCTCTCT
GAAATCCAAAGTCTCAACGAAAGTGTGAGCTTTGATGTGCTTCTCGCTTTAATGCACTGGGTGAGCTGAGTTC
TGGCTCCACACCCAGCCCCGAGGTTTATGCAGGGCTCATTGATCTGTATAAATCCTCGGACCTCCCGGAGGAGA
GTTTTCTACCTGTTTACAGTCTGTCAGCGAAACTTCATTGCTCCCGCCCACTAAAGGATTTAATTTCG
CCTGGTGAAGCACTGGTACAAAGAGTGTGAAAGGAACTGAAGCCAAAGGGGTCTTTGCCCCCAAGTATGCCTT
GGAGCTGCTCACCATCTATGCCTGGGAGCAGGGGAGTGGAGTGCCGGATTTTGACACTGCAGAAGGTTTCCGGAC
AGTCTGGAGCTGGTCACACAATATCAGCAGCTCGGCATCTTCTGGAAGGTCAATTACAACCTTTGAAGATGAGAC
CGTGAGGAAGTTTCTACTGAGCCAGTTGCAGAAAAACAGGCCTGTGATCTTGGACCCAGGCGAACCCACAGGTGA
CGTGGGTGGAGGGGACCGTTGGTGTGGCATCTTCTGGACAAAGAAGCAAAGGTTAGGTTATCCTCTCCCTGCTT
CAAGGATGGGACTGGAAACCCAATACCACCTTGGAAAGTGCCGGTAAAGTCATCTAAAGGAGGCGTTGTCTGGA
AATAGCCCTGTAAACAGGCTTGAATCAAAGAAGTCTCTACTGTAGCAACCTGAAATTAACCTCAGACACAAATAA
AGGAAACCCAGCTCAGAGGAGCTTAAACAGCTGGTCAAGCCCCCTAAGCCCCCACTACAAGTGATCCTCAGGCAG
GTAACCCCAAGATTGATGCACTGTAGGGCTGGGCGCAGCATCCCTAGGTCTCTACCCAGTAGATGCCACTAGCCCT
CCTCTCCCAAGTGACAACCAAAAGTCTTCACATGTTCAAACGTTCCCTGGGTTACAGATCTTTCTGCCTTTGGC
TTTTGGCTCCACCTCTTTAGCTGTTAATTGAGTACTTATGGCCCTGAAAGCGGCCACGGTGCCTCCAGATGGC
AGGTTTGCAATCCAAGCAGGAAGAAGGAAAAGATACCCAAAGGTCAAGAACACAGTGATTTTATTAGAAGTTTCA
TCCGCAAATTTCTTCCATTTCAATTGCTCAGAAATGTCATGTGTTTACCTGTAACCTGAAGGTGGCTACAAAGATG
ACTGTGGAGGTGGTTGCACTTGCCACCCAAGGATGTCTGCCACACCTCTCCAAGCCCTCCTACCTACCAAGATAT
ACCTGATATATCCACCAGATATCTCCTCAGATATACTTGGTTCTCTCCACCAGGTTCTTTCTTTAAAGCAGGATT
CTCAACTTTGATACTTACTCACATTGGGCTAGACAGTCTTTGTTTGGAGGCTCTCTTGTGCAITGATGATGTTG
AGCAGCATGTGTGGCCTGTACCCAGTACATGCCACCCAGTTGTGACAATTAAGGTGTCTTGAGACTTTATCATG
TGTCTTCTGCCCTAGGTGAGAACCCTTGCACTACAGGAACCCTACACCCAACCTGGGGGGAATGTAGGGAAGAGG
TGCCAAGCCAACCGTGGGGTTAGCTCTAATTATTAAAGTTATGCATTATAAATAAATACCAAAAAATTG

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FIGURE 122

MGNGESQLSSVPAQKLGWFIQEYLKPYEECQTLIDEMVNTICDVCRNPEQFPLVQGVAIGGSYGRKTVLRGNSDG
TLVLFFSDLKQFQDQKRSQRDILDKTGDKLKFCLFTKWLKNNFEIQKSLDGSTIQVFTKNQRISFEVLA AFNALS
LNDNPSWIIYRELKRS�DKNASPGFAVCFTELQKFFDNRPGKLDLILLIKHWHQOCQKKIKDLPSLSPYAL
ELLTVYAWEQGCRKDNFDIAEGVRTVLELIKCEKLCIYWMVNYNFEDETIRNILLHQLQSARPVILDPVDP TNN
VSGDKICWQWLKKEAQTWLTSPNLDNELPAPSWNVLPAPLFTTPGHLLDKF I KEFLQPNKCFLEQIDS AVNI I RT
FLKENCFRQSTAKIQIVRGGSTAKGTALKTGSDADLVVFHNSLKSYS TSQKNERHKIVKEIHEQLKAFWREKEEEL
EVSFEPPKWKAPRVLSFSLKSKVLNESVSFDVLP AFNALGQLSSGSTPSPEVYAGLIDLYKSSDLPGGEFSTCFT
VLQRNFIRS RPTKLDLIRLVKHWHYKECERKLKPKGSLPPKYALELLTIYAWEQGSGVPDFDTAEGFRTVLELVT
QYQQLGIFWKVNYNFEDETVRKFLLSQLQKTRPVILDPGEPTGDVGGGDRWCWHLLDKEAKVRLSSPCFKDGTGN
PIPPWKVPVKVI

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FIGURE 123

CTACTACTACTAAATTCGCGGCCXCTCXGGAATTGGCGACTTCGATATTAACAAGGATGCGCGGCCGCGCAGCAA
GTCGAGGAGTCGGGGCAAAGCTGGGCCTGCGTGAGATTCGCATCCACTTATGTCAGCGCTCGCCCGGCAGCCAGG
GCGTCAGGGACTTCATTGAGAAACGCTACGTGGAGCTGAAGAAGGCGAATCCCGACCTACCCATCCTAATCCGCG
AATGCTCCGATGTGCAGCCCAAGCTCTGGGCCCCGTACGCATTGGCCAAGAGACGAATGTCCCTTTGAACAAC
TCAGTGCTGATCAGGTAACCAGAGCCCTGGAGAACGTTCTAAGTGGTAAAGCCTGAAGCCTCCACTGAGGATTAA
GAGCAACAGCCCCAGAGCCTGGGCTCTGCTGGACTTAGTATAATGTGAAAAAATGTGTTCTCCTATTCTCATA
AAGCTTGTGCTGTAAATACTTTCTCAGGGTGTTCCTGTCTCATCTACCTCTAACCCTTAATGGTGCAACCA
CTGAGGCAAAGTAGCTTAATATAAAAATTAACTTTATTCTGGCCTCATCAAAAAAAAAAAAAA

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FIGURE 124

MAAAAASRGVGAKLGLREIRIHL CQRSPGSQGV RDFIEKRYVELKKANPDLPILIRECSDVQPKLWARYAFGQET
NVPLNNFSADQVTRALENVLSGKA

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FIGURE 125

CTGGTGGGCGTCAGGGGCAGGCAACAGAGTGGCGGCCGCTACGGCCCTGGAACGGGGCCATGGAGAAGCTGCGGC
GAGTCCTGAGCGGCCAGGACGACGAGGAGCAGGGCCTGACTGCGCAGGTCCTGGATGCCTCATCCCTTAGTTTCA
ACACCAGATTGAAATGGTTTGCCATCTGCTTCGTA TGTGGCGTTTTCTTTCTATTCTTGGAAGTGGATTGCTGT
GGCTTCCGGGCGGCATAAAGCTTTTTGTCAGTGT TTTATACCCTCGGCAATCTTGCTGCGTTAGCCAGTACATGCT
TTTTAATGGGACCTGTGAAGCAACTGAAGAAAATGTGTGAAGCAACAAGATTGCTTGCAACAATTGTTATGCTTT
TGTGTTTCATATTTACCTGTGTGCTGCTCTTTGGTGGCATAAGAAAGGACTGGCTGTGTTATTCTGCATATTGC
AGTTCTTGTCAATGACCTGGTATAGCCTGTCTGACATCCCATATGCAAGGGATGCAGTTATTAAATGCTGTTCTT
CTCTCCTAAGTTGAAAATCAGAACTTGTGGAAAAGAGCACTTGAATGTTGGTACTCTATGTTTGGTGAAGTTTG
CTTTTCCCATAAAACACTCCAGGAACAAC TGACGTGACAGTTGAAGACCGTXXTGTACTAAGTCTCATTTTGTA
TACTGGTAAAACTACATGCTTGATTAAACCATTAAATGCTTGTAACTTTAAATTCATTATGTGTCATTAATATA
CTTTTCAAAGATAAGATTTTAACTACTGCCAGTTGTAAATTATTTT TAGCCAATTTTAAATCTTTCAAAGC
AGCTTTGAAATGTGAATATTTAAAGGTAGACCTGTGCTGCAAGATAATTAACTTTTTTGCTTTTAAAAAATGTC
TGCATXTXTAAGATTXTTTTACTTTAAATGTGAACTTATTTXAAGCTAAAAATTGCTTATTATATGTAATAAA
ATAATATATAAATCTTTACAATTTTGAAATAAACCCATCCTTGGAATAAAT

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FIGURE 126

GGRQQATEWRPLRPWNGAMEKLRRVLSGQDDEEQGLTAQVLDASSLSFNTRLKWF AICFVCGVFFSILGTGLLW
LPGGIKLFAVFYTLGNLAALASTCFLMGPVKQLKKMCEATRLLATIVMLLCFIFTLCAALWWHKKGLAVLFCILQ
FLSMTWYSLSYIPYARDAVIKCCSSLS

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FIGURE 127

TGTCGGGGACGGTAACCGGGACCCGTGCTCTGCTCCTGTCGCCTTCGCCTCCTGAATCCCTAGCCATATGCGTGA
GTGCATCTCCATCCACGTTGGCCAGGCTGGTGTCCAGATTGGCAATGCCTGCTGGGAGCTCTACTGCCTGGAACA
CGGCATCCAGCCCGATGGCCAGATGCCAAGTGACAAGACCATTGGGGGAGGAGATGACTCCTTCAACACCTTCTT
CAGTGAGACGGGCGCTGGCAAGCACGTGCCCCGGGCTGTGTTTGTAGACTTGGAACCCACAGTCATTGATGAAGT
TCGCACTGGCACCTACCGCCAGCTCTTCCACCCTGAGCAGCTCATCACAGGCAAGGAAGATGCTGCCAATAACTA
TGCCCCGAGGGCACTACACCATTGGCAAGGAGATCATTGACCTTGTGTTGGACCGAATTGCGAAGCTGGCTGACCA
GTGCAACCCGTCTTCAGGGCTTCTTGGTTTTCCACAGCTTGGTGGGGGAAGTGGTTCTGGGTTACCTCCCTGCT
CATGGAACGCCTGTGAGTTGATTATGGCAAGAAATCCAAGCTGGAGTTCTCCATTTACCCGGCACCCCAGGTTTC
CACAGCTGTAGTTGAGCCCTACAACCTCCATCCTCACCACCACACCACCCTGGAGCACTCTGATTGTGCCTTCAT
GGTAGACAATGAGGCCATCTATGACATCTGTGCTAGAAACCTCGATATCGAGCGCCCAACCTACACTAACCTTAA
CCGCCTTATTAGCCAGATTGTGTCTCCATCACTGCTTCCCTGAGATTGATGGAGCCCTGAATGTTGACCTGAC
AGAATTCCAGACCAACCTGGTCCCCTACCCCGCATCCACTTCCCTCTGGCCACATATGCCCCGTGCATCTCTGC
TGAGAAAGCCTACCATGAACAGCTTCTGTAGCAGACATCACCATGCTTGCTTTGAGCCAGCCAACCAGATGGT
GAAATGTGACCCCTGGCCATGGTAAATACATGGCTTGTGCCTGTTGTACCGTGGTGACGTGGTTCCCAAAGATGT
CAATGCTGCCATTGCCACCATCAAAACCAAGCGCACGATCCAGTTTGTGGATTGGTGCCCCACTGGCTTCAAGGT
TGGCATCAACTACCAGCCTCCCACTGTGGTGCCTGGTGGAGACCTGGCCAAGGTACAGAGAGCTGTGTGCATGCT
GAGCAACACCACAGCCATTGCTGAGGCCTGGGCTCGCCTGGACCACAAGTTTGACCTGATGTATGCCAAGCGTGC
CTTTGTTCACTGGTACGTGGGTGAGGGGATGGAGGAAGGCGAGTTTTTCAGAGGCCCGTGAAGATATGGCTGCCCT
TGAGAAGGATTATGAGGAGGTTGGTGTGGATTCTGTTGAAGGAGAGGGTGAGGAAGAAGGAGAGGAATACTAATT
ATCCATTCCTTTTGGCCCTGCAGCATGTGCTGCCAGAATTTAGCTTCAGCTTAACTGACAGATGTTAAAGC
TTTCTGGTTAGATTGTTTTCACTTGGTGATCATGTCTTTTCCATGTGTACCTGTAATATTTTTCCATCATATCTC
AAAGTAAAGTCATTAACATCA

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FIGURE 128

MRECISIHVGQAGVQIGNACWELYCLEHGIQPDGQMPSDKTIGGGDDSFNTFFSETGAGKHVPRAVFVDLEPTVI
DEVRTGTYRQLFHPEQLITGKEDAANNYARGHYTIGKEIIDLVLDRIKRLADQCTRLQGFLVFHSFGGGTGSGET
SLLMERLSVDYGKKSLEFSIYPAPQVSTAVVEPYNSILTTHTTLEHSDCAFMDNEAIYDICRRNLDIERPTYT
NLNRLISQIVSSITASLRFDGALNVDLTFQTNLVPYPRIHFPLATYAPVISAEKAYHEQLSVADITNACFEPAN
QMVKCDPGHGKYMACECLLYRGDVVPKDVNAAIATIKTKRTIQFVDWCPTGFKVGINYQPPTVVPGGDLAKVQRAV
CMLSNTTAIAEAWARLDHKFDLMYAKRAFVHWYVGEEMEEGEFSEAREDMAALEKDYEEVGVD SVEGE GEEEGEE
Y

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FIGURE 129

GGCACGAGGGTTTGCACCTCGCTGCTCCAGCCTCTGGGGCGCATTCCAACCTTCCAGCCTGCGACCTGCGGAGAA
AAAAAATTACTTATTTTCTTGCCCCATACATACCTTGAGGCGAGCAAAAAAATTAAATTTTAACCAATGAGGGAAA
TCGTGCACATCCAGGCTGGTCAGTGTGGCAACCAGATCGGTGCCAAGTTCTGGGAGGTGATCAGTGATGAACATG
GCATCGACCCACCGGCACCTACCACGGGGACAGCGACCTGCAGCTGGACCGCATCTCTGTGTACTACAATGAAG
CCACAGGTGGCAAATATGTTCTCGTGCCATCCTGGTGGATCTAGAACCTGGGACCATGGACTCTGTTTCGCTCAG
GTCTTTTTGGCCAGATCTTTAGACCAGACAACCTTGTATTGGTTCAGTCTGGGGCAGGTAACAACCTGGGCCAAAG
GCCACTACACAGAGGGCGCCGAGCTGGTTGATTCTGTCTGGATGTGGTACGGAAGGAGGCAGAGAGCTGTGACT
GCCTGCAGGGCTTCCAGCTGACCCACTCACTGGGCGGGGCACAGGCTCTGGAATGGGCACCTCTCCTTATCAGCA
AGATCCGAGAAGAATACCCTGATCGCATCATGAATACCTTCAGTGTGGTGCCTTCACCCAAAGTGTCTGACACCG
TGGTCGAGCCCTACAATGCCACCTCTCCGTCCATCAGTTGGTAGAGAATACTGATGAGACCTATTGCATTGACA
ACGAGGCCCTCTATGATATCTGCTTCCGCACTCTGAAGCTGACCACCAACCTACGGGGATCTGAACCACCTTG
TCTCAGCCACCATGAGTGGTGTACACACCTGCCTCCGTTTCCCTGGCCAGCTCAATGCTGACCTCCGCAAGTTGG
CAGTCAACATGGTCCCTTCCCACGTCTCCATTTCTTTATGCCTGGCTTTGCCCCTCTCACCAGCCGTGGAAGCC
AGCAGTATCGAGCTCTCACAGTGCCGGAACCTACCCAGCAGGTCTTCGATGCCAAGAACATGATGGCTGCCTGTG
ACCCCGCCACGGCCGATACCTCACCGTGGCTGTCTTCCGTGGTCCGATGTCCATGAAGGAGGTGATGAGC
AGATGCTTAACGTGCAGAACAAGAACAGCAGCTACTTTGTGGAAATGGATCCCCAACAATGTCAAGACAGCCGTCT
GTGACATCCCACCTCGTGGCCTCAAGATGGCAGTCACCTTCATTGGCAATAGCACAGCCATCCAGGAGCTCTTCA
AGCGCATCTCGGAGCAGTTCACTGCCATGTTCCGCGGGAAGGCCTTCTCCACTGGTACACAGGCGAGGGCATGG
ACGAGATGGAGTTACCGAGGCTGAGAGCAACATGAACGACCTCGTCTCTGAGTATCAGCAGTACCAGGATGCCA
CCGAGAAGAGGAGGAGGATTTCCGTGAGGAGGCCGAAGAGGAGGCCTAAGGCAGAGCCCCCATCACCTCAGGCT
TCTCAGTTCCCTTAGCCGTCTTACTCAACTGCCCCCTTCTCTCCCTCAGAATTTGTGTTTGTCTGCCTCTATCTT
GTTTTTTGTTTTTTCTTCTGGGGGGGTCTAGAACAGTGCCTGGCACATAGTAGGCGCTCAATAAATACTTGTTT
GTTGAAAAAAAAAAAAAAAAA

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FIGURE 130

MREIVHIQAGQCGNQIGAKFWEVISDEHGIDPTGTYHGDSDLQLDRISVYYNEATGGKYVPRAILVDLEPGTMDS
VRSGPFGQIFRPDNFVFGQSGAGNNWAKGHYTEGAELVDSVLDVVRKEAESCDCLQGFQLTHSLGGGTGSGMGTL
LISKIREEYPDRIMNTFSVVPSPKVSDTVVEPYNATLSVHQLVENTIDETCYCIDNEALYDICFRTLKLTTPTYGDL
NHLVSATMSGVTTCLRFPGQLNADLRKLAVNMVFPRLHFFMPGFAPLTSRGSQQYRALTVPELTQQVFDAKNMM
AACDPRHGRYLTVAAVFRGRMSMKEVDEQMLNVQNKNSYFVEWIPNNVKTAVCDIPPRGLKMAVTFIGNSTAIQ
ELFKRISEQFTAMFRRKAFLHWYTGEGMDEMEFTEAESNMNDLVSEYQQYQDATAEEEEEDFGEEAEAAA

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FIGURE 131

ATCCAATACAGGAGTGACTTGGAACCTCATTCTATCACTATGAAGAAAAGTGGTGTCTTTTCTCTTGGGCATC
ATCTTGCTGGTTCTGATTGGAGTGCAAGGAACCCAGTAGTGAGAAAGGGTCGCTGTTCTTGCATCAGCACCAAC
CAAGGGACTATCCACCTACAATCCTTGAAAGACCTTAAACAATTTGCCCCAAGCCCTTCTGCGAGAAAATTGAA
ATCATTGCTACACTGAAGAATGGAGTTCAAACATGTCTAAACCCAGATTTCAGCAGATGTGAAGGAAGTATTGAAA
AAGTGGGAGAAACAGGTCAGCCAAAAGAAAAAGCAAAAGAATGGGAAAAACATCAAAAAAGAAAGTTCTGAAA
GTTGAAAATCTCAACGTTCTCGTCAAAAGAAGACTACATAAGAGACCACCTTCACCAATAAGTATTCTGTGTAA
AAATGTTCTATTTTAATTATACCGCTATCATTCCAAGGAGGATGGCATATAATACAAAGGCTTATTAATTTGAC
TAGAAAATTTAAACATTACTCTGAAATTGTAACATAAGTTAGAAAGTTGATTTTAAGAATCCAAACGTTAAGAA
TTGTTAAAGGCTATGATTGTCTTTGTTCTTCTACCACCCACCAGTTGAATTTTCATCATGCTTAAGGCCATGATTT
TAGCAATACCCATGCTACACAGATGTTACCCAACCATCCCACTCACAACAGCTGCCTGGAAGAGCAGCCCT
AGGCTTCCACGTACTGCGACCTCCAGAGAGTATCTGAGGCACATGTCAGCAAGTCTTAAGCCTGTTAGCATGCTG
GTGAGCCAAGCAGTTTGAAATTGAGCTGGACCTCACCAGCTGCTGTGGCCATCAACCTCTGTATTGATCAGC
CTACAGGCCCTCACACACAATGTGTCTGAGAGATTGCTGATTGTTATTGGGTATCACCCTGGAGATCACCAG
TGTGTGGCTTTTCAGAGCCTCCTTTCTGGCTTTGGAAGCCATGTGATTCCATCTTGCCCGCTCAGGCTGACCCTT
TATTTCTTTTTGTTCCCTTTGCTTCATTCAAGTCAGCTCTTCTCCATCCTACCACAATGCAGTGCCTTTCTTCT
CTCCAGTGCACCTGTCATATGCTCTGATTTATCTGAGTCAACTCCTTTCTCATCTTGTCCTAACACCCACAGA
AGTGCTTTCTTCTCCAATTTCATCCTCACTCAGTCCAGCTTAGTTCAGTCTGCCTCTTAAATAAACCTTTTTG
GACACACAAATTATCTTAAACCTCCTGTTTCACTTGGTTCACTACCATGGGTGAACACTCAATGGTTAACTAA
TTCTTGGGTGTTTATCCTATCTCTCCAACCAGATTGTCAGTCCCTTGAGGGCAAGAGCCACAGTATATTTCCCTG
TTTCTTCCACAGTGCCTAATAATACTGTGGAAGTGGTTTTTAATAATTTTTTAATTGATGTTGTTATGGGCAGGA
TGGCAACCAGACCATTGTCTCAGAGCAGGTGCTGGCTCTTTCTGGCTACTCCATGTTGGCTAGCCTCTGGTAAC
CTCTTACTTATTATCTTCAGGACACTCACTACAGGGACCAGGGATGATGCAACATCCTTGTCTTTTATGACAGG
ATGTTTGCTCAGCTTCTCCAACAATAAGAAGCAGTGGTAAACACTTGCGGATATTCTGGACTGTTTTAAAAA
ATATACAGTTTACCGAAAATCATATAATCTTACAATGAAAAGGACTTTATAGATCAGCCAGTGACCAACCTTTTC
CCAACCATACAAAAATTCCTTTTCCCGAAGGAAAAGGGCTTTCTCAATAAGCCTCAGCTTTCTAAGATCTAACAA
GATAGCCACCAGATCCTTATCGAACTCATTTTAGGCAAATATGAGTTTATTGTCCGTTTACTGTTCAGAG
TTTGATTTGTGATTATCAATTACCACACCATCTCCCATGAAGAAAGGGAACGGTGAAGTACTAAGCGCTAGAGGA
AGCAGCCAAGTCGGTTAGTGAAGCATGATTGGTGCCAGTTAGCCTCTGCAGGATGTGGAACCTCCTTCCAGG
GGAGGTTCACTGAATTGTGTAGGAGAGGTTGTCTGTGGCCAGAATTTAAACCTATACTCACTTTCCCAAATTGAA
TCACTGCTCACACTGCTGATGATTTAGAGTGCTGTCCGGTGGAGATCCCAACCGAACGTCTTATCTAATCATGAA
ACTCCCTAGTTCCTTCATGTAACCTCCCTGAAAAATCTAAGTGTTCATAAATTTGAGAGTCTGTGACCCACTTA
CCTTGATCTCACAGGTAGACAGTATATACTAACAACCAAGACTACATATTGTCACTGACACACAGTTATAA
TCATTTATCATATAATACATACATGATACACTCTCAAAGCAAATAATTTTCACTTCAAAACAGTATTGACTT
GTATACCTTGTAATTTGAAATATTTTCTTTGTTAAAATAGAATGGTATCAATAAATAGACCATTAAATCAG

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FIGURE 132

MKKSGVLFLLGIILLVLIGVQGTPVVRKGRCSCISTNQGTIHLQSLKDLKQFAPSPSCEKIEIIATLKNGVQTCL
NPDSADVKELIKKEKQVSQKKKQKNGKKHQQKKVLKVRKSQRSRQKKT

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FIGURE 133

TCTCGGCCCGGCATCATTGTGGGAAGAGCTGAAGCAGGCGCTCTTGGCTCGGCGCGGCCCGCTGCAATCCGTGGA
GGAACGCGCCGCCGAGCCACCATCATGCCTGGGCACTTACAGGAAGGCTTCGGCTGCGTGGTCACCAACCGATT
GACCAGTTATTTGACGACGAATCGGACCCCTTCGAGGTGCTGAAGGCAGCAGAGAACAAGAAAAAGAAGCCGGC
GGGGGCGGCGTTGGGGGCCCTGGGGCCAAGAGCGCGACTCAGGCCGCGGCCAGACCAACTCCAACGCGGCAGGC
AAACAGCTGCGCAAGGAGTCCCAGAAAGACCGCAAGAACCCGCTGCCCCCAGCGTTGGCGTGGTTGACAAGAAA
GAGGAGACGCAGCCGCCCGTGGCGTTTTAAGAAAGAAGGAATAAGACGAGTTGGAAGAAGACCTGATCAACAACCT
CAGGGTGAAGGGAAAAATAATTGATAGAAGACCAGAAAGGCGACCACCTCGTGAACGAAGATTGAAAAGCCACTT
GAAGAAAAGGGTGAAGGAGGCGAATTTTCAGTTGATAGACCGATTATTGACCGACCTATTGAGGTCGTGGTGGT
CTTGGAAGAGGTCGAGGGGGCCCGTGGACGTGGAATGGGCCGAGGAGATGGATTGTGATTCTCGTGGCAAACGTGAA
TTTGATAGGCATAGTGAAGTGATAGATCTTCTTTTTCACATTACAGTGGCCTGAAGCACGAGGACAAACGTGGA
GGTAGCGGATCTCACAACCTGGGGAACCTGTCAAAGACGAATTAAGTACTGATCAATCAAATGTGACTGAGGAA
ACACCTGAAGGTGAAGAACATCATCCAGTGGCAGACACTGAAATAAGGAGAATGAAGTTGAAGAGCTAAAAGAG
GAGGGTCCAAAAGAGATGACTTTGGATGAGTGAAGGCTATTCAAAATAAGGACCGGGCAAAAGTAGAATTTAAT
ATCCGAAAACCAAATGAAGGTGCTGATGGGCAGTGAAGAAGGGATTGTTCTTCATAAATCAAAGAGTGAAGAG
GCTCATGCTGAAGATTGCGTTATGGACCATCATTTCCGGAAGCCAGCAAATGATATAACGTCTCAGCTGGAGATC
AATTTTGGAGACCTTGGCCGCCAGGACGTGGCGGCAGGGGAGGACGAGGTGGACGTGGGCGTGGTGGGCGCCCA
AACCGTGGCAGCAGGACCGACAAGTCAAGTGCTTCTGCTCCTGATGTGGATGACCCAGAGGCATTCCCAGCTCTG
GCTTAAGTGGATGCCATAAGACAACCCTGGTTCCCTTTGTGAACCCCTTCTGTTCAAAGCTTTTGCATGCTTAAGGA
TTCCAAACGACTAAGAAATTAAAAAAGACTGTCATTACATACCATTACACCTAAAGACTGAATTTTATCT
GTTTTAAATGAACCTCTCCCGCTACACAGAAGTAACAAATATGGTAGTCAGTTTTGTATTTAGAAATGTATTG
GTAGCAGGGATGTTTTATAATTTTCAGAGATTATGCATTCTTCATGAATACTTTGTATTGCTGCTTGCAAATA
TGCAATTTCCAACTTGAAATATAGGTGTGAACAGTGTGTACCAGTTTAAAGCTTTCACCTTCAATTTGTGTTTTTA
ATTAAGGATTTAGAAGTTCCCCAATTACAACTGGTTTTAAATATTGGACATACTGGTTTTAATACCTGCTTG
CATATTCACACATGGTCAACTGGGACATGTAAACCTTGATTGTCAAATTTATGCTGTGTGGAATACTAATA
TATGTATTTTAAGTTAGTTTTAATATTTTCATTTTGGGGAAAAATCTTTTTCACTTCTCATGGATAGCTGTTA
TATATATATGCTAAATCTTTATATACAGAAATATCAGTACTTGAACCAATTCAAAGCACATTTGGGTTATTAACC
CTTGCTCCCTGCATGGCTCATTAGGGTCCAAATTATAACTGATTTACATT

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FIGURE 134

MPGHLQEGFGCVVTNRFDQLFDDESDPFVLKAAENKKKEAGGGVGGPGAKSATQAAAQTNNAAGKQLRKESQ
KDRKNPLPPSVGVVDKKEETQPPVAFKKEGIRRVGRRPDQQLQEGEKIIDRRPERRPPRERRFEKPLEEKGE
FSVDRPIIDRPIRGRGGLGRGRGGRGRGMGRGDGFD SRGKREFDRHSGSDRSSFSHYSGLKHEDKRGGSGSHNW
TVKDELTDLDQSNVTEETPEGEEHHPVADTENKENEVEEVKEEGPKEMTLDEWKAIQNKDRAKVEFNIRKPNEGA
DGQWKKGFVLHKSSEEHAEDSVMDHHFRKPANDITSQLEINFGDLGRPGRGGRGGRGGRGGRGGRPNRGSRTDK
SSASAPDVEDDPEAFPALA

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FIGURE 135

GGCGGACCGAAGAACGCGAGGAAGGGGGCCGGGGGGACCCGCCCCCGGCCGGCCGCGAGCCATGAACTCCAACGTGG
AGAACCTACCCCCGACATCATCCGCCTGGTGTACAAGGAGGTGACGACACTGACCGCAGACCCACCCGATGGCA
TCAAGGTCTTTCCCAACGAGGAGGACCTCACCGACCTCCAGGTCACCATCGAGGGCCCTGAGGGGACCCCATATG
CTGGAGGTCTGTTCCGCATGAAACTCCTGCTGGGGAAGGACTTCCCTGCCTCCCCACCCAAGGGCTACTTCCTGA
CCAAGATCTTCCACCCGAACGTGGGCGCCAATGGCGAGATCTGCGTCAACGTGCTCAAGAGGGACTGGACGGCTG
AGCTGGGCATCCGACACGTACTGCTGACCATCAAGTGCCTGCTGATCCACCCTAACCCCGAGTCTGCACTCAACG
AGGAGGCGGGCCGCCTGCTCTTGGAGAACTACGAGGAGTATGCGGCTCGGGCCCGTCTGCTCACAGAGATCCACG
GGGCGCCGGCGGGCCCAGCGGCAGGGCCGAAGCCGGTCGGGCCCTGGCCAGTGGCACTGAAGCTTCCTCCACCG
ACCTTGGGGCCCCAGGGGGCCCGGGAGGGGCTGAGGGTCCCATGGCCAAGAAGCATGCTGGCGAGCGCGATAAGA
AGCTGGCGGCCAAGAAAAAGACGGACAAGAAGCGGGCGCTGCGGGCGCTGCGGCGGCTGTAGTGGGCTCTCTTCC
TCCTTCCACCGTGACCCCAACCTCTCCTGTCCCCTCCCTCCAACCTCTGTCTCTAAGTTATTTAAATTATGGCTGG
GGTCGGGGAGGGTACAGGGGGCACTGGGACCTGGATTTGTTTTTCTAAATAAAGTTGGAAAAGCA

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FIGURE 136

MNSNVENLPPHIIRLVYKEVTTLTADPPDGIKVFNPNEEDLTDLQVTIEGPEGTPYAGGLFRMKLLLGKDFPASPP
KGYFLTKIFHPNVGANGEICVNVLKRDWTAELGIRHVLLTIKCLLIHPNPESALNEEAGRLLLENYEEYAARARL
LTEIHGGAGGPPSGRAEAGRALASGTEASSTDPGAPGGPGGAEGPMAKKHAGERDKKLAAKKTDKKRALRALRRL

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FIGURE 137

CATTGATTCATAAAGGATCTTTATAAATCTTATTCTTTGTTGGCTATATAGTTGCCAATATCTTCTCCCAATTTG
TGGCTTGCCTTTCCCTCCCTTATGATGTTCTTTGATAAAAACAATTTATTAATGGTTAAGTACTAGGAAGTATGA
GTGTTTTAAATTAGAGCGTGAGTTGTTTTAAAAAACCATTCCTACCCTGGAGTCATGAAGATAGTCTTATAIA
TCGTCTTCTTAAAGCTTTAGTTTTGCCTTTCATATTTAAATTTTTTTCATGAGGAATTAATTTGGTGTATGCTAG
GAGATGCCTCACTACCGTTTATTGACCAAATCTGGGTTTTATTCTCCTTTCTGTAGTTGCACCAAAGTCCTGTT
T

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FIGURE 138

MLGDASLPFIDQIWVLFLLSVVAPKSC

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FIGURE 139

CCCCGGCATGGGAGGAGGAGTGCCGGGTGCTCTCCATACAGAGCCACGTCATCCGCGGCTACGTGGGCAACCGGGCG
GCCACGTTCCCGCTGCAGGTTTTGGGATTTGAGATTGACGCGGTGAACCTGTGCCAGTTTTCAAACACACAGGC
TATGCCCACTGGAAGGGCCAAGTGCTGAATTCAGATGAGCTCCAGGAGTTGTACGAAGGCCTGAGGCTGAACAAC
ATGAATAAATATGACTACGTGCTCACAGGTTATACGAGGGACAAGTCGTTCCCTGGCCATGGTGGTGGACATTGTG
CAGGAGCTGAAGCAGCAGAACCCCGAGCTGGTGTACGTGTGTGATCCAGTCTTGGGTGACAAGTGGGACGGCGAA
GGCTCGATGTACGTCCCGGAGGACCTCCTTCCCGTCTACAAAGAAAAAGTGGTGCCGCTTGCAGACATTATCACG
CCCAACCAGTTTGAGGCCGAGTTACTGAGTGGCCGGAAGATCCACAGCCAGGAGGAAGCCTTGCGGGTGATGGAC
ATGCTGCACTCTATGGGCCCCGACACCGTGGTCATCACCAGCTCCGACCTGCCCTCCCCGCAGGGCAGCAACTAC
CTGATTGTGCTGGGGAGTCAGAGGAGGAGGAATCCCGTGGCTCCCGTGGTGATGGAACGCATCCGGATGGACATT
CGCAAAGTGGACGCCGTCTTTGTGGGCACTGGGGACCTGTTTGCTGCCATGCTCCTGGCGTGGACACACAAGCAC
CCCAATAACCTCAAGGTGGCCTGTGAGAAGACCGTGTCTACCTTGCAACACGTTCTGCAGAGGACCATCCAGTGT
GCAAAGCCCAGGCCGGGGGAAGGAGTGAGGCCCAGCCCCATGCAGCTGGAGCTGCGGATGGTGCAGAGCAAAGG
GACATCGAGGACCCAGAGATCGTCGTCCAGGCCACGGTGCTGTAGGGGCCCCGCCGCTTG

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FIGURE 140

MEEECRVLSIQSHVIRGYVGNRAATFPLQVLGFEIDAVNSVQFSNHTGYAHWKGQVLNSDELQELYEGLRLNNMN
KYDYVLTGYTRDKSFLAMVVDIVQELKQQNPRLVYVCDPVLGDKWDGEGSMYVPEDLLPVYKEKVPLADIITPN
QFEAELLSGRKIHSQEEALRVMDMLHSMGPDTVVITSSDLPSQGSNYLIVLGSQRRRNPAGSVVMERIRMDIRK
VDAVFVGTGDLFAAMLLAWTHKHPNNLKVACEKTVSTLHHVLQRTIQCAKAQAGEGVRPSPMQLELRMVQSKRDI
EDPEIVVQATVL

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FIGURE 141

GGATCGAGGGGACTCTGACCACAGCCTGTGGCTGGGAAGGGAGACAGAGGCGGCGGGCTCAGGGGAAACGAGG
CTGCAAGTGGTGGTAGTAGGAAGATCTCGGGCGAGGACGAGCAACAGGAGCAAACCTATCGCTGAGGACCTGGTCGT
GACCAAGTATAAGATGGGGGGCGACATCGCCAACAGGGTACTTCGGTCCTTGGTGGAAGCATCTAGCTCAGGTGT
GTCGGTACTCAGCCTGTGTGAGAAAGGTGATGCCATGATTATGGAAGAAACAGGGAAAATCTTCAAGAAAGAAAA
GGAAATGAAGAAAGGTATTGCTTTTCCCACCAGCATTTCGGTAAATAACTGTGTATGTCACTTCTCCCCTTTGAA
GAGCGACCAGGATTATATTCTCAAGGAAGGTGACTTGGTAAAAATTGACCTTGGGGTCCATGTGGATGGCTTCAT
CGCTAATGTAGCTCACACTTTTGTGGTTGATGTAGCTCAGGGGACCCAAGTAACAGGGAGGAAAGCAGATGTTAT
TAAGGCAGCTCACCTTTGTGCTGAAGCTGCCCTACGCCTGGTCAAACCTGGAAATCAGAACACACAAGTGACAGA
AGCCTGGAACAAAGTTGCCCACTCATTTAACTGCACGCCAATAGAAGGTATGCTGTACACCAGTTGAAGCAGCA
TGTCATCGATGGAGAAAAAACCATTATCCAGAATCCCACAGACCAGCAGAAGAAGGACCATGAAAAAGCTGAATT
TGAGGTACATGAAGTATATGCTGTGGATGTTCTCGTCAGCTCAGGAGAGGGCAAGGCCAAGGATGCAGGACAGAG
AACCCTATTTACAAACGAGACCCCTCTAAACAGTATGGACTGAAAAATGAAAACCTTCACGTGCCTTCTTCAGTGA
GGTGGAAGGCGTTTTGATGCCATGCCGTTTACTTTAAGAGCATTGGAAGATGAGAAGAAGGCTCGGATGGGTGT
GGTGAGTGCGCCAAACATGAAGTGTGCAACCATTTAATGTTCTCTATGAGAAGGAGGGTGAATTTGTTGCCCA
GTTTAAATTTACAGTTCTGCTCATGCCCAATGGCCCCATGCGGATAACCAGTGGTCCCTTCGAGCCTGACCTCTA
CAAGTCTGAGATGGAGGTCCAGGATGCAGAGCTAAAGGCCCTCCTCCAGAGTTCTGCAAGTCGAAAAACCCAGAA
AAAGAAAAAAGAAGGCCTCCAAGACTGCAGAGAATCCCACCAGTGGGGAAACATTAGAAGAAATGAAGCTGG
GGACTGAGGTGCGTCCCCTCTCCCCAGCTTGCTGCTCCTGCCTCATCCCCTTCCCACCAAACCCAGACTCTGTG
AAGTGCAGTTCTTCTCCACCTAGGACCGCCAGCAGAGCGGGGGGATCTCCCTGCCCCCACCACAGTTCCCCAACCC
CACTCCCTTCCAACAACAACCAGCTCCAACCTGACTCTGGTCTTGGGAGGTGAGGCTTCCCAACCACGGAAGACTA
CTTTAAACGAAAAAAGAAATTGAATAATAAAATCAGGAGTCAAATTCATCGTCTTCAAGGCCCTCTTTCTAG
CCTTTTCTACTACTCTCTGCTTGGTCAAGGTTTGTGCCCCACTACAGAACAGGGCTAAATTAGCCACCACCACTG
AAAACCTCAGCCGAATTTTTTTTATACCACTCTGACGTCAGCATTTTTT

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FIGURE 142

MSGEDQQEQTIAEDLVVTKYKMGGDIANRVLRLSLVEASSSGVSVLSLCEKGDAMIMEETGKIFKKEKEMKKGIA
FPTSISVNNCVCHFSPKSDQDYILKEGDLVKIDLGHVHVDGFIANVAHTFVVDVAQGTQVTGRKADVIKAAHLCA
EAALRLVKPGNQNTQVTEAWNKVHSAFNCTPIEGMLSHQLKQHVIDGEKTI IQNPTDQQKKDHEKAEFEVHEVYA
VDVLVSSGEGKAKDAGQRTTIYKRDP SKQYGLMKTSRAFFSEVERRFDAMPFTLRAFEDEKKARMGVVECAKHE
LLQPFNVLYEKEGEFVAQFKFTVLLMPNGPMRITSGPFEPDLYKSEMEVQDAELKALLQSSASRKTQKKKKKKAS
KTAENPTSGETLEENEAGD

[illegible]

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FIGURE 144

MVADPPRDSKGLAAAEPTANGGLALASIEDQGAAAGGYCGSRDQVRRCLRANLLVLLTVVAVVAGVALGLGVSGA
GGALALGPERLSAFVFPGELLRLRLRMIILPLVVC SLIGGAASLDPGALGR LGAWALLFFLVTTLLASALGVGLA
LALQPGAASAAINASVGAAGSAENAPSKEVLDSFLDLARNIFPSNLVSAAFRSYSTTYEERNITGTRVKVPVGQE
VEGMNILGLVVFAIVFGVALRKLGP EGELLIRFFNSFNEATMVLVSWIMWYAPVGIMFLVAGKIVEMEDVGLLFA
RLGKYILCCLLGHAIHGLLVPLIYFLFTRKNPYRFLWGIVTPLATAFGTSSSSATLPLMMKCVEENNGVAKHIS
RFILPIGATVNMDGAALFQCVAAVFIAQLSQQSLDFVKIITILVTATASSVGAAGIPAGGVLT LAIILEAVNLPV
DHISLILAVDWLVDRSCTVLNVEGDALGAGLLQNYVDRTESRSTEP ELIQVKSELPLDPLPVPTEEGNPLLKH YR
GPAGDATVASEKESVM

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FIGURE 145

AAAAATCTATGATTGAGCTTTTCATCCTGACACTGGTGAGAAGATGATTTTGATAGGAAGAATGTCAGCCCAGGT
TCCCATGAACATGACCATCACAGGTTGTATGATGACGTTTTACAGGACTACGCCGGCTGTGCTGTTCTGGCAGTG
GATTAACCAGTCCTTCAATGCCGTCGTCAATTACACCAACAGAAGTGGAGACGCACCCCTCACTGTCAATGAGTT
GGGAACAGCTTACGTTTTCTGCAACAACCTGGTGCCGTAGCAACAGCTCTAGGACTCAATGCATTGACCAAGCATGT
CTCACCCTGATAGGACGTTTTGTTCCTTTTGTGCTGCCGTAGCTGCTGCTAATTGCATTAAATATTCCATTAATGAG
GCAAAGGGAACTCAAAGTTGGCATTCCCGTCACGGATGAGAATGGGAACCGCTTGGGGGAGTCGGCGAACGCTGC
GAAACAAGCCATCACGCAAGTTGTCTGTCCAGGATTCTCATGGCAGCCCTGGCATGGCCATCCCTCCATTCTAT
TATGAACACTTTGGAAAAGAAAGCCTTTTTGAAGAGGTTCCCATGGATGAGTGCACCCATTCAAGTTGGGTTAGT
TGGCTTCTGTTTGGTGTTTGGCTACACCCCTGTGTTGTGCCCTGTTTCCTCAGAAAAGTCCATGTCTGTGACAAG
CTTGGAGGCCGAGTTGCAAGCTAAGATCCAAGAGAGCCATCCTGAATTGCGACGCGTGACTTCAATAAGGGATT
GTAAGCAGGGAGGAAACCTCTGCAGCTCATTCTGCCACTGCAAAGCTGGTGTAGCCATGCTGGTGAGAAAAATC
CTGTTCAACCTGGGTTCTCCAGTTACGGAAACCTTTTAAAGATCCACATTAGCCTTTTAGAATAAAGCTGCTAC
TTTAAACAGAGCACCTGGCGTGGGCCAAGTGCCTGATACTCCCTTACACTGAATCATGTTATGATTTATAGAAATA
CCTTTCTGTAGCTTTTATAGTCATTGTTTTTCAAAGACGATATACCAGCCCTCACCCAGGTTTTAAAAAAGCAC
TGGTAGGCATAGAATAGGTGCTCAGTATATGGTCAGTAAATGTTCTATTGATTATCAATCAGTGAAAAAGAAAT
CTGTTTAAATACTGAATTTTCATCTCACTCCCATTGCAAATCAAGGAGATCTCAGCAGTGAAGTGGGAAATAC
AAAAGCTCTGGGCTAATCTATAAAACTTACCCTGAAATATTAAGGGCAGTTTGCTTCTAGTTTGGGGATTGCGC
TAGCCCAATGAAGGTGATGAAGCTTTTGGATTTGGAGGGTAAAGCTCCTTCACACCCCTTCCAAAAGTCAGTCA
CAGACCACTGCAACATGCCTTCCCTGCTGGATCATATATACATTGAGATTGTGAGTGGATTGCCTTGGTTGACT
TTTAATTTATGTTTTTGTCTTATAAAGATGATAATCTTACCTGCAGTTATTGACTTTATATTCAATTATTT
ACATCAAATAATGAAATAACTGAAATGTACAAATGTCAAATTTTGAAGTATATTCAATACCAATGCTGTATGAG
TGGGCTGAATCCAGTTTATTGTTTTTTTTTGGTAAGAAGTGAGACTACAGTTCCAGCTACCTACATGTCTTTTC
TTGTCACTCTTATAGATCTCTTTGGCTTTCAGAAAGATACAGTGATAATGTGTGTATGAATCAGTCACAATGAAT
TTTACTTGAATATTGTATGTTGCATTCCACTTCATTGAAAATAATGAAACCATGTACCACTGTTTACATCATCT
GTAGTGATTTTCATAGATAATATATTTAATATGACAGATTATGTTTCAACTCTGTAGATGTTTAAACGTCATAGACA
GTTGGCCCTCTGTATCCGTGAGCTCTATATCTGTGAATTCAACCAAGTTTGGATGGAAAATTTTTTTTTTTTTT
TTTTTTTTTTTTGAGACGGAGTCTCGCTCTGTCACCCAGGCTGGAGTGCAGTGGCGTAGTCTCGGCTCACTGCAAG
CCCCGCCTCCTGGGTTACGCCGTTCTCCTGCCTCAGCCTCTCTGAGAAGCTGGGACTACAGGCGCCCGCCACCA
CGCCCGGCTAATTTTTTTGTATTTTTTAGTAGAGACGGGGTTTTCACTGTGGTCTCGATCTCCTGACCTCGTGATCC
GCCCCCTTGGCCTCCCAAGGTGCTGGGATTACAAGCGTGAGCCACCGCACC CGCCTGAAAATATTTTCTAAAA
AGATAAAAAATATACATAACGATGAAAAATAATACAAATTTAAAAACCAATACAGTATAACAATATTTACATAG
TGCTTACATTGTATTAGGTGTTATAAGCAATCTAGAGATGATTTAGCAAGTATACAGGAGGATGTGCCTAGGTTA
TATGCAAATACTGTGCCATTTTATATCAGGAACCTGAGCATCTGCAGATATTGGTATCGGAGGGCGGTCTTGAA
CCAAGCATCCACGGATACTGAGGGGTGACATTTCAAGAAGTGTAGATCATTGTATTGAGAGATTGTAAATGAAAA
AAATATAGAACTATTTAGTTTTTGGTAGATTTTTTTCTGACAATGTGACCAGACTGAATTTCTCATAAAGAAA
AAATGGCGTGCTTGTG

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FIGURE 146

MILIGRMSAQVPMNMTITGCMMTFYRTTPAVLFWQWINQSFNAVVNYTNRSGDAPLTVNELGTAYVSATTGAVAT
ALGLNALTKHVSPLIGRFVPFAAVAAANCINIPLMRQRELKVGIPVTDENG NRLGESANA AKQAITQVVVSRILM
AAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVGFCLVFATPLCCALFPQKSSMSVTSLEAELQAKIQESH
ELRRVYFNKGL

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FIGURE 147

ATGCTGCGCTTCCTGGCACCCCGGCTGCTTAGCCTCCAGGGCAGGACCGCCCTCTACTCCTCGGCAGCAGCCCTC
CCAAGCCCCATTCTGAACCCAGACATCCCCTACAACCAGCTGTTTCATCAACAATGAATGGCAAGATGCAGTCAGC
AAGAAGACCTTCCCGACGGTCAACCTTACCACCGGGGAGGTTCATCGGGCACGTGGCTGAAGGTGACCGGGCTGAT
GTGGATCGGGCCGTGAAAGCAGCCCGGAAGCCTTCCGCCTGGGGTCCCCATGGCGCCGGATGGATGCCTCTGAG
CGGGGCCGGCTGCTGAACCTCCTGGCAGACCTAGTGGAGCGGGATCGAGTCTACTTGGCCTCACTCGAGACCTTG
GACAATGGGAAGCCTTTCCAAGAGTCTTACGCCTTGGACTTGGATGAGGTTCATCAAGGTGTATCGGTACTTTGCT
GGCTGGGCTGACAAGTGGCATGGCAAGACCATCCCCATGCATGGCCAGCATTTCCTGCTTCACCCGGCATGAGCCC
GTTGGTGTCTGTGGCCAGATCATCCCGTGGAACTTCCCTTGGTTCATGCAGGGTTGGAACTTGCCCCGGCACTC
GCCACAGGCAACACTGTGGTTATGAAGGTGGCAGAGCAGACCCCCCTCTCTGCCCTGTATTTGGCCTCCCTCATC
AAGGAGGCAGGCTTTCCCCCTGGGCTGGTGAACATCATCACGGGGTATGGCCCAACAGCAGGTGCGGCCATCGCC
CAGCACATGGATGTTGACAAAGTTGCCTTCACCGGTTCCACCGAGGTGGGCCACCTGATCCAGAAAGCAGCTGGC
GATTCCAACCTCAAGAGAGTCAACCCTGGAGCTGGGTGGTAAGAGCCCCAGCATCGTGTCTGGCCGATGCTGACATG
GAGCATGCCGTGGAGCAGTGCCACGAAGCCCTGTTCTTCAACATGGGCCAGTGCTGCTGTGCTGGCTCCCGGACC
TTCGTGGAAGAATCCATCTACAATGAGTTTCTCGAGAGAACCGTGGAGAAAGCAAAGCAGAGGAAAGTGGGGAAC
CCCTTTGAGCTGGACACCCAGCAGGGGCCTCAGGTGGACAAGGAGCAGTTTGAACGAGTCCTAGGCTACATCCAG
CTTGGCCAGAAGGAGGGCGCAAACTCCTCTGTGGCGGAGAGCGTTTCGGGGAGCGTGGTTTCTTCATCAAGCCT
ACTGTCTTTGGTGGCGTGCAGGATGACATGAGAATTGCCAAAGAGGAGATCTTTGGGCCTGTGCAGCCCCCTGTTT
AAGTTCAAGAAGATTGAGGAGGTGGTTGAGAGGGCCAACAACACCAGGTATGGCCTGGCTGCGGCTGTGTTTACC
CGGGATCTGGACAAGGCCATGTACTTCACCCAGGCACTCCAGGCCGGGACCGTGTGGGTAAACACCTACAACATC
GTCACCTGCCACACGCCATTTGGAGGGTTTAAGGAATCTGGAAACGGGAGGGAGCTGGGTGAGGATGGGCTTAAG
GCCTACACAGAGGTAAAGACGGTCACCATCAAGGTTCTCAGAAGAACTCGTAA

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FIGURE 148

MLRFLAPRLLSLQGR TALYSSAAALPSPILNPDIPYNQLFINNEWQDAVSKKTFPTVNPTTGEVIGHVAEGDRAD
VDR AVKAAREAFRLGSPWRRMDASERGRLLNLLADLVERDRVYLASLETLDNGKPFQESYALDLDEVIKVYRYFA
GWADKWHGKTIPMHGQHFCFTRHEPVGVCQIIPWNFPLVMQGWKLAPALATGNTVVMKVAEQTPLSALYLASLI
KEAGFPPGVVNIITGYGPTAGAAIAQHMDVDKVAFTGSTEVGHLIQKAAGDSNLKRVTTLELGGKSPSIVLADADM
EHAVEQCHEALFFNMGQCCAGSRTFVEESIYNEFLERTVEKAKQRKVG NPFELDTQQGPQVDKEQFERVLGYIQ
LGQKEGAKLLCGGERFGERGFFIKPTVFGGVQDDMRIAKEEIFGPVQPLFKFKKIEEVVERANNTRYGLAAAVFT
RDLDKAMYFTQALQAGTVWVNTYNIVTCHTPFGGFKESGNGRELGEDGLKAYTEVKITVTIKVPQKNS

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FIGURE 149

GCCAGGACTCCACAAGGCTGGTCCCTGCCCTGGAGCAACTTAAACAGGCCCTCTGGCCAGCCTGGAACCCCTGAG
ATGGCCTCCAGCTCAGGCAGCAGTCCCTCGCCCGGCCCTGATGAGAATGAGTTTCCCTTTGGGTGCCCTCCCACC
GTCTGCCAGGACCCAAAGGAGCCCAGGGCTCTCTGCTGTGCAGGCTGTCTCTGAGAACCCGAGGAATGGCGAG
GATCAGATCTGCCCCAAATGCAGAGGGGAAGACCTCCAGTCTATAAGCCCAGGAAGCCGTCTTCGAACTCAGGAG
AAGGCTCACCCTGAGGTGGCTGAGGCTGGAATTGGGTGCCCTTTGCAGGTGTGCGCTGCTCCTCAAGGGAAGC
CCACAGTCTGTGCAAGAGCATGAGGTCACCTCCCAGACCTCCACCTAAACCTGCTGTTGGGGTTCATGAAACAG
TGGAAGGCCCGGCTGGGCTGTGGCCTGGAGTCTGGGCCCATGGCCCTGGAGCAGAACCTGTCAGACCTGCAGCTG
CAGGCAGCCGTGGAAGTGGCGGGGACCTGGAGGTCGATTGCTACCGGGCACCTGCTCCGAGAGCCAGGAGGAG
CTGGCCCTGCAGCACTTCATGAAGGAGAAGCTTCTGGCTGAGCTGGAGGGGAAGCTGCGTGTGTTTGAGAACATT
GTTGCTGTCTCAACAAGGAGGTGGAGGCCTCCCACCTGGCCCTGGCCACCTCTATCCACCAGAGCCAGCTGGAC
CGTGAGCGCATCCTGAGCTTGGAGCAGAGGGTGGTGGAGCTTCAGCAGACCCTGGCCAGAAAGACCAGGCCCTG
GGCAAGCTGGAGCAGAGCTTGGCCCTCATGGAGGAGGCCTCCTTCGATGGCACTTTCTGTGGAAGATCACC
GTCACCAGGCGGTGCCATGAGTCGGCCTGTGGCAGGACCGTCAGCCTCTTCTCCCCAGCCTTCTACACTGCCAAG
TATGGCTACAAGTTGTGCCTGCGCTGTACCTGAATGGAGATGGCACTGGAAAGAGAACCCATCTGTGCTCTTC
ATCGTGATCATGAGAGGGGAGTATGATGCGCTGCTGCCGTGGCCTTCCGGAACAAGGTCACCTTCATGCTGCTG
GACCAGAACACCGTGAGCAGGCCATTGACGCCTTCCGGCCTGACCTAAGCTCAGCGTCCTTCCAGAGGCCCCAG
AGTGAAACCAACGTGGCCAGTGGATGCCCCACTCTTCTCCCCCTCAGCAAACCTGCAGTCACCCAAGCAGCCTAC
GTGAAGGACGACACAATGTTCTCAAGTGCATTGTGGAGACCAGCACT**TAG**GGTGGGCGGGCTCCTGAGGGAGC
TCCAACCTCAGAAGGGAGCTAGCCAGAGGACTGTGATGCCCTGCCCTTGGCACCCAAGACCTCAGGGCACAAGAT
GGGTGAAGGCTGGCATGATCCAAGCAAGACTGAGGGGTGCACTTCGGGCTGGCCATCTGGTTAGGATGGCAGGAC
GTGGGCTGGGCCACAAAGGCAAAGGTCCAGAAGGAGACAGGCAGAGCTGCTCCCCTCTGCACGGACCATGCGA
CACTGGGAGGCCAGTGAGCCACTCCGGCCCCGAATGTTGAGGTGGACTCTCACCAAATGAGAAGAAAATGGAACC
AGGCTTGGAACCGTAGGACCCAAGCAGAGAAGCTCTCGGGCTAGGAAGATCTCTGCAGGGCCGCCAGGGAGACCT
GGACACAGGCCTGCTCTCTTTTCTCCAGGGTCAGAAACAGGACCGGGTGAAGGGATGGGGTGCCAGTTTGAAT
GCAGTCTGTCCAGGCTCGTCATTGGAGGTGAACAAGCAAACCCAGACGGCTCCACTAGGACTTCAAATTGGGGGT
TGGATTTGAAGACTTTTAAGTTTCTTCCAGCCCAGAAAGTCTCTCATTCTAGCCTCCTGGCCCAGGTGAGTCTT
AGAGCTACAGGGGTTCTGGAAACATTCAGGAGCTTCTGTCTCTCCAGCTCCTCACTCACCTTCAGTAACCCCCA
CTGGACTGACCTGGTCCACAGGGCACCTGCCACCCTGGGCCTGGCAGCTCAGCTTCCCAACACGCAGGAGCACAC
CCAGCCCCCACATCCTGTGCCTCCATCAGCTAAACACCACGTCACTTCATGCAGGTGAAACCCAGTCACTGTGAG
CTCCCAGGTGCAGCCAGAGGCACCTCAAGAAGAAGAGGGGCATAAACTTCTCTTCTGCTAGAGGCCCCACC
TTTGGTGCTTTCCAGAATCCCGTAACACCTGATTAACCTGAGGCATCCACTTCTTTCAGCAGACTGATCAGGACCT
CCAAGCCACTGAGCAATGTATAACCCCAAAGGGAATTCAAAAAAAAAAAAAAAAAA

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FIGURE 150

MASSSGSSPRPAPDENEFFPGCPPTVCQDPKEPRALCCAGCLSENPRNGEDQICPKCRGEDLQSI SPGSRLRTQE
KAHPEVAEAGIGCPFAGVGCSFKGSPQSVQEHEVT SQTSHLNLLLGFMKQWKARLGCGLESGPMALEQNLSDLQL
QAAVEVAGDLEVDCYRAPCSESQEELALQHFMKEKLLAELEGKLRVFENIVAVLNKEVEASHLALATSIHQSQLD
RERILSLEQRVVELQQTLAQKDQALGKLEQSLRLMEEASFDTGLWKITNVTRRCHESACGRTVSLFSPAFYTAK
YGYKLCLRLYLNGDGTGKRTHLSLFIVIMRGEYDALLPWPFNRKVTFMLLDQNNREHAIDAFRDLSSASFQRPQ
SETNVASGCPLFFPLSKLQSPKHAYVKDDTMFLKCI VETST

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FIGURE 151

GAATTCGGGCACGAGCGCGCGGCGAATCTCAACGCTGCGCCGTCTGCGGGCGCTTCCGGGGCCACCAGTTTCTCTGC
TTTCCACCCTGGCGCCCCCAGCCCTGGCTCCCCAGCTGCGCTGCCCCGGGCGTCCACGCCCTGCGGGCTTAGCG
GGTTCAGTGGGCTCAATCTGCGCAGCGCCACCTCCATGTTGACCAAGCCTCTACAGGGGCTCCCGCGCCCCCG
GGACCCCCACGCCGCCGCCAGGAGCAAGGATCGGGAAGCGTTCGAGGCCGAGTATCGACTCGGCCCTCTCTGG
GTAAGGGGGGCTTTGGCACCCTCTTCGCAGGACACCGCCTCACAGATCGACTCCAGGTGGCCATCAAAGTGATT
CCCCGAATCGTGTGCTGGGCTGGTCCCCCTTGTGAGACTCAGTCACATGCCACTCGAAGTCGCACTGCTATGGA
AAGTGGGTGCAGGTGGTGGGCACCCTGGCGTGATCCGCCTGCTTGACTGGTTTGAGACACAGGAAGGCTTCATGC
TGGTCTCGAGCGGCCTTTGCCGCCAGGATCTCTTTGACTATATCACAGAGAAGGGCCCACTGGGTGAAGGCC
CAAGCCGCTGCTTCTTTGGCCAAGTAGTGGCAGCCATCCAGCACTGCCATTCCCGTGGAGTTGTCCATCGTGACA
TCAAGGATGAGAACATCCTGATAGACCTACGCCGTGGCTGTGCCAACTCATTGATTTTGGTTCTGGTGCCCTGC
TTCATGATGAACCCTACACTGACTTTGATGGGACAAGGGTGTACAGCCCCCAGAGTGGATCTCTCGACACCAGT
ACCATGCACTCCCGGCCACTGTCTGGTCACTGGGCATCCTCCTCTATGACATGGTGTGTGGGGACATTCCCTTTG
AGAGGGACCAGGAGATTCTGGAAGCTGAGCTCCACTTCCCAGCCATGTCTCCCCAGACTGCTGTGCCCTAATCC
GCCGTTGCTGGCCCCCAAACCTTCTTCCCAGCCCTCACTGGAAGAGATCCTGCTGGACCCCTGGATGCAAAACAC
CAGCCGAGGATGTTACCCCTCAACCCCTCCAAAGGAGGCCCTGCCCTTTGGCCTGGTCTTGTACCCCTAAGCC
TGGCCTGGCCTGGCCTGGCCCCAATGGTCAGAAGAGCCATCCCATGGCCATGTCACAGGGATTAGATGGACATTT
GTTGACTTGGTTTTACAGGTCATTACCAAGTCATTAAAGTCCAGTATTACTAAGGTAAGGGATTGAGGATCAGGGG
TTAGAAGACATAAAACCAAGTTTGCCAGTTCCTTCCCAATCCTACAAAGGAGCCTTCTCCAGAACCTGTGGT
CCCTGATTTTGGAGGGGGAACTTCTTGCTTCTCATTTTGCTAAGGAAGTTTATTTTGGTGAAGTTGTCCCATTT
TGAGCCCCGGGACTCTTATTTTGAIGATGTGTACCCACATTGGCACCTCCTACTACCACCACAACTTAGT
TCATATGCTTTTACTTGGGCAAGGGTGCTTTCCTTCCAATACCCAGTAGCTTTTATTTTAGTAAAGGGACCCCTT
TCCCCTAGCTAGGGTCCCATATTGGGTCAAGCTGCTTACCTGCCTCAGCCCAGGATTTTTTATTTTGGGGGAGG
TAATGCCCTGTTGTTACCCCAAGGCTTCTTTTTTTTTTTTTTTTTTTTTTGGGTGAGGGGACCTTACTTTGTTATC
CCAAGTGCTCTTATTCTGGTGAGAAGAACCTTAATTCCATAAATTTGGGAAGGAATGGAAGATGGACACCACCGGA
CACCACCAGACAATAGGATGGGATGGATGGTTTTTTGGGGGATGGGCTAGGGGAAATAAGGCTTGCTGTTTGT
TCCTGGGGCGCTCCCTCCAATTTTGCAGATTTTGTCAACCTCCTCCTGAGCCGGGATTGTCCAATTACTAAAATG
TAAATAATCACGTATTGTGGGGAGGGGAGTTCCAAGTGTGCCCTCCTTTTTTTTCTGCTGGATTATTTAAAAA
GCCATGTGTGGAAACCCACTATTTAATAAAAGTAATAGAATCAGAAAAAAAAAAAAAAAAAAAAA

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FIGURE 152

MLTKPLQGPPAPPGTPTPPPGGKDREAFEAEYRLGPLLKGKGGFTVFA GHRLTDR LQVAIKVIPRNRVLGWSPLS
DSVTCPLEVALLWKVGAGGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSRCFFGQVVAA
IQHCHSRGVVHRDIKDENILIDLRRGCAKLIDFGSGALLHDEPYTDFD GTRVYSPPEWISRHQYHALPATVWSLG
ILLYDMVCGDIPFERDQEILEAELHFPAHVSPDCCALIRRCLAPKPSSRPSLEEILLDPWMQTPAEDVTPQPLQR
RPCPFGLVLATLSLAWPGLAPNGQKSHPMAMSQG

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FIGURE 153

AAAATTTGAAGACAAGATGGGCACCTACTCTACAATTCTGATAAAAAACAGAGGTCATCGAATGTGGGAACTACTG
TGGAGTACGCATCATTCACTCTTTGATTGCAGAGTTCTCACTGGAAGAATTGAAGAAAAGCTATCACCTGAATAA
AAGTCAAATTATGTTGGATATGCTAACTGAGAATTTGTTCTTCGATACTGGTATGGGAAAAAGTAAATTTTTGCA
AGATATGCACACACTCCTACTCACAAGACACCGCGATGAACATGAAGGTGAAACAGGAAATTGGTTTTCCCAT
TATTGAAGCATTACATAAAGATGAAGGAAATGAAGCAGTTGAAGCTGTATTGCTTGAAAGTATCCATCGGTTCAA
CCCAAATGCATTCAATTTGCCAAGCGTTGGCAAGACATTTCTACATTAAAAAGAAGGACTTTGGCAATGCTCTAAA
CTGGGCAAAACAAGCAAAAATCATAGAACCTGACAATTCTTATATCTCAGATACACTGGGTCAAGTCTACAAAAG
TAAATAAGATGGTGGATAGAGGAAAACGGAGGAAACGGGAACATTTTCAGTTGATGATCTAATTGCTCTTTTGA
TTTAGCAGAACATGCCTCAAGTGCATTCAAAGAATCTCAACAGCAAAGTGAAGATAGAGAGTATGAAGTGAAGGA
AAGATTGTATCCGAAGTCAAAAAGGCGGTATGATACTTACAATATAGCTGGTTATCAAGGAGAGATAGAAGTTGG
GCTTTACACAATCCAAATTTCTCCAGCTCATTCTTTTTTTGATAATAAAAAATGAGCTATCTAAAAGATATATGGT
CAATTTTGTATCAGGAAGTAGTGATATTCCAGGGGATCCAAACAATGAATATAAATTAGCCCTCAAAAATATAT
TCCTTATTTAACTAAATTGAAATTTTCTTTGAAAAAGTCCTTTGATTTTTTTGATGAATACTTTGTCTGCTAAA
ACCCAGGAACAATATTAAGCAAAATGAAGAGGCCAAAACCTCGGAGAAAGGTGGCTGGATATTTTAAGAAATATGT
AGATATATTTTGTCTCTTAGAAGAATCAGAAAACAACACAGGTCCTGGATCAAAGTTCAGTGAGCCACTTCAAGT
AGAGAGATGCAGGAGAAACCTAGTAGCTTTAAAGCAGACAAGTTTTCTGGGCTCTTGAATATCTTATCAAAAG
TCAAGAGGATGCTATAAGCACTATGAAATGTATAGTGAACGAATATACTTTCTCTTAGAACAATGCAGTGTCAA
AATCCAGTCAAAAGAAAAGCTAAATTTTCATCTTGGCCAACATTATTCTCTCTGTATCCAACCTACCTCCAGATT
AGTAAAGCCAGTTGAAAACTAAAAGATCAGCTTCGAGAAGTCTTGCAACCAATAGGACTGACTTATCAGTTTTC
AGAACCGTATTTTCTAGCTTCCCTCTTATTCTGGCCAGAAAATCAACAACCTAGATCAACATTCTGAACAAATGAA
AGAGTATGCTCAAGCACTAAAAAATCTTTCAAGGGGCAATATAAACATATGCATCGTACAAAGCAACCAATTGC
ATATTTCTTTCTTGGAAAAGGTAAAAGACTGGAAAGACTTGTTTCACAAAGGAAAAATTGACCAGTGCTTTAAGAA
GACACCAGATATTAATTCCTTGTGGCAGAGTGGAGATGTGTGGAAGGAGGAAAAAGTCCAAGAACTTTTGCTTCG
TTTACAAGGTGCGAGCTGAAAACAATTGTTTATATATAGAATATGGAATCAATGAAAAAATCACAAATACCCATCAC
TCCCGCTTTTTTAGGTCAACTTAGAAGTGGCAGAAGCATAGAGAAGGTGTCTTTTACCTGGGATTTCCCATTTGG
AGGCCCACTTGCTTATGACATTGAAATTGTTTTAAGAGCCTGATATTCTTCTCCAAGAATTTGATCTCAGTACCC
ATTTAATTTTTTTGGACTCAAGATCTATGCTTTAAACCGGCAAGGTTATAGATACAGCCTCTAGCTCTTCAGATC
TGTACATGCAGTATTTAATTTCTCTTAAACATGTATGAGTTCTACAAGGACAATAGTGAAAAAGGAAGGAGTG
AGATATATGAAAAGTAGCAAATATGTTCTTGGTTTGGTTAACATCATTGATGACAAAATAATAAGGAGCTATGA
CTGGAGTCAGGAGAAGTTAGTGTAATAAGCTGGCTACACAGAACCCCACTACTTACCAGGCATGGATTGAAGAAG
ATTGTCTACTCAAATGGCATTTAGACATTAGAATGTCTGGGAAAATATTTCTCAAAGACAGCAAAAACCTCTCAA
ACTGAGGAGCAACATTTATTCTTACTAAGCAGATCATCAATGTATCATGTGCTTGGCACTCAAGGATCTTCCAAA
ACAGAGGACCAACCAGTCTTCTGAAGGTCATGCCACAGAAGTCATCGACCTTACCAAAGTAGGTTGGAGAATT
AGATTGCCTTTTCATGCAGTGAGATTCAAGTTAAGCAAAAATGAAATTTGTCTCTATAGCTAATTAGCTTATCAAC
TCCCCCTCCAAACAAACAATTAATAAAAAAACATACAGACACTCAAATCCACAAGCTAATGAACAAAAGGGACTC
TTGTGAGAAGACTAATGAGTCCCTCATCCAGAAGATGCCAATGTACTGGCAGATTAACATACAACCTATGTTTTG
AACAAAAACAACCAGCGATACGTAATCAAAATGTAATTTTCCCTAATAAAATTATGGATATGGGCAGTCATCAA
TGGCTGCCAAAACCATTAAGTGGAAAGCTGATTAAAAAACAAAAATTTCTAATGGATTTATCAAAGTGTCCCAA
TCCTGATAAATATTAACATCAGAGGAAGACCAGACATTATGGGCCTGGAAGTACTATAGGAGTGCACACATCA
CCCGTGACATGGTCTTGCCAAATAATTAAACCTGAATTTGATCAGGTCCTCTGGATCTTATTTGCAATTCAAAAGA
AATTTTAAAAAATCCTACTAACACCACCACAAATATGCAATCAGCAATATCCAGAAAGGGGAAATTCACAGGAC
AAAAACCTGGTTTTCTTTTTTGGTTTTCTTCAACCAAAAAAGAAAGAAATTGCAAAGGACCAAAAAAATGTTGGGG
AATCTATACATTATAAGGGACTTAACAATAAAGGGCAACATATAGACTTTAGATCCTAATTTGAGCAAAATCTA
AAATCAATTATTAGGCAATCAGAAAAATTTGAACACAGACTAGATATTTGAGGATATTAAGGTACTATATTATTG
AAGATTCATGGTTATGTTTTTTAAAGAGTTTCATGCCTTTTAGAGATACATACTAAAGTATTTGTAAATAAATGA
CATGATCTAGAAAAA

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FIGURE 154

MGTYSTILIKTEVIECGNYCGVRIIHSLIAEFSLEELKKSYPHLNKSQIMLDMLTENLFFDTGMGKSKFLQDMHTL
LLTRHRDEHEGETGNWFSPIEALHKDEGNEAVEAVLLESIHRFNPNAFICQALARHFYIKKKDFGNALNWAKQA
KIIEPDNSYISDTLGQVYKSKIRWWIEENGNGNI SVDDLIALLDLAEHASSAFKESQQQSEDREYEVKERLYPK
SKRRYDTYNIAGYQGEIEVGLYTIQILQLIPFFDNKNELSKRYMVNFVSGSSDIPGDPNNEYKLALKNYIPYLT
LKFSLKKSFDFFDEYFVLLKPRNNIKQNEEAKTRRKVAGYFKKYVDIFCLLEESQNNNTGLGSKFSEPLQVERCRR
NLVALKADKFSGLLEYLIKQEDAISTMKCIVNEYTFLLEQCTVKIQSKEKLNFI LANIILSCIQPTSRLVKPVE
KLKDQLREVLQPIGLTYQFSEPYFLASLLFWPENQQLDQHSEQMKEYAQALKNSFKGQYKMHRTKQPIAYFFLG
KGKRLERLVHKGKIDQCCKTPDINSLWQSGDVWKEEKVQELLLRLQGRAENNCLYIEYGINEKITIPITPAFLG
QLRSGRSIEKVSFYLGFPPIGGPLAYDIEIV

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FIGURE 155

CGCCCCCTGCTCTCGCGCCGGCGTTCGGCTGCGTCTCCGGCGTTTGAATTGCGCTTCCGCCATCTTTCCAGCCTCAG
TCGGACGGGCGCGGAGGCGCTTCTGGAAGGAACGCCGCGCATGGCTGCGCAGGGAGAGCCCCAGGTCCAGTTCAAA
CTTGATTGTTGGTGATGGTGGTACTGGAAAAACGACCTTCGTGAAACGTCATTTGACTGGTGAATTTGAGAAG
AAGTATGTAGCCACCTTGCGTGTGAGGTTTCATCCCTAGTGTTCCACACCAACAGAGGACCTATTAAAGTTCAAT
GTATGGGACACAGCCGGCCAGGAGAAATTCGGTGGACTGAGAGATGGCTATTATATCCAAGCCCAGTGTGCCATC
ATAATGTTTGATGTAACATCGAGAGTTACTTACAAGAATGTGCCTAACTGGCATAGAGATCTGGTACGAGTGTGT
GAAAACATCCCCATTGTGTTGTGTGGCAACAAAGTGGATATTAAGGACAGGAAAGTGAAGGCGAAATCCATTGTC
TTCCACCGAAAGAAGAATCTTCAGTACTACGACATTTCTGCCAAAAGTAACTACAACCTTTGAAAAGCCCTTCCTC
TGGCTTGCTAGGAAGCTCATTGGAGACCCTAACTTGAATTTGTTGCCATGCCTGCTCTCGCCCCACCAGAAGTT
GTCATGGACCCAGCTTTGGCAGCACAGTATGAGCACGACTTAGAGGTTGCTCAGACAACCTGCTCTCCCGGATGAG
GATGATGACCTGTGAGAATGAAGCTGGAGCCCAGCGTCAGAAGTCTAGTTTATAGGCAGCTGTCTGTGATGTC
AGCGGTGCAGCGTGTGTGCCACCTCATTATTATCTAGCTAAGCGGAACATGTGCTTTATCTGTGGGATGCTGAAG
GAGATGAGTGGGCTTCGGAGTGAATGTGGCAGTTTAAAAAATAACTTCATTGTTTGGACCTGCATATTTAGCTGT
TTGGACGCAGTTGATTCCTTGAGTTTCATATATAAGACTGCTGCAGTCACATCACAATATTCAGTGGTGAAATCT
TGTTTGTTACTGTCAATCCCATTCCTTTCTTTAGAATCAGAATAAAGTTGTATTTCAAATATCTAAGCAAGTGA
ACTCATCCCTTGTTTATAAATAGCATTGGAAACCACTAAAGTAGGGAAGTTTATGCCATGTTAATATTTGAAT
TGCCTTGCTTTTATCACTTAATTTGAAATCTATTGGGTTAATTTCTCCCTATGTTATTTTGTACATTTGAGCC
ATGTCACACAACTGATGATGACAGGTCAGCAGTATTCTATTTGGTTAGAAGGGTTACATGGTGTAAATATTAGT
GCAGTTAAGCTAAAGCAGTGTGCTCCACCTTCATATTGGCTAGGTAGGGTCACCTAGGGAAGCACTTGCTCAA
AATCTGTGACCTGTCAGAATAAAAAATGTGGTTTGTACATATCAAATAGATATTTTAAGGGTAATATTTCTTTTA
TGGCAAAAGTAATCATGTTTTAATGTAGAACCCTCAAACAGGATGGAACATCAGTGGATGGCAGGAGGTTGGGAAT
TCTTGCTGTTAAAAATAATTACAAATTTTGCACCTTTTGTGTTGAATGTTAGATGCTTAGTGTAAGTTGATACGC
AAGCCG

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FIGURE 156

MAAQGE PQVQFKLVLVGDGGTGKTTFVKRHLTGEFEKKYVATLGVEVHPLVFHTNRGPIKFNVWDTAGQEKFGGL
RDGYIQAQCAIIMFDVTSRVTYKNVPNWHRDLVRVCENIPIVLCGNKVDIKDRKVKAKSIVFHRKKNLQYYDIS
AKSNYNFEKPFLLWLARKLIGDPNLEFVAMPALAPPEVVM DPALAAQYEHDLVAQT TALPDEDDDL

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FIGURE 157

TTAATTTTCTTTTAAATGTTTTGTAACTTACATGTGATTAAAGTGTGTGCCAGACTTTTATTGACAGTCT
CTCGTGGAAGTTGCACAAATAGCTTGGAGGGTTCCTGTGTATCTTTGCCAGCTCTCCCCAGTGATGGTGTCTTA
CATAACCACAGCCTGGGTGACAGAGTGAGCCCCATCTC

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FIGURE 158

MFCNLTCD

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FIGURE 159

GCAGAGGAGGCGGCGGAACACCCCGGGTTGGTCGGGTTTCCAAGGGCTGACCCGAGCTCCAGCACTTTTTCCGCG
CCTGATTTTTTCAGAGCTCTTCAGAAACCAGGCTGCTTTTCAGGAACATTGCTGTGGATTCCCAGGGCCTATTCCAC
TAGAAGCAAGATGGCTGAACTCAATACTCATGTGAATGTCAAGGAAAGATCTATGCAGTTAGATCAGTTGTTCC
CAACAAAAGCAATAATGAAATAGTCCTGGTGCTCCAACAGTTTGATTTTAATGTGGATAAAGCCGTGCAAGCCTT
TGTGGATGGCAGTGCAATTCAAGTTCTAAAAGAATGGAATATGACAGGAAAAAGAAGAACAATAAAAGAAAAAG
AAGCAAGTCCAAGCAGCATCAAGGCAACAAAGATGCTAAAGACAAGGTGGAGAGGCCTGAGGCAGGGCCCCCTGCA
GCCGAGCCACCACAGATTCAAAACGGCCCCATGAATGGCTGCGAGAAGGACAGCTCGTCCACAGATTCTGCTAA
CGAAAAACCAGCCCTTATCCCTCGTGAGAAAAAGATCTCGATACTTGAGGAACCTTCAAAGGCACTTCGTGGGGT
CACAGAAGGCAACAGACTACTGCAACAGAACTATCCTTAGATGGGAACCCCAAACCTATACATGGAACAACAGA
GAGGTCAGATGGCCTACAGTGGTCAGCTGAGCAGCCTTGTAACCAAGCAAGCCTAAGGCAAAAACATCTCCTGT
TAAGTCCAATACCCCTGCAGCTCATCTTGAAATAAAGCCAGATGAGTTGGCAAAGAAAAGAGGCCCAAATATTGA
GAAATCAGTGAAGGATTGCAACGCTGCACCGTTTCTCTAACTAGATATCGCGTCATGATTAAGGAAGAAGTGA
TAGTTCCGTGAAGAAGATCAAAGCTGCCTTTGCTGAATTACACAACCTGCATCATTGACAAAGAAGTTTCATTAAT
GGCAGAAATGGATAAAGTTAAAGAAGAAGCCATGGAAATCCTGACTGCTCGTCAGAAGAAAGCAGAAGAACTAAA
GAGACTACTAACCTTGCCAGTCAGATGGCAGAGATGCAGCTGGCCGAACCTCAGGGCAGAAATTAAGCACTTTGT
CAGCGAGCGTAAATATGACGAGGAGCTCGGGAAAGCTGCCCGGTTTTCCTGTGACATCGAACAGCTGAAGGCCCA
AATCATGCTCTGCGGAGAAATTACACATCCAAAGAACAATACTTTCCTCAAGAACTCCCTGCAGCTCCCTGCTGCC
TCTGTGAATGCGCAGCAGCAACCTCTGGGAAACAGAGTAACTTTTCCCGAAAATCATCCACTCACAATAAGCC
CTCTGAAGGCAAAGCGGCAAACCCCAAAATGGTGAGCAGTCTCCCCAGCACCGCCGACCCCTCTCACCAGACCAT
GCCGGCCAACAAGCAGAATGGATCTTCTAACCAAAGACGGAGATTAAATCCACAGTATCATAACAACAGGCTAAA
TGGGCTGCCAAGTCGCAGGGCAGTGGGAATGAAGCCGAGCCACTGGGAAAGGGCAACAGCCGCCACGAACACAG
AAGACAGCCGCACAACGGCTTCCGGGCCAAAAACAAAGGCGGTGCCAAAAATCAAGAGGCTTCCTTGGGGATGAA
GACCCCGAGGCCCCGGCCATTCTGAAAAGCCCCGGCGAAGGCAGCAGCTGCAGACACCTCGGAGGCCAGGCC
CTTCCGGGCTAGTGTCGGTAGGGTTTCACAGTGCAATCTCTGCCCCACGAGAATAGAAGTTTCCACAGATGCAGC
AGTTCTCTCAGTCCCGGCTGTGACGTTGGTGGCCTGAGCTAGGAGGAAAAAGAGCAGTTTCACTCAGTTTGGT
TCCCTGCCCCGAGGTGCTGACCCAATTGCTGCCAAAAGAGTGTCAATCAGAATATACAAATCCCGTATGGTTGTG
TCATCCTCTCTTAATCATTTTTACTAATTCTAATAATCAGCTCTAGCTTGCTTCATAATTTTCATGGCTTTGCTT
GATCTGTTGATGCTTCTCTCATCAAGACTTTGCAGCATTTTAGCCAGGCAGTATTTACTCATTATTAGGAAAAT
CAAGATGTGGCTGAAGATCAGAGGCTCAGTTAGCAACCTGTGTTGTAGCAGTGATGTCAGTCCATAGATTGTCTT
TAGAGAGTTAATGTTACAAAAAGAATTCTTAATAATCAGACAAACATGATCTGCTGAGGACACATGCGCTTTTG
TAGAATTTAACATCTGGTGTTTTTCTGAAAAAATATATATACATATATTGCTTTATTTGAAACAAATTAAAAATAT
GCTGCATTTGAAAAAAAAAAAAAAAAAAAAA

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FIGURE 160

MAELNTHVNVKEKIYAVRSVVPNKSNEIVLVLQQFDFNVDKAVQAFVDGSAIQVLKEWNMTGKKKNNKRKRSKS
KQHQGNDKADKVERPEAGLPQPPIQNGPMNGCEKDSSTDSANEKPALIPREKKISILEEPSKALRGVTEG
NRLLOQKLSLDGNPKPIHGTTERSDGLQWSAEQPCNPSPKPAKTSPVKSNTPAAHLEIKPDELAKKRGPNIEKSV
KDLQRCTVSLTRYRVMIKEEVDSSVKKIKAFAELHNCCIIDKEVSLMAEMDKVKEEAMEILTARQKKAEEELKRLT
NLASQMAEMQLAELRAEIKHFVSEKRYDEELGKAARFSCDIEQLKAQIMLCGEITHPKNNYSSRTPCSSLLPLLN
AHAATSGKQSNFSRKSSTHNKPSEGKAANPKMVSSLPSTADPSHQTMPANKQNGSSNQRRRFNPQYHNNRLNGPA
KSQSGSNEAEPLGKGNSRHEHRRQPHNGFRPKNKGGAKNQEASLGMKTPEAPAHSEKPRRRQHAADTSEARPFGRG
SVGRVSQCNCPCPTRIEVSTDAAVLSVPAVTLVA

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FIGURE 161

GGGGGAGTGAAAGCGAAAGCCCGGGCGACTAGCCGGGAGACCAGAGATCTAGCGACTGAAGCAGCATGGCCAAGC
CGTGTGGGGTGCGCCTGAGCGGGGAAGCCCGCAAACAGGTGGAGGTCTTCAGGCAGAATCTTTTCCAGGAGGCTG
AGGAATTCTCTACAGATTCTTGCCACAGAAAAATCATATACCTGAATCAGCTCTTGCAAGAGGACTCCCTCAATG
TGGCTGACTTGACTTCCCTCCGGGCCCCACTGGACATCCCCATCCCAGACCCTCCACCCAAGGATGATGAGATGG
AAACAGATAAGCAGGAGAAGAAAGAAGTCCCTAAGTGTGGATTCTCCCTGGGAATGAGAAAGTCTGTCCCTGC
TTGCCCTGGTTAAGCCAGAAGTCTGGACTCTCAAAGAGAAATGCATTCTGGTGATTACATGGATCCAACACCTGA
TCCCCAAGATTGAAGATGGAAATGATTTTGGGGTAGCAATCCAGGAGAAGGTGCTGGAGAGGGTGAATGCCGTCA
AGACCAAAGTGGAAAGCTTCCAGACAACCATTTCAGTACTTCTCAGAACGTGGGGATGCTGTGGCCAAGGCCT
CCAAGGAGACTCATGTAATGGATTACCGGGCCTTGGTGCATGAGCGAGATGAGGCAGCCTATGGGGAGCTCAGGG
CCATGGTGCTGGACCTGAGGGCCTTCTATGCTGAGCTTTATCATATCATCAGCAGCAACCTGGAGAAAATTGTCA
CCCCAAGGGTGAAGAAAAGCCATCTATGTACTGAACCCCGGGACTAGAAGGAAAATAAATGATCTATATGTTGTG
TGG

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FIGURE 162

MAKPCGVRLSGEARKQVEVFRQNLFQEAEEFLYRFLPQKIIYLNQLLQEDSLNVADLTSLRAPLDIPIPDPPKD
DEMETDKQEKKEVPKCGFLPGNEKVLSELLALVKPEVWTLKEKCILVITWQHLPKIEDGNDFGVAIQEKVLERV
NAVKTKEAFQTTISKYFSEKGDVAKASKETHVMDYRALVHERDEAAYGELRAMVLDLRAFYAELYHISSNLE
KIVTPKGEEKPSMY

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FIGURE 163

CACGCTTGCCGCCGCCCGCCGAGAAATGCTTCGGTTACCCACAGTCTTTCGCCAGATGAGACCGGTGTCCAGGGTA
CTGGCTCCTCATCTCACTCGGGCTTATGCCAAAGATGTAAATTTGGTGCAGATGCCCCGAGCCTTAATGCTTCAA
GGTGTAGACCTTTTAGCCGATGCTGTGGCCGTTACAATGGGGCCAAAGGAAGAACAGTGATTATTGAGCAGGGT
TGGGGAAGTCCCAAAGTAACAAAAGATGGTGTGACTGTTGCAAAGTCAATTGACTTAAAAGATAAATACAAGAAC
ATTGGAGCTAACTTGTTCAGATGTTGCCAATAACACAAATGAAGAAGCTGGGGATGGCACTACCACTGCTACT
GTACTGGCACGCTCTATAGCCAAGGAAGGCTTCGAGAAGATTAGCAAAGGTGCTAATCCAGTGGAATCAGGAGA
GGTGTGATGTTAGCTGTTGATGCTGTAATTGCTGAACCTTAAAAAGCAGTCTAAACCTGTGACCACCCCTGAAGAA
ATTGCACAGGTTGCTACGATTTCTGCAAACGGAGACAAAGAAATTGGCAATATCATCTCTGATGCAATGAAAAA
GTTGGAAGAAAGGGTGTCAACAGTAAAGGATGGAAAAACACTGAATGATGAATTAGAAATTATTGAAGGCATG
AAGTTTGATCGAGGCTATATTTCTCCATACTTTATTAAATACATCAAAAGGTCAGAAATGTGAATTCCAGGATGCC
TATGTTCTGTTGAGTGAAGAAAATTTCTAGTATCCAGTCCATTGTACCTGCTCTTGAAATTGCCAATGCTCAC
CGTAAGCCTTTGGTCATAATCGCTGAAGATGTTGATGGAGAAGCTCTAAGTACACTCGTCTTGAAATAGGCTAAAG
GTTGGTCTTCAGGTTGTGGCAGTCAAGGCTCCAGGGTTTGGTGACAATAGAAAGAACCAGCTTAAAGATATGGCT
ATTGCTACTGGTGGTGCAGTGTGTTGAGAAGAGGGATTGACCCTGAATCTTGAAGACGTTACAGCTCATGACTTA
GGAAAAGTTGGAGAGGTCATTGTGACCAAAGACGATGCCATGCTCTTAAAGGAAAAGGTGACAAGGCTCAAATT
GAAAAACGTATTCAAGAAATCATTGAGCAGTTAGATGTCACAACTAGTGAATATGAAAAGGAAAAACTGAATGAA
CGGCTTGCAAAACTTTTCAGATGGAGTGGCTGTGCTGAAGGTTGGTGGGACAAGTGAATGTTGAAGTGAATGAAAAG
AAAGACAGAGTTACAGATGCCCTTAATGCTACAAGAGCTGCTGTTGAAGAAGGCATTGTTTTGGGAGGGGGTTGT
GCCCTCCTTCGATGCATTCCAGCCTTGGACTCATTGACTCCAGCTAATGAAGATCAAAAAATTGGTATAGAAATT
ATTAAGAAGAACTCAAAATTCAGCAATGACCATTGCTAAGAATGCAGGTGTTGAAGGATCTTTGATAGTTGAG
AAAATTATGCAAAGTTCCTCAGAAGTTGGTTATGATGCTATGGCTGGAGATTTTGTGAATATGGTGGAAAAAGGA
ATCATTGACCCAACAAAGGTTGTGAGAACTGCTTTATTGGATGCTGCTGGTGTGGCCTCTCTGTTAACTACAGCA
GAAGTTGTAGTCACAGAAATTCCTAAAGAAGAGAAGGACCCTGGAATGGGTGCAATGGGTGGAATGGGAGGTGGT
ATGGGAGGTGGCATGTTCTAACTCCTAGACTAGTGCTTTACCTTTATTAATGAAGTGTGACAGGAAGCCCAAGGC
AGTGTTCCTCACCAATAACTTCAGAGAAGTCAGTTGGAGAAAATGAAGAAAAAGGCTGGCTGAAAATCACTATAA
CCATCAGTTACTGGTTTCAGTTGACAAAATATATAATGGTTTACTGCTGTCATTGTCCATGCCTACAGATAATTT
ATTTTGTATTTTGAATAAAAAACATTTGTACATTCTGATACTGGGTACAAGAGCCATGTACCAGTGACTGCT
TTCAACTTAAATCACTGAGGCATTTTACTACTATCTGTTAAATCAGGATTTTAGTGCTTGCCACCACCAGAT
GAGAAGTTAAGCAGCCTTTCTGTGGAGAGTGAGAATAATTGTGTACAAAGTAGAGAAGTATCCAATTATGTGACA
ACCTTTGTGTAATAAAAAATTTGTTTAA

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FIGURE 164

MLRLPTVFRQMRPVSRVLAPHLTRAYAKDVKFGADARALMLQGVDLLADAVAVTMGPKGRTVIEQGWGSPKVTK
DGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTITATVLARSIAKEGFEEKISGANPVEIRRGVMLAVDA
VIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKTLNDELEIEGMKFDRGYIS
PYFINTSKGQKCEFQDAYVLLSEKKISSIQSIVPALEIANAHRKPLVIIAEDVDGEALSTLVNRLKVGLQVVAV
KAPGFGDNRKNQLKDMAIATGGAVFGEEGLTLNLEDVQPHDLGKVGEVIVTKDDAMLLKGKGDKAQIEKRIQEI
EQLDVTTSEYEKEKLNRLAKLSGVAVLKVGGS DVEVNEKKDRVTDALNATRAAVEEGIVLGGGCALLRCIPA
LDSLTPANEDQKIGIEIKRTLKIPAMTIAKNAGVEGSLIVEKIMQSSSEVGYDAMAGDFVNMVEKGIIDPTKVV
RTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMGAMGGMGGMGGMGMF

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FIGURE 165

TACATGGCGAGCAAAAAACAACGCTGAGAGAATCTTTTCTCTAATGCCAGAGAAAAATGAACATTCTATTGCA
CAATGATCCGAGGAATGGTGAAGCTGATGTATACACATTTAATGCATTGATTGAAGCAACAGTATGTGCGATAAA
TGAGAAATTTGAGGAAAAATGGAGTAAATACTGGAGCTGCTAAGACACATGGTTGCACAGAAGGTGAAACCAA
TCTTCAGACTTTTAATACCATTTCTGAAATGTCTCCGAAGATTTTCATGTGTTTGCAAGATCGCCAGCCTTACAGGT
TTTACGTGAAATGAAAGCCATTGGAATAGAACCTCGCTTGCAACATATCACCATATTATTTCGCTGTTTGATCA
ACCTGGAGACCCTTTAAAGAGATCATCCTTCATCATTATGATATAATGAATGAATTAATGGGAAAGAGATTTTC
TCCAAAGGACCCGGATGATGGCATATAAGTTTTTTTTCAGTCAGCCATGAGCATATGCTCATCTCTCAGAGATCTAG
AACTTGCCTACCAAGTACATGGCCTTTTAAAAACCGGAGACAACCTGGAAATTCATTGGACCTGATCAACATCGTA
ATTTCTATTATTCCAAGTTCTTCGATTTGATTTGTCTAATGGAACAAATTGATGTTACCTTGAAGTGGTATGAGG
ACCTGATACCTTCAGCCTACTTTCCCCACTCCCAACAATGATACATCTTCTCCAAGCATTGGATGTGGCCAATC
GGCTAGAAGTGATTCTAAAATTTGGAAAGATAGTAAAGAATATGGTCATACTTTCCGCAGTGACCTGAGAGAAG
AGATCCTGATGCTCATGGCAAGGGACAAGCACCCACCAGAGCTTCAGGTGGCATTGCTGACTGTGCTGCTGATA
TCAATCTGCGTATGAAAGCCAACCCATCAGACAGACTGCTCAGGATTGGCCAGCCACCTCTCTCAACTGTATAG
CTATCCTCTTTTTAAGGGCTGGGAGAACTCAGGAAGCCTGGAAAATGTTGGGGCTTTTCAGGAAGCATAATAAGA
TTCCTAGAAGTGAGTTGCTGAATGAGCTTATGGACAGTGCAAAAGTGTCTAACAGCCCTTCCAGGCCATTGAAG
TAGTAGAGCTGGCAAGTGCCCTCAGCTTACCTATTTGTGAGGGCCTCACCCAGAGAGTAATGAGTGATTTTGCAA
TCAACCAGGAACAAAAGGAAGCCCTAAGTAATCTAACTGCATTGACCAGTGACAGTGATACTGACAGCAGCAGTG
ACAGCGACAGTGACACCAGTGAAGGCAAAATGAAAGTGGAGATTCAGGAGCAGCAATGGTCTCACCATAGCTGCTG
GAATCACACCTGAGAACTGAGATATACCAATATTTAACATTGTTACAAAGAAGAAAAGATACAGATTTGGTGAAT
TTGTTACTGTGAGGTACAGTCAGTACACAGCTGACTTATGTAGATTTAAGCTGCTAATATGCTACTTAACCATCT
ATTAATGCACCATTAAGGCTTAGCATTTAAGTAGCAACATTGCGGTTTTTCAGACACATGGTGAGGTCCATGGCT
CTTGTCATCAGGATAAGCCTGCACACCTAGAGTGTGGTGAGCTGACCTCACGATGCTGCTCCTCGTGCGATTGCC
CTCTCCTGCTGCTGGACTTCTGCCTTTGTTGGCCTGATGTGCTGCTGTGATGCTGGTCCTTCATCTTAGGTGTTT
ATGCAGTTCTAACACAGTTGGGGTTGGGTCAATAGTTTCCCAATTCAGGATATTTTCGATGTCAGAAATAACGCA
TCTTAGGAATGACTAAACAAGATAATGGCAGTTTAGGCTGCACAACCTGGTAAAATGACTGTAGATAAATGTTGTA
ATTAGTGACACGTTTGTATTTTTGTAAATATAGCCGCTGCCATAGTTTTCTAACTTGAACAGCC

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FIGURE 166

MMAYKEFFQSAMSSICSSLRDLELAYQVHGLLKTGDNWKEFIGPDQHRNFYYSKFFDLICLMEQIDVTLKWYEDLIPS
AYFPHSQTMIHLLQALDVANRLEVIPKIWKDSKEYGHTFRSDLREEILMLMARDKHPPPELQVAFADCAADIKSAY
ESQPIRQTAQDWPATSLNCIAILFLRAGRTQEAWKMLGLFRKHKNKIPRSELLNELMDSAKVSNSPSQAIEVVELA
SAFSLPICEGLTQRVMSDFAINQEKEALSNTALTSDSDTDSSSDSDSDTSEK

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FIGURE 167

ATGGAAGATTCGATGGACATGGACATGAGCCCCCTGAGGCCCCAGAACTATCTTTTCGGTTGTGAACTAAAGGCC
GACAAAGATTATCACTTTAAGGTGGATAATGATGAAAATGAGCACCAGTTATCTTTAAGAACGGTCAGTTTAGGG
GCTGGTGCAAAGGATGAGTTGCACATTGTTGAAGCAGAGGCAATGAATTACGAAGGCAGTCCAATTAAAGTAACA
CTGGCAACTTTGAAAATGTCTGTACAGCCAACGGTTTCCCTTGGGGGCTTTGAAATAACACCACCAGTGGTCTTA
AGGTTGAAGTGTGGTTCAGGGCCAGTGCATATTAGTGGACAGCACTTAGTAGCTGTGGAGGAAGATGCAGAGTCA
GAAGATGAAGAGGAGGAGGATGTGAACTCTTAAGTATATCTGGAAAGCGGTCTGCCCCTGGAGGTGGTAGCAAG
GTTCCACAGAAAAAAGTAAAAGTCTGCTGCTGATGAAGATGATGACGATGATGATGAAGAGGATGATGATGAAGAT
GATGATGATGATGATTTTGTGATGATGAGGAAGCTGAAGAAAAAGCGCCAGTGAAGAAATCTATACGAGATACTCCA
GCCAAAAATGCACAAAAGTCAAATCAGAATGGAAAAGACTCAAACCATCATCAACACCAAGATCAAAAGGACAA
GAATCCTTCAAGAAACAGGAAAAAACTCCTAAAACACCAAAGGACCTAGTTCTGTAGAAGACATTAAAGCAAAA
ATGCAAGCAAGTATAGAAAAAGGTGGTTCTCTTCCCAAAGTGGAAGCCAAATTCATCAATTATGTGAAGAATTGC
TTCCGGATGACTGACCAAGAGGCTATTCAAGATCTCTGGCAGTGGAGGAAGTCTCTTTAA

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FIGURE 168

MEDSMDMDMSPLRPQNYLFGCELKADKDYHFKVDNDENEHQLSLRTVSLGAGAKDELHIVEAEAMNYEGSPIKVT
LATLKMSVQPTVSLGGFEITPPVVLRLKCGSGPVHISGQHLVAVEEDAEESEDEEEEDVKLLSISGKRSAPGGGSK
VPQKKVKLAADEDDEDDDDDEDDDDDDDDDDFDDEEAEEKAPVKKSIRDTPAKNAQKSNQNGKDSKPSSTPRSKGQ
ESFKKQEKTPKTPKGPSSVEDIKAKMQASIEKGGSLPKVEAKFINYVKNCFRMTDQEAIQDLWQWRKSL

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FIGURE 169

AATGACAGGTTGCTCAGAGACTGCTGATTTCCATCCCTATATAAAGAGAGTCCCTGGCATAACAGGGACTGCTCTG
CTCCAGGCATCTGCCACAATGTGGGTGCTTACACCTGCTGCTTTTGGCTGGGAAGCTCTTGAGTGTGTTTCAGGCAA
CCTCTGAGCTCTCTGTGGAGGAGCCTGGTCCCGCTGTTCTGCTGGCTGAGGGCAACCTTCTGGCTGCTAGCTACC
AAGAGGAGAAAGCAGCAGCTGGTCCTGAGAGGGCCAGATGAGACCAAAGAGGAGGAAGAGGACCTCCTCTGCCC
ACCACCCCAACCAGCGTCAACTATCACTTCACTCGCCAGTGCAACTACAAATGCGGCTTCTGTTTCCACACAGCC
AAAAATCCTTTGTGCTGCCCTTGAGGAAGCAAAGAGAGGATTGCTTTTGTCTAAGGAAGCTGGTATGGAGAAG
ATCAACTTTTTCAGGTGGAGAGCCATTCTTCAAGACCGGGGAGAATACCTGGGCAAGTTGGTGAGGTTCTGCAAA
GTAGAGTTGCGGCTGCCAGCGTGAGCATCGTGAGCAATGGAAGCCTGATCCGGGAGAGGTGGTTCCAGAATTAT
GGTGAGTATTTGGACATTCTCGCTATCTCCTGTGACAGCTTTGACGAGGAAGTCAATGTCCTTATTGGCCGTGGC
CAAGGAAAGAAGAACCATGTGGAAAACCTTCAAAAGCTGAGGAGGTGGTGTAGGGATTATAGAGTCGCTTTCAAG
ATAAATTCTGTCAATTAATCGTTTCAACGTGGAAGAGGACATGACGGAACAGATCAAAGCACTAAACCTGTCCGC
TGGAAAGTGTTCCAGTGCCCTCTTAATTGAGGGTGAGAATTGTGGAGAAGATGCTCTAAGAGAAGCAGAAAGATTT
GTTATTGGTGATGAAGAATTTGAAAGATTCTTGGAGCGCCACAAAGAAGTGCTCTGCTTGGTGCCTGAATCTAAC
CAGAAGATGAAAGACTCCTACCTTATTCTGGATGAATATATGCGCTTTCTGAACTGTAGAAAGGGACGGAAGGAC
CCTTCCAAGTCCATCCTGGATGTTGGTGTAGAAGAAGCTATAAAATTCAAGTGGATTGATGAAAAGATGTTTCTG
AAGCGAGGAGGAAAATACATATGGAGTAAGGCTGATCTGAAGCTGGATTGGTAGAGCGGAAAGTGGAACGAGACT
TCAACACACCAAGTGGGAAAACCTTAGAGTAAGTCCATTGTCTGCAATACTATCCCGTTGGTATTTCCAGTGG
CTGAAAACCTGATTTTCTGCTGCACGTGGCATCTGATTACCTGTGGTCACTGAACACACGAATAACTTGGATAGC
AAATCCTGAGACAATGGAAAACCATTAACCTTACTTCACTTGGCTTATAACCTTGTGTTATTGAAACAGCACTTC
TGTTTTTGTAGTTTGTGTTTGTAGCTAAAAGAAGGAATACACACAGGAATAATGACCCCAAAAATGCTTAGATAAGGC
CCCTATACACAGGACCTGACATTTAGCTCAATGATGCGTTTGTAAAGAAATAAGCTCTAGTGATATCTGTGGGGGC
AATATTTAATTTGGATTTGATTTTTTAAACAAATGTTTACTGCGATTTCTATATTTCCATTTTGAACTATTTCT
TGTTCCAGTTTGTTCATTTGACAGAGTCAGTATTTTTTGCCAAATATCCAGATAACCAAGTTTTCACATCTGAGA
CATTACAAAGTATCTGCCTCAATTATTTCTGCTGGTTATAATGCTTTTTTTTTTTTGCCTTTATGCCATTGCAG
TCTTGACTTTTTACTGTGATGTACAGAAATAGTCAACAGATGTTTCCAAGACATATGATATGATAATCCTACC
AATTTTCAAGAAGTCTCTAGAAAGAGATAACACATGGAAAGACGGTGTGGTGCAGCCCAGCCACGGTGGCTGTT
CCATGAATGCTGGCTACCTATGTGTGTGGTACCTGTTGTGTCCCTTTCTCTTCAAAGATCCTGAGCAAAACAAAG
ATACGCTTTCCATTTGATGATGGAGTTGACATGGAGGCAGTGCTTGCAATTGCTTTGTTGCGCTATCATCTGGCCA
CATGAGGCTGTCAAGCAAAAGAATAGGAGTGTAGTTGAGTAGCTGGTTGGCCCTACATCTCTGAGAAGTGACGTT
ACACTGGGTTGGCATAAGATATCCTAAAATCACGCTGGAACCTTGGGCAAGGAAGAATGTGAGCAAGAGTAGAGA
GAGTGCCTGGATTTTCATGTGAGTGAAGCCATGTCAACCATATCATATTTTGAATGAACTCTGAGTCAGTTGAAT
AGGGTACCATCTAGGTCAGTTTAAAGAAGAGTCAGTCAGAGAAAGCAAGCATAAGGGAAAATGTCACGTAAACTA
GATCAGGGAACAAAATCCTCTCCTTGTGGAATATCCCATGCAGTTTGTGATACAACTTAGTATCTTATTGCCT
AAAAAAAATTTCTTATCATTGTTTCAAAAAGCAAAATCATGGAATTTTTGTTGTCCAGGCAAATAAAAGGT
CATTTTAATTTAGCTGCAATTTCAAGTGTTCCTCACAGGTGGCATTAAATGTCGCTGATGTCAATTAAGCACCA
TCCAAAAGTCTGCTTCATAATCTATTTTCAAGACTTGGTGATTCTGAAAGTTTTGGTTTTTGTGACTTTGTTTC
TCAGGAAAAAAATATCCTACTTAAATTTAAGTCTATAATTCAATTTAAATATGTGTGTCTCATCCAGGAT
AGGATAGGTTGTCTTCTATTTTCCATTTTACCTATTTACTTTTTTTGTAAGAAAAGAGAAAAATGAATTCTAAAG
ATGTTCCCATGGGTTTTGATTGTGTCTAAGCTATGATGACCTCATATAATCAGCATAAACATAAAACAAATTT
TTTACTTAACATGAGTGCACCTTACTAATCCTCATGGCACAGT

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FIGURE 170

MWVLTAAAFAGKLLSVFRQPLSSLVRSVPLFCWLRATFWLLATKRRKQQLVLRGPDETKEEEEDPPLPTTPTSV
NYHFTRQCNYKCGFCFHTAKTSFVLPLEEAKRGLLLLKEAGMEKINFSGGEPFLQDRGEYLGKLVRFCKVELRLP
SVSIVSNGSLIRERWFQNYGEYLDILAI SCDSFDEEVNVLIGRGQGKKNHVENLQKLRRWCRDYRVAFKINSVIN
RFNVEEDMTEQIKALNPVRWKVFQCLLIEGENCGEDALREAERFVIGDEEFERFLERHKEVSCLVPESNQMKDS
YLILDEYMRFLNCRKGRKDP SKSILDVGVEEAIKFSGFDEKMFLKRGGKYIWSKADLKLDW

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FIGURE 171

CTGAGGCCCCACGCAGGGCCTAGGGTGGGAAGATGCGCAGGTGGGGGCGGCGACCTGAGCACCAGGAGGCTGAATGA
ATGTATTTTACCAGTAGCAAATGAGATGAACCATCTTCTGCACACAGCCACGATTTGCAAAGGATGTTACGGA
AGACCAGGGTGTAGATGACAGGCTGCTCTATGACATTGTATTCAAGCACTTCAAAGAAATAAGGTGGAGATTTC
AAATGCAATAAAAAAGACATTTCCATTCCCTCGAGGGCCTCCGTGATCGTGATCTCATCACAATAAAATGTTTGA
AGATTCTCAAGATTCTTGTAGAAACCTGGTCCCTGTACAGAGAGTGGTGTACAATGTTCTTAGTGAAGTGGAGAA
GACATTTAACCTGCCAGTTCTGGAAGCACTGTTTACGCGATGTCAACATGCAGGAATACCCCGATTTAATTCACAT
TTATAAAGGCTTTGAAAATGTAATCCATGACAAATGCTCTCCAAGAAAGTGAAGAAGAAGAGAGGGAGGAGAG
GTCTGGCCTCCAACCTAAGTCTTGAACAAGGAAGTGGTGAAGAACTCTTTTTCGAAGCCTGACTTGGCCACCTTCGGG
TTCCCCATCTCATGCTGGTACAACCCACCTGAAAATGGACTCTCAGAGCACCCCTGTGAAACAGAACAGATAAA
TGCAAAGAGAAAAGATACAACCAAGTGACAAAGATGATTGCTAGGAAGCCAACAAACAAATGAACAATGTGCTCA
AAAGGCTGAGCCAACAGAGTCTGCGAACAAATTGCTGTCCAAGTGAATAATGGGGATGCTGGAAGGGAGATGCC
CTGCCCGTTGCCCTGTGATGAAGAAAGCCCAGAGGCAGAGCTACACAACCATGGAATCCAAATTAATTCCTGTTT
TGTGCGACTGGTGGATATAAAAAAGGAAAAGCCATTTTCTAATTCAAAAGTTGAGTGCCAAGCCCAAGCAAGAAC
TCATCATAACCAGGCATCTGACATAATAGTCATCAGCAGTGAGGACTCTGAAGGATCCACTGACGTTGATGAGCC
CTTAGAAGTCTTCATCTCAGCACCGAGAAGTGAGCCTGTGATCAATAATGACAACCCCTTTAGAATCAAATGATGA
AAAGGAGGGCCAAGAAGCCACTTGCTCACGACCCAGATTGTACCAGAGCCCATGGATTTGAGAAAATTATCTAC
ATTCAGAGAAAGTTTTTAAGAAAAGAGTGATAGGACAAGACCACGACTTTTCAGAATCCAGTGAGGAGGAGGCGCC
CGCAGAAGCCTCAAGCGGGGCACTGAGAAGCAAGCATGGTGAGAAGGCTCCTATGACTTCTAGAAGTACATCTAC
TTGGAGAATACCCAGCAGGAAGAGACGTTTTCAGCAGTAGTGACTTTTTCAGACCTGAGTAATGGAGAAGAGCTTCA
GGAAACCTGCAGCTCATCCCTAAGAAGAGGGTCAGGTAAAGAAGATTAGGATGCCAAGACTTGGCCTGCAGAAATG
TCAGGAATGTGAATTAAGCTGCTGTTTCCAGACGCTTTTTATCTGAGCACCTTCACTACCTTGTATCCAGTT
CATCTGGGAAGTCTTTTTTGCATTTTAGAAAATGGAAAGAGGCAGGAAATTATGATAAACTCATGTTTAACAGAA
AGAGTTTCACTGACTAAATGTATGTAATTATATTTTGTGTTGTAGAAGAAATAAATAGCAAATTTGTGGTATTC
TTTTTTTTTAAACCTGCTCTCATTCCTATTAACACTAAGATCTTAGATTTTTATAGTGATAAATGGGTTGACATCA
TTGTCGTTTGTAAATTGTAAAGCCTCAAAGACAACCTGTTTCTACTATGTAATTATAGACAGAAATAAAACTTCA
GATC

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FIGURE 172

MAGGGGDLSTRRLNECISPVANEMNHLPAHSHDLQRMFTEDQGVDRLLYDIVFKHFKNKVEISNAIKKTFPFL
EGLRDRDLITNKMFEQSQSCRNLVPVQRVVYNVLSELEKTFNLPVLEALFSDVNMQEYPDLIHIYKGFENVIH
KLPLQESEEEEREERSGLQLSLEQGTGENSFRSLTWPPSGSPSHAGTTPPENGLSEHPCETEQINAKRKDTTSDK
DDSLGSQQTNEQCAQKAEPTECEQIAVQVNNGDAGREMPCLPCDEESPEAELHNHGIQINSCSVRLVDIKKEK
PFSNSKVECQAQARTHHNQASDIIVISSEDSGSTDVDEPLEVFISAPRSEPVINNDNPLESNDEKEGQEATCSR
PQIVPEPMDFRKLSTFRESFKKRVIGQDHDFSESSEEEAPAEASSGALRSKHGEKAPMTSRSTSTWRIPSRKRRF
SSSDFSDLSNGEELQETCSSSLRRGSGKED

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FIGURE 174

MDSQRPEPRXXXXXXXXLRLWELDSEELGTRTEGPSVVQGWGHLLQAVWRGPAGLVTQLLRQGASVEERTLRCC
WATGQTQASGTGMAALRCTGLPPEDTCLPSSCWSPRGPRWMRGTPWASHPCITPLGKATWRLPAACWTGCAQVDA
TGWLRKTPLHLAAERGHGPTVGLLLSRGASPTLRTQWAEVAQMPEGDLPQALLNLEGGKGV

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FIGURE 175

GGCACGAGGGCCAGGAACGCCAGCCGTTACGCGTTTCGGTCCTCCTTGGCTGACTCACCGCCCTCGCCGCCGCAC
CATGGACGCCCCCAGGCAGGTGGTCAACTTTGGGCCTGGTCCCGCCAAGCTGCCGCACTCAGTGTGTAGAGAT
ACAAAAGGAATTATTAGACTACAAAGGAGTTGGCATTAGTGTCTTGAAATGAGTCACAGGTCATCAGATTTTGC
CAAGATTATTAACAATACAGAGAATCTTGTGCGGGAATTGCTAGCTGTTCCAGACAACATAAGGTGATTTTCT
GCAAGGAGGTGGGTGCGGCCAGTTCAGTGCTGTCCCTTAAACCTCATTGGCTTGAAAGCAGGAAGGTGTGCGGA
CTATGTGGTGACAGGAGCTTGGTCAGCTAAGGCCGAGAAGAAGCCAGAAGTTTGGGACTATAAATATCGTTCA
CCCTAACTTGGGAGTTATACAAAAATTCAGATCCAAGCACCTGGAACCTCAACCCAGATGCCTCTACGTGTA
TTATTGCGCAAATGAGACGGTGCATGGTGTGGAGTTTGACTTTATACCCGATGTCAAGGGAGCAGTACTGGTTG
TGACATGTCCTCAAACCTTCTGTCCAAGCCAGTGGATGTTTCCAAGTTTGGTGTGATTTTTGCTGGTGCCAGAA
GAATGTTGGCTCTGCTGGGGTCACCGTGGTGATTGTCCGTGATGACCTGCTGGGGTTTGCCTCCGAGAGTGCCC
CTCGGTCTCGAATACAAGGTGCAGGCTGGAAACAGCTCCTTGTACAACACGCTCCATGTTTACGCATCTACGT
CATGGGCTTGGTTCTGGAGTGGATTAAAAACAATGGAGGTGCCGCGGCCATGGAGAAGCTTAGCTCCATCAAATC
TCAAACAATTTATGAGATTATTGATAATTCTCAAGGATTCTACGTTTGTCCAGTGGAGCCCCAAAATAGAAGCAA
GATGAATATTCCATTCCGCATTGGCAATGCCAAAGGAGATGATGCTTTAGAAAAAGATTCTTGATAAAGCTCT
TGAACCTCAATATGTTGTCTTGAAGGGCATAGGTCTGTGGGAGGCATCCGGGCCTCTCTGTATAATGCTGTCAC
AATTGAAGACGTTTCAAGAGCTGGCCGCCTTCATGAAAAAATTTTTGGAGATGCATCAGCTATGAACACATCCTAA
CCAGGATATACTCTGTTCTTGAACAACATACAAAGTTTAAAGTAACCTTGGGGATGGCTACAAAAAGTTAACACAG
TATTTTTCTCAAATGAACATGTTTATTGCAGATTCTTCTTTTTTGAAGAACAACAGCAAAACATCCCAACTCT
GTAAAGCTGGTGGGACCTAATGTCACCTTAATTCTGACTTGAACCTGGAAGCATTTTAAGAAATCTTGTTGCTTTT
CTAACAAATTCCCGCTATTTTGCCTTTGCTGCTACTTTTTCTAGTTAGATTTCAAACCTTGCTGTGGACTTAAT
AATGCAAGTTGCGATTAATTATTTCTGGAGTCATGGGAACACACAGCACAGAGGGTAGGGGGGCCCTCTAGGTGC
TGAATCTACACATCTGTGGGGTCTCCTGGGTTGAGCGGCTGTTGATTCAAGGTCAACATTGACCATTTGGAGGAGT
GGTTTAAGAGTGCCAGGCGAAGGGCAAACCTGTAGATCGATCTTTATGCTGTTATTACAGGAGAAGTGACATACTT
TATATATGTTTATATTAGCAAGGTCTGTTTTTAATACCATATACTTTATATTTCTATACATTTATATTTCTAATA
ATACAGTTATCACTGATATATGTAGACACTTTTAGAATTTATTAAATCCTTGACCTTGTGCATTATAGCATTCCA
TTAGCAAGAGTTGTACCCCTCCCGAGTCTTCGCCCTCCTCTTTTAAAGCTGTTTTATGAAAAGACCTAGAAGT
TCTTGATTCATTTTTACCATTCTTTCCATAGGTAGAAGAGAAAGTTGATTGGTTGGTTGTTTTCAATTATGCCA
TTAAACTAAACATTTCTGTTAAATTACCCTATCCTTTGTTCTCTACTGTTTTCTTTGTAATGTATGACTACGAGA
GTGATACTTTGCTGAAAAGTCTTTCCCTATTGTTTATCTATTGTCAGTATTTTATGTTGAATATGTAAAGAACA
TTAAAGTCCTAAACATCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 176

MDAPRQVVNFGPGPAKLPHSVLLEIQKELLDYKGVGISVLEMSHRSSDFAKIINNNTENLVRELLAVPDNYKVIFL
QGGGCGQFSAPVPLNLIGLKAGRCADYVVTGAWSAKAAEEAKKFGTINIVHPKLGSYTKIPDPSTWNLNPDASYVY
YCANETVHGVEFDFIPDVKGAVLVCDMSSNFLSKPVDVSKFGVIFAGAQNKGVSAGVTVVIVRDDLLGFALRECP
SVLEYKVQAGNSSLYNTPPCFSIYVMGLVLEWIKNNGGAAAMEKLSSIKSQTIYEIIDNSQGFYVCPVEPQNRSK
MNIPFRIGNAKGDDALEKRFLDKALELNMLSLKGHRVGGIRASLYNAVTIEDVQKLAAFMKKFLEMHQL

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FIGURE 177

GGCGTCTGCCAGGAGCTACGGCCGGAAGATGCGGGCGGCCGAGAGTTGTCGCTACTGGAGAAGTCCCTGGGACT
GAGTAAGGGGAATAAATACAGTGCTCAGGGCGAGCGACAGATTCCAGTTCTTCAGACAAACAATGGTCCAAGTCT
AACAGGATTGACTACTATAGCAGCTCATCTAGTCAAGCAAGCCAACAAAGAATATTTGCTGGGGAGTACTGCAGA
AGAAAAAGCAATCGTTCAGCAGTGTTAGAATACAGGGTCACTCAAGTAGATGGGCACTCCAGTAAAAATGACAT
CCACACACTGTTGAAGGATCTTAATTCATATCTTGAAGATAAAGTCTACCTTACAGGGTATACTTTACATTAGC
AGATATACTATTGTACTATGGACTTCATCGCTTTATAGTTGACCTGACAGTTCAAGAAAAGGAGAAATATCTTAA
TGTGTCTCGCTGGTTTTGTCACATTCAGCATTATCCAGGCATCAGGCAACATCTGTCTAGTGTGTTCTTCATCAA
GAACAGACTATATACTAATTCCCACTAGAGCTGTCCATGCCATACAGAAGATCTATTAATAAATGTTTTAAATGG
AAAATGTACTCTAGACCACAGGACTAATGTAAATTAATATACAGTCATTCAATTATTTGTTGAAGTTGATAGAATT
TTTGAAGTGTAACCTTGTTGTCTGAATGTTTTATTTGTTCTTTAGCTGAAGTTTTGCAATTTTTATGTCAAAATTC
AATTGCTATTAAACAAGTTGAGATCCAGTTATAAATTAACCTTGTTTTTAGTAGATGACATTTATTTCAATAAAA
GTTGCAAAATCGGGAA

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FIGURE 178

MAAAAELSLLEKSLGLSKGNKYSAQGERQIPVLQTNNGPSLTGLTTIAAHLVKQANKEYLLGSTAEKAIVQOWL
EYRVTQVDGHSSKNDIHTLLKDLNSYLEDKVYLTYGYNFTLADILLYYGLHRFIVDLTVQEKEKYLNVSRWFCHIQ
HYPGIRQHLSSVVF IKNRLYTNSH

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FIGURE 179

GGCACGAGCCCAGAAACAAAGACTTCACGGACAAAGTCCCTTGGAACCAGAGAGAAGCCGGGATCGAAACTCCAA
ACACCACAGAGGACTATGACACGACCACAGAGTTTGACTATGGGGATGCAACTCCGTGCCAGAAGGTGAACGAGA
GGGCCTTTGGGGCCCAACTGCTGCCCCCTCTGTACTCCTTGGTATTTGTCATTGGCCTGGTTGGAAACATCCTGG
TGGTCCTGGTCCTTGTGCAATACAAGAGGCTAAAAACATGACCAGCATCTACCTCCTGAACCTGGCCATTTCTG
ACCTGCTCTTCTGTTCACGCTTCCCTTCTGGATCGACTACAAGTTGAAGGATGACTGGGTTTTTGGTGATGCCA
TGTGTAAGATCCTCTCTGGGTTTTATTACACAGGCTTGACAGCGAGATCTTTTTCATCATCCTGCTGACGATTG
ACAGGTACCTGGCCATCGTCCACGCCGTGTTTGCCTTGCGGGCACGGACCGTCACTTTTGGTGTCATCACCAGCA
TCATCATTTGGGCCCTGGCCATCTTGGCTTCCATGCCAGGCTTATACTTTTCCAAGACCCAATGGGAATTCACCTC
ACCACACCTGCAGCCTTCACTTTCCCTCACGAAAGCCTACGAGAGTGGAAGCTGTTTCAGGCTCTGAAACTGAACC
TCTTTGGGCTGGTATTGCCTTTGTTGGTCATGATCATCTGTACACAGGGATTATAAAGATTCTGCTAAGACGAC
CAAATGAGAAGAAATCCAAAGCTGTCCGTTTGATTTTGTCAATCATGATCATCTTTTTTCTCTTTGGACCCCT
ACAATTTGACTATACTTATTTCTGTTTTCCAAGACTTCCTGTTCACCCATGAGTGTGAGCAGACAGACATTTGG
ACCTGGCTGTGCAAGTGACGGAGGTGATCGCCTACACGCACTGCTGTGTCAACCCAGTGATCTACGCCCTTCGTTG
GTGAGAGGTTCCGGAAGTACCTGCGGCAGTTGTTCCACAGGCGTGTGGCTGTGCACCTGGTTAAATGGCTCCCT
TCCTCTCCGTGGACAGGCTGGAGAGGGTCAGCTCCACATCTCCCTCCACAGGGGAGCATGAACCTCTCTGCTGGGT
TCTGACTCAGACCATAGGAGGCCAACCCAAAATAAGCAGGCGTGACCTGCCAGGCACACTGAGCCAGCAGCCTGG
CTCTCCCAGCCAGGTTCTGACTCTTGGCACAGCATGGAGTCACAGCCACTTGGGATAGAGAGGGAATGTAATGGT
GGCCTGGGGCTTCTGAGGCTTCTGGGGCTTCAGTCCTTTCCATGAACTTCTCCCCTGGTAGAAAGAAGATGAATG
AGCAAAACCAAATATTCCAGAGACTGGGACTAAGTGACAGAGAAGGGCTTGGACTCAAGCAAGATTTAGATT
TGIGACCATTAGCATTGTCAACAAAGTACCCACTTCCCCTATTGCTTGACAAACCAATTAACCCAGTAGT
GGTGAAGTGTGGGCTCCATTCAAAGTGAGCTCCTAAGCCATGGGAGACACTGATGTATGAGGAATTTCTGTTCTTC
CATCACCTCCCCCCCCCGCCACCCTCCCACTGCCAAGAACTTGAAATAGTGATTTCCACAGTGACTCCACTCT
GAGTCCCAGAGCCAATCAGTAGCCAGCATCTGCCTCCCCTTCACTCCCACCGCAGGATTTGGGCTCTTGGAATCC
TGGGGAACATAGAACTCATGACGGAAGAGTTGAGACCTAACGAGAAATAGAAATGGGGGAACACTACTGCTGGCAGT
GGAATAAGAAAGCCCTTAGGAAGAATTTTTATATCCACTAAATCAAACAATTCAGGGAGTGGGCTAAGCACGG
GCCATATGAATAACATGGTGTGCTTCTTAAATAGCCATAAAGGGGAGGGACTCATCATTTCCATTACCCCTCT
TTTCTGACTATTTTTCAGAACTCTCTCTTTTCAAGTTGGGTGATATGTTGGTAGATTCTAATGGCTTTATTGC
AGCGATTAATAACAGGCAAAAGGAAGCAGGTTGGTTTCCCTTCTTTTGTCTTTCATCTAAGCCTTCTGGTTTT
ATGGGTCAGAGTTCGACTGCCATCTTGGACTTGTACGCAAAAAAAAAAAAAAAAAA

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FIGURE 180

METPNNTTEDYDTTTEFDYGDATPCQKVNERAFGAQLLPPLYSLVFVIGLVGNILVVLVLVQYKRLKNMTSIYLLN
LAISDLLFLFTLPFWIDYKLDWVFGDAMCKILSGFYTGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFG
VITSIIWALAILASMPGLYFSKTQWEFTHTCSLHFPHESLREWKLFQALKLNLFGLVLP LLVMIICYTGIKI
LLRRPNEKKSKAVRLIFVIMIIFFLFWTPYNLTILISVFQDFLFTHECEQSRHLDLAVQVTEVIAYTHCCVNPVI
YAFVGERFRKYLRQLFHRRVAVHLVKWLPFLSVDRLERVSSTSPSTGEHELSAGF

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FIGURE 181A

AGAGCGAGCAGGGGAGAGCGAGACCAGTTTTAAGGGGAGGACCGGTGCGAGTGAGGCAGCCCCGAGGCTCTGCTC
GCCCCACCACCAATCCTCGCCTCCCTTCTGCTCCACCTTCTCTCTGCCCCTCACCTCTCCCCGAAAACCCCTT
ATTTAGCCAAAGGAAGGAGGTGAGGGGAACGCTCTCCCTCCCTTCCAAAAACAAAAACAGAAAAACCCCTTTT
CCAGGCCGGGGAAAGCAGGAGGGAGAGGGGCCCGGGCTGGCCATGAGCTGCTGTGCCACGAGGTGGACCCGG
TCCGCAGGGCCGTGCGGGACCGCAACCTGCTCCGAGACGACCGCTCTGCAGAACCTGCTCACCATCGAGGAGC
GCTACCTTCCGCAGTGTCTTCAAGTGCCTGCGAAGGACATCCAACCCTACATGCGCAGAATGGTGGCCA
CCTGGATGCTGGAGGTCTGTGAGGAACAGAAGTGCAGAAGAGAGGTCTTCCCTCTGGCCATGAATTACCTGGACC
GTTTCTTGGCTGGGGTCCCGACTCCGAAGTCCCATCTGCAACTCCTGGGTGCTGTCTGCATGTTCTTGGCCTCCA
AACTCAAAGAGACCAGCCCGCTGACCGCGGAGAAGCTGTGCATTTACACCGACAACCTCCATCAAGCCTCAGGAGC
TGCTGGAGTGGAACCTGGTGGTGTCTGGGGAAGTTGAAGTGAACCTGGCAGCTGTCACTCCTCATGACTTCATTG
AGCACATCTTGCGCAAGCTGCCCCAGCAGCGGGAGAAGCTGTCTCTGATCCGCAAGCATGCTCAGACCTTCATTG
CTCTGTGTGCCACCGACTTTAAGTTTGCCATGTACCCACCGTCGATGATCGCAACTGGAAGTGTGGGAGCAGCCA
TCTGTGGGCTCCAGCAGGATGAGGAAGTGAGCTCGCTCACTTGTGATGCCCTGACTGAGCTGCTGGCTAAGATCA
CCAACACAGACGTGGATTGTCTCAAAGCTTGCCAGGAGCAGATTGAGGCGGTGCTCCTCAATAGCCTGCAGCAGT
ACCGTCAGGACCAACGTGACGGATCCAAGTCGGAGGATGAACCTGGACCAAGCCAGCACCCCTACAGACGTGCGGG
ATATCGACCTGTGAGGATGCCAGTTGGGCCGAAAGAGAGAGACGCGTCCATAATCTGGTCTCTTCTCTTTCTGG
TTGTTTTTGTCTTTGTGTTTTAGGGTGAACTTAAAAAAAATCTGCCCCACCTAGATCATATTTAAAGAT
CTTTTAGAAGTGAGAGAAAAAGGTCTACGAAAACGGAATAATAAAAAGCATTGGTGCCTATTGAGTACAGC
ATAAGGGAATCCCTTGTATATGCGAACAGTTATTGTTTGATTATGTAAGTAATAGTAAATGCTTACAGGAAA
ACCTGCAGAGTAGTTAGAGAATATGTATGCCTGCAATATGGGAACAAATTAGAGGAGACTTTTTTTTTTCATGTT
ATGAGCTAGCACATACACCCCTTGTAGTATAATTTCAAGGAACCTGTGTACGCCATTTATGGCATGATTAGATTG
CAAAGCAATGAACCTCAAGAAGGAATTGAAATAAGGAGGGACATGATGGGGAAGGAGTACAAAACAATCTCTCAAC
ATGATTGAACCATTTGGGATGGAGAAGCACCTTTGCTCTCAGCCACCTGTTACTAAGTCAGGAGTGTAGTTGGAT
CTCTACATTAATGTCTCTTGTCTGTACAGTAGCTGTACCTAAAAAAGATGTTTTATTTTGCCAGTTGGACA
CAGGTGATTGGCTCCTGGGTTTCATGTTCTGTGACATCCTGCTTCTTCTTCCAAATGCAGTTTCATTGCAGACACC
ACCATATTGCTATCTAATGGGGAAATGTAGCTATGGGCCATAACCAAACTCACATGAAACGGAGGCAGATGGAG
ACCAAGGGTGGGATCCAGAATGGAGTCTTTCTGTATTGTATTTAAAAGGGTAATGTGGCCTTGGCATTCTTCTC
TTAGAAAAAACTAATTTTTGGTGTGATTGGCATGTCTGGTTCACAGTTTAGCATTGTTATAAACCATTCATT
CGAAAAGCACTTTGAAAAATTGTTCCCGAGCGATAGATGGGATGGTTTATGCAAGTCATGCTGAATACTCCTCCC
CTCTTCTCTTTTGCCCCCTCCCTTCTGCCCCAGTCTGGGTACTCTCGCTTCTGGTATCTGGCGTTCTTTGG
TACACAGTTCTGGTGTCTTACCAGGACTCAAGAGACACCCCTTCTGCTGACATTCCCATCACACATTCTCTCA
GACAAGCCTGTAACTAAAATCTGTTACCATCTGATGGCACAGAAGGATCTTAATCCCATCTCTATACTTCTC
CTTTGGACATGGAAGAAAAAGTTATTGCTGGTGCAAAGATAGATGGCTGAACATCAGGGTGTGGCATTGTTGTTCC
CTTTCCGTTTTTTTTTTTTTTTATTGTTGTTGTTAATTTTATTGCAAAGTTGTATTACAGCGTACTGAATTTTTC
TTCTCTCCACTTCTTAGAGGCATTGAGTTAGCAAAGAGGTTGGAGCAACAACCTTTTTTTTTTTTTTTTGCACAA
TTGTAATTGACAGGTAATGAAGCTATTTGTTAAAAATATTTGCCTTTTTAAGTAAAAAAGAAAAATCAGAACAGGG
CTATTTGAAGAATTATTTTATACACAGATTCTGCCTTGTTCATAGTATGAGGGTTGAAGACGGAAAAACAATCTA
AGGGTCTCTCATTTTTTTAATTTTGTGTTGTTGTTGTTGTTTTTTTTTTTTTTTGGCGTGCTAAGAAGCTAAAG
TCATCCATCCTTATTCACGTTGACAGTACCTAGCTGTAATGTTTCACAGAGTGTGCTGCTATTTTATAAACATTT
TTATAATATATTATTTTACTGCTTAAATCCAAGTCTGAAGTAGATGGTTGAGATATGAGTCTTCTGCTACTGGA
AAAGCCCTTCCGTAGTTTGTGTTTCTTCTGGTAGCATATTCATGGTTGTTTTTTTTTTCTTTTTTGGTTTTTTGG
TTTTTTTTTTTTTCTCTGATCACATTCTTCAAAGACGGAGTATTCTTTACCTCAGGTTTACTGGACAAAATCAAT
AACTACAAAAGGCAATGATTACGCTTTTGTGTTTCATAATACCTCACACCGTACAGTTTCTGCTTGGGAGCCCA
TTCGATGAGGAATACAGAAGCAGTGTGAGCAGGGCTGACTCCCTCTCAGGTGGAAGGCAGGGCGGTCTCACTCC
CAGGGACCTTTTTTGGTCATGGAGGCCATCGGGCTCCAGTTAGACCCTGGTATCCTCATCATGATGGAATAAATA
CATTGAACCAAGGGATCCTCCCTCCCTTCAAAGGCAGACGTTGAGTACAAACATTTATGCGGTAGGCTCAGATGT
CGTAATTTGCACTTAGGTACCAGGTGTCAGGAAACAGACTAAAAAGAATCCACCAGGCTGTTGGAGATCCTCA
TCTTGGAGCTTTTTCAAAGCGGGGCTTCATCTGCAAGGGCCCTTTTATCTTGAAGTTTTTCCCCTCCGCTCTT

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FIGURE 181B

CCCCCCCCCTGGCATGGACACCTTGTGTTTAGGATCATCTCTGCAGGTTTCCTAGGTCTGAATCTGCCAGTAGAT
GAACCTGCAGCAAGCAGCGTTTATGGTGCTTCCTTCTCCCTCCTCTGTCTCAAACCTGCCGAGGCAAGCACTATGC
AAGCCCAGGCCCTCTGCTGAGCGGTACTAAACGGTCGGGTTTTCAATCACACTGAATTGGCAGGATAAGAAAAAT
AGGTCAGATAAGTATGGGATGATAGTTGAAGGGAGGTGAAGAGGCTGCTTCTCTACAGAGGTGAAATCCAGATG
AGTCAGTCTCTTGGGAAGTGTGTTTAGAAGGGTTCAGGACTTTGTGAGTTAGCATGACCCTAAATTTCTAGGGGA
TTTCTGGTGGGACAATGGGTGGTGAATTTTGAAGTTTGGAGAGGGAAGTGGAGCAGCCAGCAAGTAAGCTAGCC
AGAGTTTTCTCAAGAGCCAGCTTTGCTCAGCACACTCTCCTGGGCCCAAGGAGTCCCACGGAATGGGGAAAGTG
GGAACCCTGGAGTTCTTGGGAATCTTGGAGCCTAAAGAGAAACCGAGGTGCAAATTCATTTTCATGGTGACTGACC
CTTGAGCTTAAACAGAAGCAGCAAATGAAAGAACC GGACAAATAAGGAAGGGCACAAGCCTACCCGACTCTATTT
ACAGTCTGTAACCTTTCCACTCTTCTGTAGTCCCGAGGCCCCCTGGGTCTTCTAGCTTTTCTCTTTCCCATCCTT
GGGGCCTTGTGTGATGATGGGTGTGGGGCTGCCGATGGGAAAGTCGGGGGTGTTAGGCTTTTCTGCCTGCTCCT
GCTTAAACACAAGAAGGAATCCTGGATTTTGCCTCTCCTTAGCTCTTAGTCTCTTTGGTAGGAGTTTGTTCCTCA
GAGGAGCTCTCCCCCTTGGATTTGAACCTGCTCTTTTGTGTTGTTGTTCTTTCTCTTCTTTTCTTACCTCCC
ACTAAAGGGGTTCCAAATTATCCTGGTCTTTTTCTACCTTGTGTTGTTTCTATCTCGTCTTTACTTCCATCTGTT
TGTTTTTTTTCTCCATCAGTGGGGGCCGAGTTGTCCCCCAGCCTGCCAAATTTTGATCCTTCCCCCTCTTTTGCC
AAATCCTAGGGGGAAGAAATCCTAGTATGCCAAAAATATATGCTAAGCATAATTAACTCCATGCGGGTCCATAA
CAGCCAAGAAGCCTGCAGGAGAAAGCCAAGGGCAGTTCCTTCCGCAGAACACCCCATGCGTGCTGAGAGGCGAGC
TCCTTGAAGAAGGGGCTGTTCTTCCAGGAGGCTTATTTGAACTGCCTCAGGACCCCACTGGAGAGCACAGCAT
GCCTTACTACTGGGTATCCTTGGTCTATGTGCTCTGTACTGGAGGCTCTGTTCTGCCTCTTATCAGCCAGGTCA
GGGGCACACATGGCTTAAGTGACAAAGCCAGAGGAGAAGACAACCCTGACAGCATCACGCTGCATCCCATTGCTA
GCAGGATTGGCAACTCTTCAGACGGAGCTGCGCTTCCCTGCAGTCTAGCACCTCTAGGGCCTCTCCAGACTGTGC
CCTGGGAGCTCTGGGACTGAAAGGTTAAGAACATAAGGCAGGATCAGATGACTCTCTCCAAGAGGGCAGGGGAAT
TTTCTCTCCATGGGCCACAGGGGACAGGGCTGGGAGAAGAAATAGACTTGCACCTTATGTATGTAATAATTGA
TTTTCTAGTTCAAGAAGATAATATTGGTAGTGTGGGAATTGGAGGTAGGAAGGGGAGGAAGTCTGAGTAAGCCAG
TTGGCTTCTAAGCCAAAAGGATTCTCTTTGTTTATCTCTGAGACAGTCCAACCTTGAGAATAGCTTTAAAGGG
AAATTAATGCTGAGATGATAAAGTCCCTTAAGCCAACAAACCCTCTGTAGCTATAGAATGAGTGCAGGTTTCTA
TTGGTGTGGACTCAGAGCAATTTACAAGAGCTGTTTATGCAGCCATCCATTTGTGCAAAATAGGGTAAGAAGATT
CAAGAGGATATTTATTACTTCTCATACCACATGGCTTTTGATGATTCTGGATTCTAAACAACCCAGAATGGTCA
TTTCAGGCACAACGATACTACATTCTGTGTGTCTGCTTTTAACTTGGCTGGGCTATCAGACCCTATTCTCGGC
TCAGGTTTTGAGAAGCCATCAGCAAATGTGTACGTGCATGCTGTAGCTGCAGCCTGCATCCCTTCGCTGCAGCC
TACTTTGGGGAAATAAAGTGCCTTACTGACTGTAGCCATTACAGTATCCAATGTCTTTTGACAGGTGCCTGTCT
TGAAAAACAAAGTTTCTATTTTTATTTTTAATTGGTTTAGTTCTTAACTGCTGGCCAACTCTTACATCCCCAGCA
AATCATCGGGCCATTGGATTTTTTCCATTATGTTTATCACCCTTATATCATGTACCTCAGATCTCTCTCTCTC
CTCTCTCTCAGTTATATAGTTTCTTGTCTTGGACTTTTTTTTTCTTTTCTTTTTTTTTTTTTTGTCTTAAAA
CAAGTGTGATGCCATATCAAGTCCATGTTATTCTCTCACAGTGTACTCTATAAGAGGTGTGGGTGTCTGTTGGT
CAGGATGTTAGAAAGTGTGATAAGTAGCATGATCAGTGTATGCGAAAAGGTTTTTAGGAAGTATGGCAAAAATG
TTGTATTGGCTATGATGGTGACATGATATAGTCAGCTGCCTTTTAAAGAGGTCTTATCTGTTTCAAGTGTAAAGTAT
TTAAAAAATAATAACCTGTTTTCTGACTAGTTTAAAGATGGATTTGAAAATGTTTTGAATGCAATTAGGTTAT
GCTATTTGGACAATAAACTCACCTTGACCT

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FIGURE 182

MELLCHEVDPVRRAVRDRNLLRDDRVLQNLLTIEERYLPQCSYFKCVQKDIQPYMRRMVATWMLEVCEEQKCEE
VFPLAMNYLDREFLAGVPTPKSHLQLLGAVCMFLASKLKETSPLTAEKLCIYTDNSIKPQELLEWELVVLGKLKWN
LAAVTPHDFIEHILRKLPQOREKLSLIRKHAQTFIALCATDFKFAMYPPSMIATGSVGAAICGLQQDEEVSSLTC
DALTELLAKITNTDCLKACQEQIEAVLLNSLQQYRQDQRDGSKSEDELDQASTPTDVRDIDL

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FIGURE 183

ATGGCCGCGCTTGACCGCTGCCCCGCTCCCCGCACAGTTCAAGAGCATACAGCATCATCTGAGGACGGCTCAG
GAGCATGACAAGCGAGACCCTGTGGTGGCTTATTACTGTCGTTTATACGCAATGCAGACTGGAATGAAGATCGAT
AGTAAACTCCTGAATGTCGCAAATTTTTATCAAAGTTAATGGATCAGTTAGAAGCTCTAAAGAAGCAGTTGGGT
GATAATGAAGCTATTACTCAAGAAATAGTGGGCTGTGCCCATTGGAGAATTATGCTTTGAAAATGTTTTGTAT
GCAGACAATGAAGATCGTGCTGGACGATTTCAAAAAACATGATCAAGTCCTTCTATACTGCAAGTCTTTTGATA
GATGTCATAACAGTATTGGAGAACTCACTGATGAAATGTGAACACAGGAAGTATGCCAGATGGAAGGCAACATAC
ATCCATAATGTTAAGAATGGGGAGACTCCTCAAGCAGGCCCTGTTGGAATTGAAGAAGATAATGATATTGAAGAA
AATGAAGATGCTGGAGCAGCCTCTCTGCCCCACTCAGCCAACTCAGCCATCATCATCTTCAACTTATGACCCAAGC
AACATGCCATCAGGCAACTATACTGGAATACAGATTCCTCCGGGTGCACACGCTCCAGCTAATACACCAGCAGAA
GTGCCTCACAGCACAGGTGTAGCAAGTAATACTATCCAACCTACTCCACAGACTATACCTGCCATTGATCCCGCA
CTTTTCAATACAATTTCCCAGGGGGATGTTGCTCTAACCCAGAACTTTGCTAGAGCTCAGAAGTACTGCAAA
TATGCTGGCAGTGCTTGCAGTATGAAGATGTAAGCACTGCTGTCCAGAATCTACAAAAGGCTCTCAAGTTACTG
ACGACAGGCAGAGAATGA

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FIGURE 184

MAALAPLPPLPAQFKSIQHHLRTAQEHDKRDPVVAYYCRLYAMQTGMKIDSKTPECKRFLSKLMDQLEALKKQLG
DNEAITQEIVGCAHLENYALKMFLYADNEDRAGR FHKNMIKSFYTASLLIDVITVLENSLMKCEHRKYARWKATY
IHNVKNGETPQAGPVGIEEDNDIEENEDAGAASLP TQPTQPSSSSTYDPSNMPSGNYTGIQIPPAHAPANTPAE
VPHSTGVASNTIQPTPQTIPAI DPALFNTISQGDVRLTPEDFARAQKYCKYAGSALQYEDVSTAVQNLQKALKLL
TTGRE

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FIGURE 185

ACGTGTATCGCTGCCGTCAAGATGGAGGGGCCCTTTGTCCGTGTTCCGGTGACCGCAGCACTGGGGAAACGATCCGC
TCCCAAAACGTTATGGCTGCAGCTTCGATTGCCAAATTATTGTAAAAAGTTCTCTTGGTCCAGTTGGCTTGGATAAA
ATGTTGGTGGATGATATTGGTGATGTAACCATTACTAACGATGGTGCAACCATCCTGAAGTTACTGGAGGTAGAA
CATCCTGCAGCTAAAGTTCTTTGTGAGCTGGCTGATCTGCAAGACAAAGAAGTTGGAGATGGAACACTTTCAGTG
GTTATTATTGCAGCAGAACTCCTAAAAATGCAGATGAATTAGTCAAACAGAAAATTCATCCCACATCAGTTATT
AGTGGCTATCGACTTGCTTGCAAGGAAGCAGTGCGTTATATCAATGAAAACCTAATTGTTAACACAGATGAACTG
GGAAGAGATTGCCTGATTAATGCTGCTAAGACATCCATGTCTTCCAAAATCATTGGGATAAATGGTGATTTCTTT
GCTAACATGGTAGTAGATGCTGTACTTGTCTATTAAATACACAGACATAAGAGGCCAGCCACGCTATCCAGTCAAC
TCTGTTAATATTTTGAAAGCCCATGGGAGAAGTCAAATGGAGAGTATGCTCATCAGTGGCTATGCACTCAACTGT
GTGGTGGGATCCAGGGCATGCCCAAGAGAATCGTAAATGCAAAAATTGCTTGCCTTGACTTCAGCCTGCAAAAA
ACAAAAATGAAGCTTGGTGTACAGGTGGTCATTACAGACCCTGAAAACTGGACCAAATTAGACAGAGAGAATCA
GATATCACCAAGGAGAGAATTGAGAAGATCCTGGCAACTGGTGCCAATGTTATTCTAACCACTGGTGGAATTGAT
GATATGTGTCTGAAGTATTTTGTGGAGGCTGGTGCATGGCAGTTAGAAGAGTTTTAAAAAGGGACCTTAAACGC
ATTGCCAAAGCTTCTGGAGCAACTATTCTGTCAACCCTGGCCAATTTGGAAGGTGAAGAACTTTTGAAGCTGCA
ATGTTGGGACAGGCAGAAGAAGTGGTACAGGAGAGAATTTGTGATGATGAGCTGATCTTAATCAAAAATACTAAG
GCTCGTACGTCTGCATCGATTATCTTACGTGGGGCAAATGATTTTCATGTGTGATGAGATGGAGCGCTCTTTACAT
GATGCACTTTGTGTAGTGAAGAGAGTTTTGGAGTCAAAATCTGTGGTTCCCGGTGGGGGTGCTGTAGAAGCAGCC
CTTTCCATATACCTTGAAACTATGCAACCAGCATGGGTCTCGGGAACAGCTTGCGATTGCAGAGTTTGCAAGA
TCACTTCTTGTTATTCCCAATACACTAGCAGTTAATGCTGCCCAGGACTCCACAGATCTGGTTGCAAAATTAAGA
GCTTTTCATAATGAGGCCCAGGTTAACCCAGAACGTAAAAATCTAAAATGGATTGGTCTTGATTGAGCAATGGT
AAACCTCGAGACAACAAACAAGCAGGGGTGTTTGAACCAACCATAGTTAAAGTTAAGAGTTTGAAATTTGCAACA
GAAGCTGCAATCACCATTCTTCGAATTGATGATCTTATTAAATTACATCCAGAAATCCTTCGGATTAAACATGGA
AGTTATGAAGATGCTGTTCACTCTGGAGCCCTTAATGATTGATCTGATGTTCCCTTTATTTATAACAATGTTAAA
TGCAATGTCTTGACCTTGAGTTGAGTATTACACATTAAAGTAAAGTACAAGCTGTAAACTTGGGTTTTTGTGAT
GTAGGAAATGGTTTCCATCTGTACTTTGGTCCTCTGATTTTCAGATATTGCAACCTAGTACTTTATTAGTTTAAAA
AGAAATTGAGGTTGTTCAAAGTTTAAAGCAATTCATTCTCTCTGAACACACATTGCTATTCCCATCCCACCCCAA
TGCACAGGGCTGCAACACCACGACTTCTGCCATTCTCTCCAGTGTGTGTAACAGGGTCACAAGAATTC

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FIGURE 186

MEGPLSVFGDRSTGETIRSONVMAAASIANIVKSSLGPGVGLDKMLVDDIGDVTITNDGATILKLLEVEHPAAKVL
CELADLQDKEVGDGTTTSVVIIAAELLKNADELVKQKIHTSVISGYRLACKEAVRYINENLIVNTDELGRDCLIN
AAKTSMSKKIIGINGDFFANMVVDAVLAIKYTDIRGQPRYPVNSVNILKAHGRSQMESMLISGYALNCVVGSGQM
PKRIVNAKIACLDFSLQKTKMKLGQVQVITDPEKLDQIRQRESKITKERIQKILATGANVILTTGGIDDMCLKYF
VEAGAMAVRRVLKRD LKRIAKASGATILSTLANLEGEETFEAAMLGQAEEVVQERICDDELILIKNTKARTSASI
ILRGANDFMCEMERSLHDALCVVKRVLESKSVPGGGAVEAALSIYLENYATSMGSREQLAIAEFARSLVIPN
TLAVNAAQDSTD LVAKLRAFHNEAQVNPERKNLKWIGLDLSNGKPRDNKQAGVFEP TIVKVKSLKFATEAAITIL
RIDDLIKLHPEILRIKHGSYEDAVHSGALND

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FIGURE 187

GCTTCGGGTGCC**ATG**GGGACTCCTCCCGGCCTGCAGACCGACTGCGAGGCGCTGCTCAGCCGCTTCCAGGAGACG
GACAGTGTACGCTTCGAGGACTTCACGGAGCTCTGGAGAAACATGAAGTTCGGGACTATCTTCTGTGGCAGAATG
AGAAATTTAGAAAAGAACATGTTTACAAAAGAAGCTTTAGCTTTGGCTTGGCGATATTTTTTACCTCCATACACC
TTCCAGATCAGAGTTGGTGCTTTGTATCTGCTATATGGATTATATAATACCCAACGTGTGCAACCAAAACAAAAG
ATCAGAGTTGCCCTGAAGGATTGGGATGAAGTTTTAAATTTTCAGCAAGATTTAGTAAATGCACAGCATTTTGAT
GCAGCTTATATTTTAGGAAGCTACGACTAGACAGAGCATTCACTTTACAGCAATGCCCAAATTGCTGTCATAT
AGGATGAAGAAAAAATTCACCGAGCTGAAGTTACAGAAGAATTTAAGGACCCAAGTGATCGTGTGATGAAACTT
ATCACTTCTGATGTATTAGAGGAAATGCTGAATGTTTCATGATCATTATCAGAACATGAAACATGTAATTTTCAGTT
GATAAGTCCAAGCCAGATAAAGCCCTCAGCTTGATAAAGGATGATTTTTTTGACAATATTAAGAACATAGTTTTG
GAGCATCAGCAGTGGCACAAAGACAGAAAGAATCCATCCTTAAAGTCAAAAACATAATGATGGAGAAGAAAAAATG
GAAGGAAATTCACAAGAAACGGAGAGATGTGAAAGGGCAGAATCATTAGCGAAAATAAAATCAAAGGCCTTTTCA
GTTGTCATACAGGCATCCAAATCAAGAAGGCATCGTCAAGTCAAACTCGACTCTTCTGACTCTGATTCTGCATCT
GGTCAAGGGCAAGTCAAAGCAACTAGGAAAAAGAGAAGAAAGAAAGATTGAAACCAGCAGGAAGGAAGATGTCT
CTCAGAAACAAAGGCAATGTGCAGAATATACACAAGGAAGATAAACCTTTAAGTCTGAGTATGCCTGTAATTACA
GAAGAAGAAGAGAATGAAAGTTTGAGTGGAACAGAGTTCACTGCATCCAAGAAGAGGAGAAAACACT**TGA**ACAAAG
AGCCTGGTGTAGTTTTTAATTTTGAGTTTTCTGACAGAAGAAAGATTGATATTTTGTGTATTGAACAGGAAGAC
TGCCAGTATTAAAAAATCCTTCTGGGAATCTGTAGGTTATTTCTTGGAATTGCAATACGTAGTTCTAGAATAA
AAGTACAAAAAATTAGAATAAGAATTC

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FIGURE 188

MGTPPGLQTDCEALLSRFQETDSVRFEDFTELWRNMKFGTIFCGRMRNLEKNMFTKEALALAWRYFLPPYTFQIR
VGALYLLYGLYNTQLCQPKQKIRVALKDWDDEVLFQQDLVNAQHFDAAAYIFRKLRLDRAFHTAMPKLLSYRMKK
KIHRAEVTEEFKDP SDRVMKLITSDVLEEMLNVDHYQNMKHVISVDKSKPDKALSLIKDDFFDNKNIVLEHQQ
WHKDRKNPSLKSKTNDGEEKMEGNSQETERCERAESLAKIKSKAFSVVIQASKSRHRQVKLDSSSDSASGQQQ
VKATRKKEKKERLKPAGRKMSLRNKGNVQNIHKEDKPLSLMPVITEEEENESLSGTEFTASKKRRKH

FIGURE 189

CGCGCGCAGCTGGTTCCCGCTCTCGACGCAACGCGCTGAGGACAGTGGGCGCGCTCAGTCCCGGGACCGCGTCTCTCCTCTCGCCTCTGGGCCTGGGACCCGCAAGCGGCGCATGAGAGCGGAGGTGCGGGAGGAAGTCGCGGCGCAACGGCGCTCGACCGCGGGCAAGGCCGCCGCGACCCAGCCCGCAAGTCTCCGGGCGCACAGCTCTGGCTCTTTCCCA GCGCCGCGGGCCTCCACCGCGCGCTGCTCCGGAGGGTGGAGGTGACGCGCCAACCTCTGCTGCTCGCCGGGGCGCC TCGCGGTCTTGGAACGCGGCGGGGCGGGCGTCCAGGTTACCAGCTGCTCGCCGGGAGCGGCGGCGCCCGGACGC CGAAATGCATTAAATTAGGAAAAAACATGAAGATACATTCCGTGGACCAAGGAGCAGAGCACATGCTGATTCTCT CATCAGATGGAAAACCATTTGAGTATGACAACATATAGCATGAAACATCTAAGGTTTGAAAGCATTTTACAAGAAA AAAAAATAATTAGATCACATGTGGAGATTACCATTCTCTTGCACTCTCAAAGGCGGTGAGCTTTTTGCCTGGG GACAGAACCTGCATGGGCAGCTTGAGATTGGAAGGAAATTTCCCTCAACCACCACACCACAGATTGTGGAGCACG TCGCAGGAGTACCCTTGGCTCAGATTTCTGCCGGAGAAGCCACAGCATGGCCTTATCCATGTCTGGCAACATTT ATTCATGGGGAAAAAATGAATGTGGACAACCTAGGCCTGGGCCACACTGAGAGTAAAGATGATCCATCCCTTATTG AAGGACTAGACAATCAGAAAGTTGAATTTGTGCGTTGTGGTGGCTCTCACAGTGCCCTACTCACACAGGATGGGC TGCTGTTTACTTTCCGTGCTGGAAAACATGGGCAACTTGGTCATAATTCAACACAGAATGAGCTAAGACCTGTT TGGTGGCTGAGCTTGTGGGTATAGAGTGACTCAGATAGCATGTGGAAGGTGGCACACACTTGCCTATGTTTCTG ATTTGGGAAAGGTCTTTTCCTTTGGTTCTGGAAAAGATGGACAACCTGGGAAATGGTGGAACACGTGACCAGCTGA TGCCGCTTCCAGTGAAAGTATCATCAAGTGAAGAACTCAAACCTTGAAAGCCATACCTCAGAAAAGGAGTTAATAA TGATTGCTGGAGGGAATCAAAGCATTTTGTCTGGATAAAGAAAGAGAATTCATATGTTAATCTGAAGAGGACAA TTCCTACTCTGAATGAAGGGACTGTAAAGAGATGGATTGCTGATGTGGAGACTAAACGGTGGCAGAGCACAAAAA GGGAAATCCAAGAGATATTTTCATCTCCTGCTTGTCTAACTGGAAGTTTTTTAAGGAAAAGAAGAACTACAGAAA TGATGCCTGTTTATTTGGACTTAAATAAAGCAAGAAACATCTTCAGGGAGTTAACCCAAAAGGACTGGATTACTA ACATGATAACCACCTGCCTCAAAGATAATCTGCTCAAAGACTTCCATTTTATTCTCCACCCCAAGAAGCTTTAG AAATTTTCTTCTTCTCCAGAATGTCTGTGATGCATTTTCCAACAACCTGGGAGAGCCTTGTGGTTCCATTTG CAAAGTTGTTTGTAAATGAGTGACCAGTCTTCACTGGTTCTGGAAGAGTATTGGGCAACTCTGCAAGAATCCA CTTTCAGCAAACTGGTCCAGATGTTTAAACAGCCGTCATATGCCAGTTGGATTACTGGGATGAAAGTGTGAGG AGAATGGTAATGTTCAAGCTCTCCTAGAAATGTTGAAGAAGCTGCACAGGGTAAACCAGGTGAAATGTCAACTAC CTGAAAGTATTTTCCAAGTAGACGAACTCTTGACCGTCTCAATTTTTTTGTAGAAGTATGCAGAAGGTACTTGT GGAAAATGACTGTGGACGCTTCAGAAAATGTACAA TGCTGCGTCATATTGAGTCACTTTCCATTTATCTTTAATA ATCTGTCGAAAATTAAACTACTACATACAGACACACTTTTAAAAATAGAGAGTAAAAAACATAAAGCTTATCTTA GGTCGGCAGCAATTGAGGAAGAAAGAGAGTCTGAATTGCTTTGAGGCCACGTTTGATCTAACAGTCAGAAGGA ATCACTTGATTGAGGATGTTTTGAATCAGCTAAGTCAATTTGAGAATGAAGACCTGAGGAAGAGTTATGGGTTT CATTTAGTGAGAAATTGGGTATGACCTCGGAGGAGTCAAGAAAGAGTTCTTCTACTGTCTGTTTGCAGAGATGA TCCAGCCGGAATATGGGATGTTTATGTATCCTGAAGGGGCTTCTGCATGTGGTTTCTGTCAAGCCTAAATTTG AGAAGAAAAGATACTTCTTTTTTGGGGTTCTATGTGGACTTTCCCTGTTCAATTGCAATGTTGCCAACCTCCCTT TCCCACTGGCACTGTTTAAAGAACTTTTGGACCAAATGCCATCATTGGAAGACTTGAAAGAACTCAGTCTGATT TGGGAAAGAATTTGCAACACTTCTGGATGATGAAGGTGATAACTTTGAGGAAGTATTTTACATCCATTTTAATG TCGACTGGGACAGAAACGACACAACTTAATTCCATAATGGAAGTAGCATAACTGTCAACCAGACTAACAGAGAG ACTATGTTTCTAAGTATATCAATTACATTTTCAACGACTCTGTAAAGGCGGTTTATGAAGAATTCGGAGAGGAT TTTATAAAATGTGCGACGAAGACATTATCAAAATTATCCACCCCGAAGAACTGAAGGATGTGATTGTTGGAAATA CAGATTATGATTGGAAAACATTTGAAAAGAATGCACGTTATGAACCAGGATATAACAGTTTACATCCCACCATAG TGATGTTTTGGAAGGCTTTCCACAAATTGACTCTGGAAGAAAAGAAAAAATTCCTTGTATTTCTTACAGGAAC TG ACAGACTACAAATGAAAGATTTAAATAATATGAAAATAACATTTTGTCTGTCTGAAAGTTGGAATGAAAGAGACC CTATAAGAGCACTGACATGTTTTCAGTGTCTCTTCTCCCTAAATATTCTACAATGGAACAGTTGAAGAAGCGC TTCAAGAAGCCATCAACAACAACAGAGGATTTGGC TGACAGCTTGCTTGTCCAACAGCCTTATTTTGTGTGTGT TATCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTTCTCTACTTTGTTTTGTTTTAGGCTTTTAGCAGCCTGAAGCCAT GGTTTTTTCAATTTCTGTCTCTAGTGATAAGCAGGAAAGAGGGATGAAGAAGAGGGTTTTACTGGCCGGTTAGAACCC GTGACTGTATTCTCTCCCTTGGATACCCCTATGCC TACATCATATTCCCTTACCTCTTTTGGGAAATATTTTTCAA AATAAAAAATAACCGAAAAACTAAAAAAGAAAAA AAAAAAAAAAAAAAAAAAAAAA

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FIGURE 190

MERRSRRKSRNNGRSTAGKAAATQPAKSPGAQLWLFPSAAGLHRALLRRVEVTRQLCCSPGRLAVLERGGAGVQV
HQLLAGSGGARTPKCIKLGKNMKIHSVDQGAEHMLILSSDGKPFYDNYSMKHLRFESILQEKKIIQITCGDYHS
LALSKGGELFAWGQNLHGQLGVGRKFPSTTTPQIVEHLAGVPLAQISAGEAHSMALSMGNIYSWGKNECCQLGL
GHTESKDDPSLIEGLDNQKVEFVACGGSHSALLTQDGLLFTFGAGKHGQLGHNSTQNELRPCLVAELVGYRVTI
ACGRWHTLAYVSDLGKVSFSGSGKDGQLGNGGTRDQLMPLPVKVSSEELKLESHTSEKELIMIAGGNQSILLWI
KKENSYVNLKRTIPTLNELTVKRWIADVETKRWQSTKREIQEIFSSPACLTGSFLRKRRTTEMPVYLDLNKARN
IFRELTQKDWITNMITTCLKDNLLKRLPFHSPQEALEIFFLLPECPVMHISNNWESLVVPPFAKVCKMSDQSSL
VLEEWATLQESTFSKLVQMFKTAVICQLDYWDESAEENGNVQALLEMLKKLHRVNQVKQLPESIFQVDELLHR
LNFFVEVCRRYLWKMTVDASENVQCCVIFSHFFPIFNNLSKIKLLHTDTLLKIESKKHKAYLRSAAIEEERESEF
ALRPTFDLTVRRNHLIEDVLNQLSQFENEDLRKELWVSFSGEIGYDLGGVKKEFFYCLFAEMIQPEYGMFMYPEG
ASCMWFPVKPKFEKKRYFFFGVLCGLSLFNCNVANLPFPALFKKLLDQMPLEDLKEKSPDLGKNLQTLDDDEG
DNFEEVFYIHFNVHWRNDTNLIPNGSSITVNQTNKRDYVSKYINYIFNDSVKAVYEEFRRGFYKMCDEDIKLF
HPEELKDVIVGNTDYDWKTFEKNARYEPGYNSSHP TIVMFWKAFHKLTLLEKKKFLVFLTGTDRLQMKDLNNMKI
TFCCPESWNERDPIRALTCFSVLFLPKYSTMETVEEALQEAINNNRGFG

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FIGURE 191

CAGCGGCACAGCGAGGTCGGCAGCGGCACAGCGAGGTCGGCAGCGGCACAGCGAGGTCGGCAGCGGCACAGCGAG
GTCGGCAGCGGCACAGCGAGGTCGGCAGCGGCACAGCGAGGTCGGCAGCGGCAGCGAGGTCGGCAGCGGCACAGC
GAGGTCGGCAGCGGCAGCGAGGTCGGCAGCGGCGCGCGCTGTGCTCTTCCGCGGACTCTGAATCATGCGACCAC
GGCCACGATGGCGACCTCGGGCTCGGCGCGAAAGCGGCTGCTCAAAGAGGAAGACATGACTAAAGTGAATTCTGA
GACCAGCGAGGAGGTGGATGTGACCCACGTTTCGACACCATGGGCCTGCGGGAGGACCTGCTGCGGGGCATCTA
CGCTTACGGTTTTTGA AAAACCATCAGCAATCCAGCAACGAGCAATCAAGCAGATCATCAAAGGGAGAGATGTCAT
CGCACAGTCTCAGTCCGGCACAGGAAAAACAGCCACCTTCAGTATCTCAGTCCTCCAGTGTTTGGATATTCAGGT
TCGTGAAACTCAAGCTTTGATCTTGGCTCCCAAGAGAGTTGGCTGTGCAGATCCAGAAGGGGCTGCTTGCTCT
CGGTGACTACATGAATGTCCAGTGCCATGCCTGCATTGGAGGCACCAATGTTGGCGAGGACATCAGGAAGCTGGA
TTACGGACAGCATGTTGTGCGGGGCACTCCAGGGCGTGTTTTTGATATGATTTCGTGCGAGAAGCCTAAGGACACG
TGCTATCAAAATGTTGGTTTTGGATGAAGCTGATGAAATGTTGAATAAAGGTTTTCAAAGAGCAGATTTACGATGT
ATACAGGTACCTGCCTCCAGCCACACAGGTGGTTCATCAGTGCCACGCTGCCACACGAGATTCTGGAGATGAC
CAACAAGTTCATGACCGACCCAATCCGCATCTTGGTGAAACGTGATGAATTGACTCTGGAAGGCATCAAGCAATT
TTTCGTGGCAGTGGAGAGGGAAGAGTGGAATTTGACACTCTGTGTGACCTCTACGACACACTGACCATCACTCA
GGCGGTCATCTTCTGCAACACCAAAAGAAAGGTGGACTGGCTGACGGAGAAAATGAGGGAAGCCAACCTTCACTGT
ATCCTCAATGCATGGAGACATGCCCCAGAAAGAGCGGGAGTCCATCATGAAGGAGTTCGGTTCGGGCGCCAGCCG
AGTGCTTATTTCTACAGATGTCTGGGCCAGGGGGTGGATGTCCCTCAGGTGTCCCTCATCATTAACTATGATCT
CCCTAATAACAGAGAATTGTACATACAGAAATTGGGAGATCAGGTGATACGGCCGGAAGGGTGTGGCCATTAA
CTTTGTAAAGAATGACGACATCCGCATCCTCAGAGATATCGAGCAGTACTATTCCACTCAGATTGATGAGATGCC
GATGAACGTTGCTGATCTTATCTGAAGCAGCAGATCAGTGGGATGAGGGAGACTGTTACCTGCTGTGTACTCCT
GTTTGGAAGTATTTAGATCCAGATTCTACTTAATGGGGTTTATATGGACTTTCTTCTCATAAATGGCCTGCCGTC
TCCCTTCCTTTGAAGAGGATATGGGGATTCTGCTCTCTTTTCTTATTTACATGTAAATAATACATTGTTCTAAGT
CTTTTTCATTAAAAATTTAAACTTTTCCCAT

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FIGURE 192

MATTATMATSGSARKRLLKEEDMTKVEFETSEEVDVPTFTDTMGLREDLLRGIYAYGF EKPSAIQQRAIKQIIKG
RDVIAQSQSGTGKTATFSISVLQCLDIQVRETQALILAPTRELAVQIQKGLLALGDYMNVOCHACIGGTNVGEDI
RKLDYGQHV VAGTPGRVFD MIRRRSLRTRAIKMLVLDEADEMLNKGFK EQIYDVYRYLPPATQVVLISATLPHEI
LEMTNKFMTDPIRILVKRDELTLLEGIKQFFVAVEREEWKFDTLCDLYDTLTITQAVIFCNTKRKVDWLTEKMREA
NFTVSSMHGDM PQKERESIMKEFRSGASRVLISTDVWARGLDVPQVSLIINYDLPNNRELYIHRIGRSGRYGRKG
VAINFVKND DIRILRDIEQYYSTQIDEMPMNVADLI

FIGURE 193

CGCGGACGCGCGGAAGGTGGACTCGCGAATGTTAGGCCTGTGGGTGCCATAGCGACCGGGAGGTTGGGCTGCCAG
ATTGAGCTGCCGGGACCGGACCAGGTGCTTAGGAGAACATGCAGTAGAACTTTTCATCAAACAAATGGAACACGT
CACAGAATTTTGCTAACATGGACAACCTCTGCACAGAAAAATGAACGCACTGGCAAACATCCCAGACGTGCCAGTG
AAGTACAGAAAAAATGATATCCCAGGACCTGGGTTCTACAATGTTATTACACAGTCACCGGTGTCCAACAGTGTCT
TCATTGTCCAAGAAAGGAACCTTGCATGTTTCCCTCAATGTGCGCCCGATTGGACACCATCATTTCTAAATACCCT
GCAGCGAATGCATACACTATCCCATCGGATTTTATTTCCAAGAGAGACTTTAGTAATTTCGTGTTCCAGCATGTTT
CAGTTGCCAAGCTTTATGAAAGCTCTCAAGTTTGAAACTCCTGCACCAAACCTATTACAATGCCTCTGTCTCTTG
TGCAAGCAGAGAAACAACGTCTGTACTCGAGCCGGGTTTATGTCAAAAACCCAAAGAGGATCTTTTCGCTTTTGCT
GATAAAGGACCTCCCCAGGGCATTATGATATCAACGAATCCCTTGTGAAGCAGTCGCCAAATACATTAATGTCT
TGTTTTAAATCAAAAACCAACCGTGGATTAAAACTGACGTCAACAGGCCCGGGACCTGGTTATTACAACCCAGT
GATTGCACAAAAGTTCCAAAAAAGACTCTTTTCCGAAAAACCCATCCTGAACTTCTCTGCTCAGCCTTCGCCT
CTGCCTCCGAAGCCACCTTTCCAGGTCTGGTCAAGTATGAGATCGTGGACTACTTAGGCCCCCGCAAGCATTTC
ATCTCTAGTGCATCATTTCGTGTCCAATACCAGCCGGTGGACAGCGCGCGCCCTCAGCCAGGCCTGCCTGGCCCA
GCTACGTACAAGCCAGAGCTTCCAGGAAAGCAGTCTTCCTCTACAACGAGGACAAGAAATGGATCCCGGTTCTG
TAGGGATGTCACACAAGGTCAAGGAGAACTCCAGCCACCAGCCCACCCTGCCAGCGTCCCAGGACATTCTCTCA
GGAGGAGACCGGATCATGAGTGTGGCAGCTGACAAC TTGGGGGGTGGCTCTACCACTCTGGCCTGGCATCCTAGCC
GGACTGCTGCCATTGCCTTTGTCTTGAGCTGGAGACATTGCTCCCTGGAGACTTCACCCAGCCCCACAGACTCC
AGTGGCTTCTCTGAGCAGAAGGGAGGAGTGGACAGAGCCCCCTGGCTGCTTCCCCACGCACCCATCCAGGCTGCCT
TCCGGCACGACTCCCTGCCGCAGACTGAAGGGACTCCTGAAGCGCAGACTTCAAGGAGGATCAGTCCACCCTGAA
GGTGGCCAAGCCTGGAAGCCCCACCCTTCCCTGTNNCCCTCAC
TCCTGCCTTTTCTCATTTGTCCCTTTCTGACCTCAC TCACTTACGGTATGTCTACTGGGCGAAAGCTACCTGCAG
CAGGTGATGCTTTTTCCACCAGTCCACAGCTTCCTTTCTAAAGTGACCACCTGTTTGGAAGACCTCTCTTTACT
CCTTTTAGACCTTTTTCTCTTTGGAGTGGGAGATCATCTTGAATGGCAGTGGCCGGGCCCCGGGGGCTGCGCTTT
TCCCTGACTTTCTCTGCTGGCGGGACTGAATTTTCTCAAGGCTTACAGGCCCTTCCATGGAGTCCACATGGCCTG
TCTAGGCTGATAGCTTTCTGTCTCTCTATGTGGAGGGAAAAAGAAATGTGCCCTAGTGGTTTTGGTGGAGGCTGC
ACAGATTGCGCGTGGGTGGGGAGCTGCCAGGCTCCTTTTCTGATCTCCACGAGGCTTTGACTGACGCTGTTTAG
TCTTTCTGTACATTAACCCCGCCAGATACCGAGAGGTTACAAAGCCTCCAAGGCCTGTACAACTGTGGCCTCTCC
AGAGAAGTGGTTCTCAGCCTTGACTGCACACTGTAATCACCTGGGACTTTAAAAGTACTGAGGCCTGGGGCCC
ACCCACAAATGCTGATTTAACCTCCTCCAGGGTGGGGTCTGGGCAGTGGGGAGGCAGGAGCCACCCAGGTGATTCC
AATGATAGGTGTAGGTTGAGAAGCGCCACCTTCCAGCTTCTTAAC TGCTCTGGGAGGGGAGCTGGGTGGGAAGT
TCAGGAGGTGGGAACCTTTGTACACGCAGAGCACCTGGAGCACCTACAGCATGGCTGTGGTTCCACACTCCTCTGT
CATTTAACCTTCACACATCACCTCGTTCTGACATCAAGGTGCGTCACAGCCACAGTGAGGCCTCGCCTGGGCAG
AGCAACTCTGGGTGCCCACTGGGTCCCTCCCACAGGGGCAGGCAAGCCTAATGGGAACCCGAGGCAAAAGGAAA
CATCAGTAATACGAATCCTGTCTTTAAAACTGTGATGTTTTGTTTACCATGGATTTTTTTTTTTGGGGGGGGGGCC
TTAATTTTAAAAATATTGCATTAACTTATTTATCTTGCTTATTGAGCTTTTGGGTACCCCTTAATTTTTTGIGCC
TTAGGCTAGAGACTCACCTGCCCATAGCCTTGACTCTAGGTAGGGGCTTGGGAATTAGGACCACAGACTGTCAGC
GCTGGGAGGTTCTTAGAGGGATCATGGTTTTTACACCTTTTTAAAAAAAGTTTTTACTCAGACAGATGT

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FIGURE 194

RTAEGGLANVRPVGAIARPGGWAGQIQLPQPDQVLRRTCSRTFHQTNGTRHRILLTWITLHRKMNALANIPDVPV
KYRKNDIPGPGFYNVIHQSPVSNVSLSKKGTCTMFPSCARLDTIISKYPAANAYTIPSDFIKRDFSNSCSSMF
QLPSFMKALKFETPAPNYYNASVSCCKQRNNVCTRAGFMSKTQRGSFAFADKGPPPGHYDINESLVKQSPNTLMS
CFKSKTNRGLKLTSTGPGPGYYNPSDCTKVPKKTLPKNPILNFSAQPSPLPPKPPFPGPGQYEIVDYLGP RKHF
ISSASFVSNTSRWTAAPPQFGLPGPATYKPELPGKQSFLYNEDKKWIPVL

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FIGURE 195

CGGCTGAGAGGCAGCGAACTCATCTTTGCCAGTACAGGAGCTTGTGCCGTGGCCACAGCCCACAGCCCACAGCC
ATGGGCTGGGACCTGACGGTGAAGATGCTGGCGGGCAACGAATTCCAGGTGTCCCTGAGCAGCTCCATGTCGGTG
TCAGAGCTGAAGGCGCAGATCACCCAGAAGATTGGCGTGCACGCCTTCCAGCAGCGTCTGGCTGTCCACCCGAGC
GGTGTGGCGCTGCAGGACAGGGTCCCCCTTGCCAGCCAGGGCCTGGGCCCTGGCAGCACGGTCCTGCTGGTGGTG
GACAAATGCGACGAACCTCTGAGCATCCTGGTGAGGAATAACAAGGGCCGCAGCAGCACCTACGAGGTCCGGCTG
ACGCAGACCGTGGCCACCTGAAGCAGCAAGTGAGCGGGCTGGAGGGTGTGCAGGACGACCTGTTCTGGCTGACC
TTCGAGGGGAAGCCCCTGGAGGACCAGCTCCCGCTGGGGGAGTACGGCCTCAAGCCCCTGAGCACCGTGTTTCATG
AATCTGCGCCTGCGGGGAGGCGGCACAGAGCCTGGCGGGCGGAGCTTAAGGGCCTCCACCAGCATCCGAGCAGGAT
CAAGGGCCCGAAATAAAGGCTGTTGTAAGAGAAT

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FIGURE 196

MGWDLTVKMLAGNEFQVSLSSSMSVSELKAQITQKIGVHAFQORLAVHPSGVALQDRVPLASQGLGPGSTVLLVV
DKCDEPLSILVRNNKGRSSTYEVRLTQTV AHLKQQVSGLEGVQDDLFWLTFEGKPLEDQLPLGEYGLKPLSTVFM
NLRLRGGGTEPGGRS

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FIGURE 197

CCAGTTAGAGCTCGGGTCTCCTCGCCACAGCTCCGAGTCTTTCGTTCTGGGAGGCCAGGCGGCTTCGCGTTCTG
AGAATAAACAGAACCTCTGTTGCTCTGCGACTTGCAGGCACTGGGAGATTTCGTAGCTAAGACGCCAGGGCATCCC
GGAAGCTGGGAAATGGGACTGTTGACATTACAGGGATGTGGCCGTAGAATTCTCTTTGGAGGAGTGGGAACACCTG
GAACCAGCTCAGAAGAATTTGTATCAGGATGTGATGTTAGAAAACTACAGAAACCTGGTCTCTCTGGGTCTTGT
GTCTCTAAGCCGGACCTGATCACCTTTTTTGGAAACAAAGGAAAGAGCCTTGGAAATGTGAAGAGTGAGGAGACAGTA
GCCATCCAGCCAGATGTGTTTTTCGCATTATAACAAGGACCTGTTGACAGAGCACTGCACAGAAGCTTCATTCCAA
AAAGTGATATCGAGGAGACATGGGAGCTGTGATCTTGAGAATTTACATTTAAGAAAAAGGTGGAAAAGGGAGGAG
TGTGAAGGGCACAATGGATGTTATGATGAAAAGACTTTTAAATATGATCAATTTGATGAATCCTCTGTGAAAGT
TTGTTTCACCAGCAAATACTTTCTTCTTGTGCCAAAAGCTATAACTTTGATCAATATAGGAAGGTCTTTACTCAT
TCATCATTGCTTAATCAACAAGAGGAAATAGATATTTGGGGAAAACATCACATATATGATAAACTTCAGTGTTA
TTTAGGCGAGTCTCTACTCTAAATAGTTACCGAAATGTTTTATTGGAGAGAAAAATTATCATTGCAATAATTCT
GAAAAAACCTTGAACCAAAGCTCAAGCCCTAAAAATCATCAGGAAAAATTATTTCTAGAAAAACAATACAAATGT
AAAGAATTTGAGGAAGTCTTTCTTCAGAGTATGCATGGGCAAGAGAAACAAGAACAGTCTTACAAATGTAATAAA
TGTGTAGAAGTTTGTACCCAGTCATTAAACATATTCACATCAGACCATCCATATCAGAGAAAACATCATATAGC
TATAACAAATATGATAAAGATCTTAGTCAGTCATCAAATCTTAGAAAGCAGATAATCCATAATGAAGAGAAACCA
TACAAATGTGAAAAATGTGGGGATAGCTTAAACCATAGTTTGCACCTTACTCAACATCAGATCATTCCTACCGAA
GAGAAACCTTATAAATGGAAAGAATGTGGCAAGGTCTTTAACCTTAACTGTAGTTTATACCTTACTAAACAGCAG
CAAATGATACTGGAGAAAACCTTTACAAATGTAAAGCATGTAGCAAATCTTTTACTCGTTCCTCCAATCTTATT
GTGCATCAGAGAATTCACACTGGAGAGAAACCATACAAATGTAAAGAATGTGGCAAAGCCTTTCGCTGTAGTTCA
TACCTTACTAAACATAAGCGAATTCATACTGGAGAGAAACCTTATAAATGTAAAGAATGTGGAAAAGCTTTTAA
CGTAGTTCATGCCTTACTCAACATCAGACAACTCATACAGGAGAAAACTTTACAAATGTAAAGTATGTAGCAAA
TCTTATGCTCGTTCTTCAAATCTTATTATGCATCAGAGAGTTCATACTGGAGAGAAAGCCTTATAAATGTAAAGAA
TGTGGCAAAGTCTTTAGCCGTAGTTCTTGCCCTTACTCAACATCGGAAAATTCATACTGGAGAAAAATCTTTACAAA
TGCAAAGTATGTGCTAAACCTTTTACTTGTCTCAAATCTTATTGTGCATGAGAGAATTCATACTGGAGAGAAA
CCCTATAAATGTAAAGAATGTGGCAAAGCCTTTCCCTATAGTTACACCTTATTTCGACATTATCGAATTCATACT
GGAGAAAAACCATACAAATGTAAAGCATGTAGCAAATCTTTTAGTGACTCCTCAGGTCTTCTGTGCATCGGCGA
ACTCATACTGGAGAGAAACCTTATACATGTAAAGAATGTGGCAAAGCCTTTAGTTATAGTTCAGATGTTATTCAG
CATCGGAGAATTCATACTGGCCAGAGACCCTACAAATGTGAAGAATGTGGCAAAGCCTTCAACTATAGGTCATAC
CTCACTACACATCAGAGAAGTCATACTGGAGAGAGACCCTACAAATGTGAAGAATGTGGCAAAGCCTTCAACTCT
AGGTCATACCTCACTACACATCGGAGAAGACATACTGGAGAGAGACCCTACAAATGTGATGAATGTGGTAAAGCC
TTCAGCTATAGGTCATACCTCACTACACATCGGAGAAGTCATAGTGGAGAGAGACCCTACAAATGTGAAGAATGT
GGCAAAGCCTTTAACTCTAGGTCATACCTCATTGCACATCAGAGAAGTCATACTAGAGAAAACTTTTAAATGT
AAAACATGGAGCAGATTTTTTACTTGTACCCATGTCTTATTGTGCATCAGATAATTTATATGGGAGTGAAACCC
TACAAATGTGAAGAATGTGGCATAACCTTTAACTATTTTCAAGCCTTACACAATAGCAGAGAATATAAACTGAAA
AAATCCATACAAATATTAAAAATGTGGCAAATTATTTTAACTGTGCTCAACCCTTACTCAAGATAATCCATACT
AGAGAAACACTATAGATGTAAAAATGTGAAAAGTTTATTCAAATATCAAACCTTATGAGTC

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FIGURE 198

MGLLTFRDVAVEFSLEEWELHLEPAQKNLYQDVMLNENYRNLVSLGLVVSKEPDLITFLEQRKEPWNVKSEETVAIQP
DVFSHYNKDLLTEHCTEASFQKVISRRHGSCDLENLHLRKRWKREECEGHNGCYDEKTFKYDQFDESSVESLFHQ
QILSSCAKSYNFDQYRKVFTHSSLLNQEEIDIWGKHHIYDKTSVLFRQVSTLNSYRNVFIGEKNYHCNNSEKTL
NQSSSPKNHQENYFLEKQYKCKEFEEVFLQSMHGQEKQEQSYKCNKCEVCTQSLKHIHQHTIHIHRENSYSYNKY
DKDLSQSSNLRKQIIHNEEKPYKCEKCGDSLNLHSLHLTQHQIIPTEEKPYKWKECGKVFNLNCSLYLTKQQQIDT
GENLYKCKACSKSFTRSSNLIVHQRIHTGEKPYKCKEKGAFRCSSYLTKHKRIHTGEKPYKCKEKGAFNRSSC
LTQHQTTHHTGEKLYKCKVCSKSYARSSNLIMHQRVHTGEKPYKCKEKGKVFSSSCLTQHRKIHTGENLYKCKVC
AKPFTCFSNLIVHERIHTGEKPYKCKEKGAFPPYSSHLIRHYRIHTGEKPYKCKACSKSFSDSSGLSVHRRHTHTG
EKPYTKCEKGKAFSYSSDVIQHRRIHTGQRPYKCEECGKAFNYRSYLTTHQRSHTGERPYKCEECGKAFNSRSYL
TTHRRRHTGERPYKCECGKAFSYRSYLTTHRRSHSGERPYKCEECGKAFNSRSYLIAHQRSHTREKL

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FIGURE 199

GCAGTGTCACTCTTTTCAGAAATATGTCCATGGTGGTTTACTCAATTTGCTTCTTTTTTATTCATAGATTTGCAT
ATGTAATGCATTGCGCTATAACCATTAAAGACAGCTATGATGTCACTGCAGTTACAGTGTCACTAGGTGATAGAAAT
TGTCCAGCTCCATTACAACCTTATGGAACCACTGGTGCATACGTGGTTCATTGTGGTCCATTGTTGACTGAAACA
ATGTTATGAGGTGCGTAACTATATATCCAAAGCAAAGCTAAATGAAATAAATGAAACTAATTGTGTTGGTGTCC
TAAACACACAGAGGAGAATTACTTCAAGTATTTTTAAAACACAGTCACTTGTCTATGCATTTTGTAGTGGATATGC
CCTAAAGTATGAACTAAATTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAAATTAATTTACAAATAGTATTAATATTG
AATAATAATATATGTTAATATTGTTACTCTGAATCTATTATATACATTTTGGAGGATAAATAACATGCAATTTTG
TTAATATTAGGAATCAAGAACTATATATATAAAATCAAAGCTGCTAAATAAAATTATAAAATTGTGTTTATAATT
ACAAATTTGAATTGGAAATATCATTATAAAATCATAATGTATTTTCTTTACAGAAGCACATTTTCTAGCCCTGTT
ATTTGAAAATCAGTAATGAGCACCTTAGAATGCAGATTATAGTCTCTAAATGCAATTTTCTGCTAAAA

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FIGURE 200

SVTLFRNMSMVVISICFFFIHREFAYVMHCAIPLRQL

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FIGURE 201

GGGCAGAAAGGGCACGCTCTTGTGGGTGACTACAGGTTAGGAGACCGTTGAACCTGGAGGGGCCCTAGGATGGAC
CCCGTGGAAAGATTTCAGAGACTGCGCCCTCTCCCTGGGCGCCGCTTCCCCTACACGCGGCGGGTATATTCTGTG
CAGTTGGCCCAGGACCTGTTTCCAAGACTCTGCCCCCTCGCACTTCCGTCCCTCCTGGTTTTGTAAAGTGATGCT
CATAGGAACCCCCACCCGCGTGACACTACTCCAGCTCCTGGCTGACTTCTAGTCTTCTGGTTGAAGCTGCGCC
TTTAGATGACACGACCCTACCCACCCCTGTTTCCAGCGGATGCCCCGGGCCTGGAGCCCACAGAATTCTTCCAGTC
CCTGGGTGGGGACGGAGAAAGGAACGTTTCAGATTGAGATGGCCCATGGCACCACCACGCTCGCCTTCAAGTTCCA
GCATGGAGTGATTGCAGCAGTGGATTCTCGGGCCTCAGCTGGGTCTTACATTAGTGCCTTACGGGTGAACAAGGT
GATTGAGATTAACCCTTACCTGCTTGGCACCATGTCTGGCTGTGCAGCAGACTGTCAGTACTGGGAGCGCCTGCT
GGCCAAGGAATGCAGGCTGTACTATCTGCGAAATGGAGAACGTATTTTCAGTGTGCGCAGCCTCCAAGCTGCTGTC
CAACATGATGTGCCAGTACCGGGGCATGGGCCTCTCTATGGGCAGTATGATCTGTGGCTGGGATAAGAAGGGTCC
TGGACTCTACTACGTGGATGAACATGGGACTCGGCTCTCAGGAAATATGTTCTCCACGGGTAGTGGGAACACTTA
TGCCTACGGTGTTCATGGACAGTGGCTATCGGCCTAATCTTAGCCCTGAAGAGGCCTATGACCTTGGCCGCAGGGC
TATTGCTTATGCCACTCACAGAGACAGCTATTCTGGAGGCGTTGTCAATATGTACCACATGAAGGAAGATGGTTG
GGTGAAAGTAGAAAGTACAGATGTCAGTGACCTGCTGCACCAGTACCGGGAAGCCAATCAATAATGGTGGTGGTG
GCAGCTGGGCAGGTCTCCTCTGGGAGGTCTTGGCCGACTCAGGGACCTAAGCCACGTTAAGTCCAAGGAGAAGAA
GAGGCCTAGCCTGAGCCAAAGAGAGAGTACGGGCTCAGCAGCCAGAGGAGGCCGGTGAAGTGCATCTTCTGCGTG
TTCTC

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FIGURE 202

MLIGTPTPRDTPSSWLTSSLLVEAAPLDDTTLPVSSGCPGLEPTEFFQSLGGDGERNVQIEMAHGTTTLAFK
FQHGVIAAVDSRASAGSYISALRVNKVIEINPYLLGTMSGCAADCQYWERLLAKECRLYYLRNGERISVSAASKL
LSNMMCQYRGMGLSMGSMICGWDKKGPGLYYVDEHGTRLSGNMFSTGSGNTYAYGVMDSGYRPNLSPEEAYDLGR
RAIAYATHRDSYSGGVNMYHMKEDGWVKVESTDVSDLLHQYREANQ

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FIGURE 203

CCCGAATTTTCCGGCTCGAATGCCCGGCAGCCGTGGCGGCTAGAGCGTTCCTCCCCAGCTCGAATGCCCGGCGGC
GAGGCGGCTAGAGCGTCGCCTCCTCCCGGGGAACCGCGTGTGACCTTCCAGCCCCGCGGACCGATGCTGCCGGCGG
CCGCTCGCCCCCTGTGGGGGCCTTGCCTTGGGCTTCGGGCCGCTGCGTTCGGCCTTGCCAGGCGACAGGTGCCAT
GTGTCTGTACCGTSCGACATATGAGGAGCAGCGGCCATCAGAGGTGTGAGGCCCTCGCTGGTGCACCCCTGGATA
ACGCCCCCAAGGAGTACCCCCCAAGATACAGCAGCTGGTCCAGGACATCGCCAGCCTCACTCTCTTGAAATCT
CAGACCTCAACGAGCTCCTGAAGAAAACGTTGAAGATCCAGGATGTCGGGCTTGTGCCGATGGGTGGTGTGATGT
CTGGGGCTGTCCCTGCTGCAGCAGCCAGGAGGCGGTGGAAGAAGATATCCCCATAGCGAAAGAACGGACACATT
TCACCGTCCGCCTGACCGAGGCGAAGCCCGTGGACAAAGTGAAGCTGATCAAGGAAATCAAGAACTACATCCAAG
GCATCAACCTCGTCCAGGCAAAGAAGCTGGTGGAGTCCCTGCCCCAGGAAATCAAAGCCAATGTCGCCAAAGCTG
AGGCGGAGAAGATCAAGGCGGCCCTGGAGGCGGTGGGCGGCACCGTGGTTCTGGAGTAGCCTCCAGCTCGGAGGA
CTTGTGTTTCAGGGGTCTTGGGCCCCGCGGAGGTCCCGCCCTCCCGTGGTCACTGGCTCCGCCCCAGCACCAGGC
GCCCAGTGGAGCCGTTTGGGAGAATTGCCTGCGCCACGCAGCGGGCCGGACAGGCCGCACAGACCTACTGTGGCG
GGAGGGAGGGGCGGCTGCTGCCTGGTGACGGCACCCGGAAGCCCACCAGGACGCGCCACCGGTCAATGTGCCTCT
GGTGGCTGCTGAGAAAAATACACTGTGCAGCTC

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FIGURE 204

MLPAAARPLWGPCLGRLRAAFRLARRQVPCVCTVRHMRSSGHQRCALAGAPLDNAPKEYPPKIQQLVQDIASLT
LLEISDLNELLKKTILKIQDVGLVPMGGVMSGAVPAAAAQEAVEEDIP IAKERTHFTVRLTEAKPVDKVKLIKEIK
NYIQGINLVQAKKLVESLPQEIKANVAKAEAEKIKAALEAVGGTVVLE

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FIGURE 205

GGCACCATTTCGGGGCCTGCCCGGACTTCGCCGCACGCTGCAGAACCTCGCCCAGCGCCCACCATGCCCCGGCAG
 CTCAGCGCGCGCGGCCGCGCTCTTCGCGTCCCTGGCCGTAATTTTGCACGATGGCAGTCAAATGAGAGCAAAAGCA
 TTTCCAGAAACCAGAGATTATTCTCAACCTACTGCAGCAGCAACAGTACAGGACATAAAAAAACCTGTCCAGCAA
 CCAGCTAAGCAAGCACCTCACCAAACCTTTAGCAGCAAGATTCATGGATGGTCATATCACCTTTCAAACAGCGGCC
 ACAGTAAAAATTCCAACAACCTACCCAGCAACTACAAAAACACTGCAACCACCAGCCCAATTACCTACACCCTG
 GTCACAACCCAGGCCACACCCAACAACCTCACACACAGCTCCTCCAGTTACTGAAGTTACAGTCGGCCCTAGCTTA
 GCCCCTTATTCACTGCCACCCACCATCACCCACCAGCTCATACAGCTGGAACCAGTTCATCAACCGTCAGCCAC
 ACAACTGGGAACACCCTCAACCCAGTAACCAGACCACCCTTCCAGCAACTTTATCGATAGCACTGCACAAAAGC
 ACAACCGTGCAGAACCTGATCAACCCACCCATGCCCGAGGAACAACGGCAGCTGCCACAATACCACCCGCACA
 GCTGCACCTGCCTCCACGGTTTCTGGGCCACCCCTTGACCTCAGCCATCGTCAGTCAAGACTGGAATTTATCAG
 GTTCTAAACGGAAGCAGACTCTGTATAAAAGCAGAGATGGGGATACAGCTGATTGTTCAAGACAAGGAGTCGGTT
 TTTTCACCTCGGAGATACTTCAACATCGACCCCAACGCAACGCAAGCCTCTGGGAAGTGTGGCACCAGAAAATCC
 AACCTTCTGTTGAATTTTTCAGGGCGGATTTGTGAATCTCACATTTACCAAGGATGAAGAATCATATTATATCAGT
 GAAGTGGGAGCCTATTTGACCGTCTCAGATCCAGAGACAGTTTACCAAGGAATCAAACATGCGGTGGTGATGTTT
 CAGACAGCAGTCGGGCATTCTTTCAAGTGCCTGAGTGAACAGAGCCTCCAGTTGTGAGCCACCTGCAGGTGAAA
 ACAACCGATGTCCAACCTTCAAGCCTTTGATTTTGAAGATGACCACTTTGGAAATGTGGATGAGTGCTCGTCTGAC
 TACACAATTGTGCTTCTGTGATTGGGGCCATCGTGGTTGGTCTCTGCCTTATGGGTATGGGTGCTATAAAATC
 CGCCTAAGGTGTCAATCATCTGGATACCAGAGAATCTAAATTGTTGCCCGGGGGAATGAAAAAATGGAATTTAG
 AGAACTCTTTTCATCCCTTCCAGGATGGATGTTGGGAAATTCCTCAGAGTGTGGGTCTTCAAACAATGTAAACC
 ACCATCTTCTATTCAAATGAAGTGAGTCATGTGTGATTAAAGTTTTCAGGCAGCACATCAATTTCTAAATACTTTTT
 GTTTATTTTATGAAAGATATAGTGAGCTGTTTATTTTCTAGTTTCTTTAGAAATATTTTAGCCACTCAAAGTCAA
 CATTGAGATAATGTTGAATTAACATAATATATGTAAGTAGAATAAGCCTTCAAATTATAAACCAAGGGTCAATT
 GTAACATAACTACTGTGTGTGCATTGAAGATTTTATTTTACCCTTGATCTTAACAAAGCCTTTGCTTTGTTATC
 AAATGGACTTTTCAGTGCTTTTACTATCTGTGTTTTATGGTTTCATGTAACATACATATTCCTGGTGTAGCACTTA
 ACTCCTTTTCCACTTTAAATTTGTTTTGTTTTTGTAGACGGAGTTTCACTCTTGTACCCAGGCTGGAGTACAG
 TGGCAGCATCTCGGCTTATGGCAACCTCCGCCTCCCGGTTCAAGTGATTCTCCTGCTTCAGCTCCCGAGTAGC
 TGGGATTACAGGCACACACTACCACGCCTGGCTAAATTTTGTATTTTATTATAGACGGGTTTACCATGTTGGC
 CAGACTGGTCTTGAACCTTTCAGCTCAGGTGATCCACCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCATG
 AGCCATTGCGCCCGGCCTTAAATGTTTTTTTTTAATCATCAAAAAGAACAACATATCTCAGGTTGTCTAAGTGTTT
 TTATGTAAACCAACAAAAAGAACAATCAGCTTAATTTTTTATCTTGATGACTCCTGCTCCAGAATTGCTAGA
 CTAAGAATTAGGTGGCTACAGATGGTAGAACTAAACAATAAGCAAGAGACAATAATAATGGCCCTTAATTATTAA
 CAAAGTGCCAGAGTCTAGGCTAAGCACTTTATCTATCTCATTTTCACTTCTACAACCTTATAAGTGAATGAGTAA
 ACTGAGACTTAAGGGAAGTGAATCACTTAAATGTACCTGGCTAACTGATGGCAGAGCCAGAGCTTGAATTCATG
 TTGGTCTGACATCAAGGTCTTTGGTCTTCTCCCTACACCAAGTTACCTACAAGAACAATGACACCACACTCTGCC
 TGAAGGCTCACACCTCATACCAGCATACGCTCACCTTACAGGGAAATGGGTTTATCCAGGATCATGAGACATTAG
 GGTAGATGAAAGGAGAGCTTTGCAGATAACAAATAGCCTATCCTTAATAAATCCTCCACTCTCTGGAAGGAGAC
 TGAGGGGCTTTGTAAACATTAGTCAGTTGCTCATTTTATGGGATTGCTTAGCTGGGCTGTAAAGATGAAGGCA
 TCAAATAAACTCAAAGTATTTTTAAATTTTTTGAATAAGAGAACTTCGCTAACCAACTGTTCTTTCTTGAGT
 GTATAGCCCCATCTTGTGGTAACTTGCTGCTTCTGCACCTCATATCCATATTTCTATTGTTCACTTTATTCTGT
 AGAGCAGCCTGCCAAGAATTTTATTTCTGCTGTTTTTTTTGCTGCTAAAGAAAGGAACCTAAGTCAGGATGTTAAC
 AGAAAAGTCCACATAACCCTAGAATCTTAGTCAAGGAATAATTCAAGTCAGCCTAGAGACCATGTTGACTTTCC
 TCATGTGTTTTCTTATGACTCAGTAAGTTGGCAAGGTCCTGACTTTAGTCTTAATAAAACATTGAATTGTAGTAA
 AGGTTTTTGAATAAAACCTTACTTTGG

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FIGURE 206

MPRQLSAAAALFASLAVILHDGSQMRKAFPETRDYSQPTAAATVQDIKKPVQQPAKQAPHQTLAARFMDGHITF
QTAATVKIPTTTTPATTKNTATTSPITYTLVTTQATPNNSHTAPPVTEVTVGPSLAPYSLPPTITPPAHTAGTSSS
TVSHTTGNTTQPSNQTTLPATLSIALHKSTTGQKPDQPTHAPGTTAAAHNTTRTAAPASTVPGPTLAPQPSSVKT
GIYQVLNGSRLCIKAEMGIQLIVQDKESVFSPPRYFNIDPNATQASGNCGTRKSNLLLNFGGFFVNLTFTKDEES
YYISEVGAYLTVSDPETVYQGIKHAVVMFQTAVGHSFKCVSEQSLQLSAHLQVKTTDVQLQAFDFEDDHFGNVDE
CSSDYTIVLPVIGAIVVGLCLMGMGVYKIRLRQSSGYQRI

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FIGURE 207.

ATGGCATTGGTTTTTCCATTTTTGCAAATCTCTTTAGTCTGGCTGACGGAAGACGGCTGGACCCACATGCCTCGT
GCCCTTCTGGAGATCCTCCCAGGCTCCTGCGGACTGAGTGACGAGGCAGATAGTGTCTATATTACTGTTGAACCAC
ACAGACCTGAAAGGGCCTCGGGGACCCCCAGCCATGCTGACCACACCCCAAGAGCTGGGGCCAGATGGAAAGAC
AGGGAAGGCTGGCTTTTGATGGGTGGAGCTCAAACCAGATAGAGGACAAGGGGGCCTGGCCACCCGCACAGACACT
CCCAGACACAGAGAACAGGCAGGGGGCTTCCAGACCCCTTCCCAAGCAGTTCTCTGGGTTTGTTGGACACAGGAA
GAGGAAGCTGCTCACCTTTGTCCCTAAGCCCAGGGCCTGTGCCCTGTGTGGCTGGTCTGGAACAGCCTTGCTGCC
CTTGCTGGGGTTGGAACCAGGGCCTCTGGGGTCTGCGGACCTTTGTTCTCGCACCAGCCTTGGGCCTGCGCTG
GGCAGTGGCCCCCGCTCGGTGCGCGCCTCCCTCCTAACATTGCCAGAGTGAAACACTCCTAGTCTCTCGGCT
TTGCTTGTATTTCTTTACTGCCATGTCTTTCTTGTGTTCCGTATTTGAAGACCCATGTGATAAATTTCTTCAA
GCTAGGAAGGAGTTTTGTCTCTCTGCGTGAGATATTGGCTGCTTGCTGGAACCTGGGGCCAGGTTTGGCCTCAG
CCTCATTTCCAGATGCCTTGGTGCCACATCTCTCTTCTCTACTTGGCTCTCCCTTTTTTATTTCTTTATAAAA
ATGAAGGTGGTGAACCTAAGCAGCCTCAGGCTTTAGAAGTGAGTCCCTGGCATCGGTGAGGCCACCCACACAGCCA
TTCCCTGTACATCAGGAGGGTGGTCTCACTCTGTACCTATCACCCAGGTTCTCGGGACCGGAAGTCAGGTGGGAG
ACTGGGCTCCCCGAAGCCAGAGCGGCAGAGAGGCCAGAACTCCAAAGCCCTGCAGCCCCGGCTGACAGGAAGCG
CCAGCTGTACCCCAAGTCCAAGAGCTCCAGCAAGGTCACGAGCGTGCCCGGCAAAGCCTCGGATCCCGGCGCCGC
CAGCACCAAATCAGGGAAGGCCAGCACGCTGTCTCGGCGGAGGAGCTGCTGAAACAGCTGAAGGCCGTGGAGGA
TGCTATTGCACGCAAGCGGGCCAAGATCCCCGGGAAAGCATAGGCCGTGCCCCGACCGGACTGGACGCATTTTAA
TACATAGGGTAAGCGCAGCCATTTGGATTTTGCAGTTAATGTCTTATTTTGGCTGTGATTCTTTTAAAAAGTA
AAAAAGAAAAAAGTTTCTCAGCTGGAAAAAGCCACACAGGAAATGACAACGACGCTGAATCCCAGCCTCCC
TCCCCAGAGCAGAAGTCCCGCAGGACAGACAGACAGACAGCGCTAGTGACCAGCACGGTTCTCATGTAAATTA
CAAGCCCCAGCGCCAGCCCCGCCTTCTCTTCTCTCTCTCCGTCTTCTTCCCTGGCCCTGGTCAGGCCTGTGGA
GCCCCAGCTCTGGGTCCCTAGCCCGGGTCCAGGCAGCCAGGCTCCCTCCTGAGCTGAGAAACGGAACCTCGCGAA
CCACTGGTGGCACATCCTTCTCCTCCCCCGCCCTGATCACCCGCCCCCGGATCAGAAATATATCTATATTCTCG
ACTAAAGTCTCATCAGGAAATATTTCTGTCTTTTATTTTAAAGCATCAAATTGTTTGTAGTTGATTTAAAAAGGAA
AAAATACAGAAAAGACCAAAAAAGGCCAAGGGTGTGTTGGGGCGTCTGTCTAATGTGGTGGGTCTTTTTTTGA
GGGTCTCCTAAATAAAATATTTTGATAAGCAAAAAATCTATGTGGTGCGGAGAAAGAGGTAATGAAATG

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FIGURE 208

GIGFSIFANLFSLADGRRLLDPHASCLEILPGSCGLSDEADSVYITVEPHRPERASGTPSHADHTPRAGAQMERO
GRLALMGGQAQTR

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FIGURE 209

CGGTCCGGACAGCCGCGCTGAGGGTCTCGGGGCGGGCGCCGCGGGACCTCTCCGGGCCATGGCAGCCCCCTGTC
AAAGGGAACAGGAAGCAGTCCACGGAGGGTGACGCCCTAGACCCACCTGCATCCCCCAAACCTGCTGGCAAGCAG
AACGGAATCCAGAACCCCATCTCGCTGGAGGACTCCCCGAGGCGAGCGGGGAGCGGGAGGAGGAGCAGGAGCGG
GAGGAGGAGCAGGCCCTTCCTGGTCAGCCTCTACAAGTTCATGAAGGAGCGACACACGCCCATCGAGAGGGTGCCC
CATCTCGGCTTCAAGCAGATTAACCTGTGGAAGATCTACAAAGCAGTGGAGAAGCTGGGGGCCCTATGAGCTGGTG
ACCGGGCGCCGCTCTGGAAGAACGTGTACGACGAGCTGGGGGGCAGCCCAGGCAGCACCAGCGCGGCCACGTGC
ACGCGCCGCCACTACGAGAGGCTGGTCTGCCATACGTGCGGCACCTGAAGGGGGAGGATGACAAGCCGCTGCCC
ACCTCCAAGCCCAGGAAACAGTACAAGATGGCTAAGGAGAACAGGGGGGATGATGGGGCCACCAGAGGGCCGAAG
AAGGCCAAGGAGGAGCGGCGCATGGACCAGATGATGCCAGGAAAGACCAAAGCAGATGCTGCTGACCCAGCACCA
CTTCCCAGCCAGGAGCCCCCAGGAACAGCACAGAACAGCAGGGCCTGGCCTCTGGGTCTTCTGTGTCTTTGTG
GGTGCCAGCGGTGTCTCTGAGGCCTACAAGCGGCTCCTATCCAGCTTCTACTGCAAGGGGACACACGGCATCATG
TCACCACTGGCCAAAAAGAAGCTCCTGGCCAGGTGAGCAAGGTGGAGGCCTTGCAAGTGCAGGAGGAGGGCTGC
CGCCATGGGGCAGAGCCCCAGGCGTCCCCAGCTGTTACCTCCAGAGAGTCCCCAGAGCCCCAAAGGGCTGACT
GAGAACTCCAGGCACCGGCTGACCCCTCAGGAGGGATTGCAGGCCCCAGGTGGCAGCCTCAGAGAGGAGGCGCAG
GCAGGCCCCTGCCCGGCAGCCCCCATCTTCAAGGGCTGCTTCTACACCCACCCACCGAGGTGCTGAAGCCTGTC
AGCCAGCACCCAGGGACTTCTTCTCTAGACTTAAAGATGGGGTGCTATTGGGGCCTCCTGGCAAAGAGGGGCTG
TCAGTGAAAGAGCCCCAGCTGGTGTGGGGCGGAGACGCTAACCGCCCTTCTGCGTTCCATAAAGGTGGCTCCAGA
AAGGGCATCCTCTACCCCAAGCCCAAAGCCTGCTGGGTGTCCCCATGGCCAAGGTCCCAGCCGAGAGCCCCACG
CTCCCGCCACCTTCCCCAGTAGCCCAAGGCTGGGCAGCAAGCGCAGCCTGGAGGAAGAGGGTGCTGCCCCACAGT
GGGAAGAGACTGCGGGCCGTGTCTCCCTTTCTTAAGGAGGCGGATGCCAAGAAGTGTGGGGCCAAACCTGCAGGG
TCCGGCCTGGTCTCCTGCCTTCTGGGCCCAGCCCTGGGGCCTGTGCCCCAGAGGCCTACAGGGGCACCATGCTG
CACTGCCCCGCTGAACCTTCACTGGCACCCCGGGCCCTTGAAGGGCCAGGCTGCACTCCCTTCAGCCCCCTGGTC
ATCCCGGCCTTCCCGGCCCACTTCTTGGCCACCGCAGGCCCCCTCGCCCATGGCCGCTGGCCTGATGCACTTCCCC
CCAACGTCTTTCGACAGTGCCCTCCGCCACAGACTTTGCCCCGCCCTCATCTGCCTGGCACGCACCACCAGTCACA
ACCTATGCAGCGCCCCACTTCTTCCACCTCAACACCAAGCTGTAGGCCAGCCCATGGTGTGTGTACACTGTGGA
GTCGACAGGGGCCTACAACAGGCAGGTACTGCTGCCAGGGGCTCTGAACTAGTGCCTGCTACCCAGGACACCCG
GGCCATGCCCCCTGGCTGGGCAGCCTGGCACAAGTGAAGAAGAAGGCAGTGGGAAACTGGGTTTATCTCAAGGCA
GCAGCCTGAGCCCAGGAGCAGAGGACCCAGTTGTTATAAGGCGCTGGGAGAGGATGGGCAGCTCCCACTGCCCCA
GAGCGGASSTCGAAGCACCCAGGTTGCCACGGAAAATCCAATAAAAAGACACCAGTGTGAATCCAAAAA

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FIGURE 210

RSGQPRAEGLGAGAAGPLRAMAAPVKGNRKQSTEGDALDPPASPKPAGKQNGIQNPISLEDSPEAGGEREEEEQER
EEEQAFVLVS LYKFMKERHTPIERVPHLGFKQINLWKIYKAVEKLGAYELVTGRRLWKNVYDELGGSPGSTSAATC
TRRHYERLVLPHYVRHLKGEDDKPLPTSKPRKQYKMAKENRGDDGATERPKKAKEERRMDQMPGKTKADAADPAP
LPSQEPNRNSTEQQGLASGSSVSFVGASGCPEAYKRLLSSFYCKGTHGIMSPLAKKKLLAQVSKVEALQCQEEGC
RHGAEPQASPAVHLPESPQSPKGLTENSRRHLTPQEGQLAPGGSLREEAQAGPCPAAPIFKGC FYTHPTEVLKPV
SQHPRDFFSRLKDGVL LGPPGKEGLSVKEPQLVWGGDANRPSAFHKGGSRK GILYPKPKACWVSPMAKVPAESPT
LPPTFPSSPGLGSKRSLEEEGAHSGKRLRAVSPFLKEADAKKCGAKPAGSGLVSCLLGPALGPVPPEAYRGTML
HCPLNFTGTPGPLKGQAALPFSPLVIPAFPAHFLATAGPSPMAAGLMHFPPTSFD SALRHRLCPASSAWHAPPVT
TYAAPHFFHLN TKL

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FIGURE 211

AAGCTTGCACGAGGCCTTCCCGGCGGCTGATTTCGAGGGCTTGTTTTGGTCAGAAGGGGGGCGTCAGAGAAGCTGCC
CCTTAGCCAACCAATGCCGCTGAGGGTCGCTGCTGGGAGACCTTGAAGGCCCTACGCAGTTCCGACAAAGGTCGC
CTTTGCTACTACCGCGACTGGCTGCTGCGGCGCGAGGATGTTTTAGAAGAATGTATGTCTCTTCCCAAGCTATCT
TCTTATTCTGGATGGGTGGTAGAGCAGTCCTACCCATATGCAGGAGAACCAACCTCTGTCTGAGACTTCGCCA
TCCTCTACGTCAGCTTCAGCCCTAGATCAACCCTCATTTGTTCCCAAATCTCCTGACGCAAGCTCTGCCTTTTCC
CCAGCCTCCCCTGCAACACCAAATGGAACCAAGGGCAAAGATGAGTCCCAGCACACAGAATCTATGGTACTTCAG
TCCTCACGGGGGATCAAAGTGGAAGGCTGCGTCCGAATGTACGAACTGGTACACAGAATGAAAGGAACAGAGGGC
CTGAGGCTATGGCAGGAGGAGCAGGAGAGGAAGGTGCAAGCCCTCTCGGAGATGGCATCTGAACAACCTGAAGCGG
TTTGATGAATGGAAGGAACCTGAAGCAGCATAAAGAATTCCAGGACTTGCGGGAAGTAATGGAGAAGAGCTCCAGA
GAAGCCTTGGGACACCAAGAGAAGTTAAAAGCTGAGCACCCTCACAGAGCAAAGATTCTCAACCTGAAGCTGCGG
GAAGCAGAGCAGCAGCGCGTGAAGCAAGCAGAACAGGAGCGGCTTCGGAAGGAAGAAGGCCAGATCCGCCTGCGG
GCCCTCTATGCTCTGCAGGAGGAGATGCTGCAGCTCAGCCAGCAGCTGGATGCCCTCTGAGCAGCACAAAGCCCTG
CTTAAGGTCGACCTGGCTGCCTTCCAGACCCGAGGCAACCAGCTGTGCAGCCTCATCTCAGGGATCATCCGGGCC
TCTTCAGAGAGCAGCTATCCACAGCAGAGAGTCAAGCTGAGGCTGAGCGAGCTCTGCGGGAAATGCGGGACCTC
CTGATGAACCTTGGGGCAGGAGATCACCAGAGCCTGCGAAGACAAGAGGAGGCAGGATGAAGAAGAGGCCCAGGTA
AAGCTGCAAGAGGCACAGATGCAGCAGGGACCAGAGGGCCACAAAGAGCCCCAGCTCCCAGCCAGGGCCCAGGA
GGGAAACAGAAATGAAGACCTCCAGGTGAAGGTACAAGACATTACAATGCAGTGGTACCAGCAGCTGCAGGATGCT
TCCATGCAGTGTGTGTTGACCTTTGAGGGCCTGACCAACAGCAAGGACAGTCAGGCCAAAAAGATAAAGATGGAC
CTCCAGAAGGCTGCTACCATCCAGTGAGCCAAATCTCTACCATTGCAGGCTCAAACTGAAGGAGATCTTTGAC
AAGATCCACAGCCTGCTCTCTGGAAAACCTGTTCAATCTGGTGGGCGCTCTGTGTCTGTACACTTAACCCACAG
GGGCTGGACTTTGTTCAATACAACTGGCAGAGAAATTTGTGAAACAAGGCGAGGAGGAAGTGGCCTCTCACCAT
GAAGCAGCATTCCCCATTGCAGTTGTGGCATCCGGGATCTGGGAGCTCCACCCAGAGTGGGGGACCTCATTCTT
GCTCATCTACATAAGAAGTGTCTTACTCTGTTCTTTCTATCCCACCTTTCAAGGAGGGAATGGCTTTTGAAGAC
TATCAGAGGATGCTTGTTACCAAGTAAAGGATTCCAAAGTGGAGCAGCAAGACAACCTTTCTAAAACGCATGTCA
GGGATGATCCGCTCTCTACGCTGCTATCATCCAGCTCCGGTGGCCATATGGAAACCGACAGGAGATTACCCCTCAT
GGCTTAAATCATGGATGGCGCTGGTTGGCACAGATCTTAAACATGGAGCCCTTGTGAGATGTGACAGCCACCCTC
CTCTTTGACTTCTGGAGGTGTGTGGGAATGCCCTCATGAAGCAATACCAGGTTGAGTCTGGAAGATGCTAATT
CTCATCAAAGAGGACTACTTTCCAGGTATCAGGCTTGTTTGAGCAGACAGCAGGGGATTAAGTAACTCATAACCA
GGCCTCAGATACCAAGGGTGTATTACCTGCTGGTTTTGATTCAAGTTAAAAACACCTGTACTAAGTATGACAT
CTTTCTACTCCAGTCCCTCTCGTTGATATTTGAATAAATGCTTTTGAACCTTAAAAAAAAAAAA

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FIGURE 212

MPSEGRCWETLKALRSSDKGRLCYYRDWLLRREDVLEECMSLPKLSSYSGWVVEHVLPHEMQUENQPLSETSPSSTS
ASALDQPSFVVPKSPDASSAFSPASPATPNGTKGKDESOHTESMVLQSSRGIKVEGCVRMYELVHRMKGTEGLRLW
QEEQERKVQALSEMASEQLKRFDEWKELKQHKEFQDLREVMEKSSREALGHEKLEKAEHRHRAKILNLKLREAEQ
QRVKQAEQERLRKEEGQIRLRALYALQEEMQLQSQQLDASEQHKALLKVDLAAFQTRGNQLCSLISGIIRASSES
SYPTAESQAEAEERALREMRDLLMNLGQEITRACEDKRRQDEEEAQVKLQEAQMQQGPEAHKEPPAPSQGPGGKQN
EDLQVKVQDITMQWYQQLQDASMQCVLTFEGLTNSKDSQAKKIKMDLQKAATIPVSQISTIAAGSKLKEIFDKIHS
LLSGKPVQSGGRSVSVTLNPQGLDFVQYKLAEFVKQGEEEVASHHEAAFPPIAVVASGIWELHPRVGDLLILAH LH
KKCPYSVFFYPTTFKEGMALEDYQRM LGYQVKDSKVEQQDNFLKRMSGMIRLYAAIIQLRWPYGNRQEIHPHGLNH
GWRWLAQILNMEPLSDVTATLLFDFLEVCGNALMKQYQVQFWKMLILIKEDYFPRYQAC

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FIGURE 213

GGTTCACCATCATCCTCACCAACTTTTGGNCCATAATTCACCCAACCCTTTGGTGAGCCTGAAAAAATCTGGG
CAGAATGTAGGACTTCTTTATTTTGTAAAGGGGTAACACAGAGTGCCCTTATGAAGGAGTTGGAGATCCTGCA
AGGAAGAGAAGGAGTGAAGGAGAGATCAAGAGAGAGAAACAATGAGGAACATTTTCATTTGACCCAACATCCTTTA
GGAGCATAAATGTTGACACTAAGTTATCCCTTTTGTGCTAAAATGGACAGTATTGGCAAAATGATACCACAACCTT
CTTATTCTCTGGCTCTATATTGCTTTGGAAACACTTAAACATCAAATGGAGTTAAATACATATTTGAAATTTAGG
TTAGGAAATATTGGTGAGGAGGCCTCAAAAAGGGGGAAACATCTTTTGTCTGGGAGGATATTTTCCATTTTGTGG
ATTTCCCTGATCTTTTTCTACCACCCTGAGGGGTGGTGGGAATTATCATTTTGCTACATTTTAGAGGTCATCCAG
GATTTTGAACCTTTACATTCTTTACGGTTAAGCAAGATGTACAGCTCAGTCAAAGACACTAAATTCTTCTTAGA
AAAATAGTGCTAAGGAGTATAGCAGATGACCTATATGTGTGTTGGCTGGGAGAATATCATCTTAAAGTGAGAGTG
ATGTTGTGGAGACAGTTGAAATGTCAGTGCTAGAGCCTCTGTGGTGTGAATGGGCACGTTAGGTTGTTGCATTAG
AAAGTGACTGTTTCTGACAGAAATTTGTAGCTTTGTGCAAACTCACCCACCATCTACCTCAATAAAATATAGAGA
AAAGAAAAATAGAGCAGTTTGAGTTCTATGAGGTATGCAGGCCAGAGAGACATAAGTATGTTTCTTTAGTCTTG
CTTCCTGTGTGCCACACTGCCCTCCACAACCATAGCTGGGGGCAATTGTTTAAAGTCATTTTGTTCCTGACTAG
CTGCCTTGACATTATCTTCATTTTCTGGAATTTGATACAGAGAGCAATTTATAGCCAATTGATAGCTTATGCT
GTTTCAATGTAAATTCGTGGTAAATAACTTAGGAACTGCCTCTTCTTTTCTTTGAAAACCTACTTATAACTGTT
GCTAATAAGAATGTGTATTGTTTCAGGACAACCTTGTCTCCATACAGTTGGGTGTAACCCTCATGCTTGCCCCAA
TAACTCTCTACTTATATCAGTTTTCTTACACTTCTTCTTTTAGGTCAACAATACCAAGAGGGGTACTGTGC
TGGGTAATGTGTAACTTGTGTCTTGTTTAGAAAGATAAATTTAAAGACTATCACATTGCTTTTTCATAAAACAA
GACAGGTCTACAATTAATTTATTTTGATGCAATTGATAGGGGGGCCAAGTAAGCCCCATATGCTTAATGATCAG
CTGATGAATAATCATCTCCTAGCAACATAACTCAATCTAATGCTAAGGTACC

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FIGURE 214

MIPQLLILWLYIAETLKHQMELNITYLKFERLCNIGEEASKRGKHLISGRIFSILWISLIFFYHPEGWWELSFCYI
LEVIQDF

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FIGURE 215

AATCTGTGGTTTTTGTCTCAAACTCAGTCTATCTGGATGCGTTGAATTATAGACAGATGCTGGCCGTGCTGGAA
GAAGAGGTCAAGACCTGATGGGAGATGTATATTCTTTGATATTCCATTCCCCAAAATAGGAAAACTCATAAAAT
CCAATGTTCCCTGAGCTGAGAGGACACTTCCCTCTCAGCATAACCCTGGTCCTGCGACTCATGCTGCTGGCTTCCA
AGGGAGATGACCCAGAGGATGCCAAGGCAAAGGTGCTATCAGTGCTAAAGCATTTCATTGCTGTCCTTCAAGCAAC
CCAGAGTCATGGACATGTTAAACTTTACTTCTCTGTTTTCTTTGCAGTTCCTGGTGAAAGAGGGCTATTTAGATC
AAGAAGGTAATCCTATGGGGTTTGCTGGACTTGTGTCACATTTGCATTATCATGAACCTTCTAATCTGTTTTTG
TGAGTTTTCTGTAAATGGCCTCTTCCATGATCTCTGTCAGCCAACCAGGAAAGGCTCAAAACATTTTTCTCAAG
ACGTTATGGAAAAGCTAGTATTAGTATTGGCACATCTCTTTGGAAGAAGATATTTCCACCAAAGTTCAGGATG
CACACTTCGAGTTTTATCAATCAAAGGTGTTCCCTTGATGATCTCCCTGAGGATTTTAGTGATGCTTTAGATGAAT
ATAACATGAAAATTATGGAGGACTTTACCACCTTTCCTACGAATTGTTTCCAACTGGCTGATATGAATCAGGAAT
ATCAACTCCCATTGTCAAAAATCAAATTCACAGGTAAAGAATGTGAAGACTCTCAACTCGTATCTCATTGTGATGA
GCTGCAAGGAAGGAAGAGTAGCAATTTACCATTGTTTGTCTGTCTGGGAACCTTGATGATGATTGCTTCGAC
TAGAACTCCAAACCATGTTACTCTAGGCACAATCGGTGTCAATCGCTCTCAGGCTCCAGTGCTGTTGTCACAGA
AATTTGATAACCGAGGAAGGAAAATGTCGCTTAATGCCTATGCACTGGATTTCTACAAACATGGTTCCTTGATAG
GATTAGTCCAGGATAACAGGATGAATGAAGGAGATGCTTATTATTTGTTGAAGGATTTTGCCTCACCATTAAAT
CTATCAGTGTTTCCTTGCGTGAGCTATGTGAAAATGAAGACGACAACGTTGTCTTAGCCTTTGAACAACTGAGTA
CACTTTTTGGGAAAAGTTAAACAAAGTCTAAAAACAAAGTCTATGCAAACCACTCAAAAATAATTCCATAGTAG
TTTTTCAGGTCACGTTTTTGATTCTTATGCTTCTTGCCAGAAATACATTATGATAAAGTGGAATACATTACGAT
GAAGTGGAAGAGCAAACACTTTGGAATCAAACAGAGTTGCAATCAAACCTGCCATGTTCTGTGATGAATACTCA
CAAATTATTTAGTATACCTGAATCTTGTTTTCTTTTATAACTGAGTAATAATGGTTACATCTCAGGTAGTTTGA
GGATTGACTAAAAAATGCGAGAATGTTGTATGTGACTGAATAACAATTTTTACTCTGCGAAGCCAAAAGTAAATA
TAATATTATCAGTAACTTTATCCCCAGTGTCAGTATTTATAAAATGTTTATTAAGGCTAGAAAAATGAATACAA
TATCCTGAAGGTGAAATATATTCTCTTCAATTAGCATAAAATATGATTTACATAAGTTAGCTATACAGCTATTGAG
ATAGTACTTTCTAGTAAACTTAACTACTTTTTAAACATACATTTTGTGTTGATTTAACAAAAATATAGAGAATG
ATTTGCTTTATTGTAATTGTATATAAGTGACTGGAAAAGCACAAAGAAATAAAGTGGGTTCGATCTGTTTACCAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 216

MSGRAGRRGQDLMGDVYFFDIPFPKIGKLIKSNVPELRGHFPLSITIVLRMLLASKGDDPEDAKAKVLSVLKHS
LLSFKQPRVMDMLKLYFLFSLQFLVKEGYLDQEGNPMGFAGLVSHLHYHEPSNLVFVSFLVNGLFHDLCPTRKG
SKHFSQDVMEKLVVLVAHLFGRRYFPPKFQDAHFEFYQSKVFLDDLPEDFSALDEYNMKIMEDFTTFLRIVSKL
ADMNQEYQLPLSKIKFTGKECEDSQLVSHLMSCKEGRVAISPFVCLSGNFDDLLRLETPNHVTLTIGVNRSA
PVLLSQKFDNRGRKMSLNAYALDFYKHGSLIGLVQDNRMNEGDAYLLKDFALTIKSI SVSLRELCENEDDNVVL
AFEQLSTTFWEKLNKV

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FIGURE 217A

AATGCGCTTGCGCACGTGCTGTCTACCAGTTCCTGAGAGGGACGCGTGCCGCGGAGCCAGGCTTACTACGTGACC
CGGACACCAGGCATACGCTAGGGGCGAGTCAGCTGTGCCTTCTCTTTCCGAGTTGTTCCGTGCTCCACGTGCTTC
CCCTTCTCCACTGGCTGGGATCCCCCGGGCTCGGGGCGCAGTAATAATTTTTCACCATGTCATCGGAAAAAGGTGG
ATAACCGAATCCGGATTCTCATTGAGAATGGAGTAGCTGAGCGGCAAAGATCTCTCTTTGTTGTAGTTGGGGATC
GAGGAAAAGATCAGGTGGTAATACTTTCATCACATGTTATCCAAAGCAACTGTGAAGGCTCGGCCTTCAGTGCTGT
GGTGTATAAAGAAAGAGCTGGGGTTTAGCAGTCACCGGAAGAAAAGAAATGCGACAGCTGCAGAAGAAAATAAAGA
ATGGAACACTGAACATAAAGCAGGACGACCCCTTTGAAGTCTTCATAGCAGCCACAAACATTGCGTACTGCTACT
ACAACGAGACCCACAAGATCCTGGGCAATACCTTCGGCATGTGTGTGCTGCAGGATTTTGAAGCCTTAACCTCAA
ACTTGCTGGCCAGGACTGTAGAAACAGTGAAGGTGGTGGGCTAGTGGTCATCCTCTACGGACCATGAAGTCAC
TCAAGCAATTGTACACAGTGACTATGGATGTGCATTCAGGTACAGAACTGAGGCCCATCAGGATGTGGTGGGAA
GATTTAATGAAAGTATTATTCTGTCTCTGGCCTCTGTGAAGAGTGTCTCGTCATTGATGACCAGCTCAACATCC
TGCCCATCTCTCCACGTTGCCACCATGGAGGCCCTGCTCTCCCGAGCTCCGGATGAGAGTCTTGGTCTCTCTG
ATCTGGAGCTGAGGGAGTTGAAGGAGAGCTTGACAGGACACCCAGCCTGTGGGTGTGTTGGTGGACTGCTGTAAAG
CTCTAGACCAGGCCAAAGCTGTCTTGAAATTTATCGAGGGCATCTCTGAAAAGACCCTGAGGAGTACTGTTGCAC
TCACAGCTGCTCGAGGACGGGGAAAATCTGCAGCCCTGGGATTGGCGATTGCTGGGGCGGTGGCATTGGGTACT
CCAATATCTTTGTTACCTCCCCATGCCCTGATAACCTCCATACCTCTGTTTGAATTTGTATTTAAAGGATTTGATG
CTCTGCAATATCAGGAACATCTGGATTATGAGATTATCCAGTCTCTAAATCCTGAATTTAAACAAAGCAGTGATCA
GAGTGAATGTATTTGAGAACACAGGCAGACTATTAGTATATACATCCTGCAGATGCTGTGAAGCTGGGCCAGG
CTGAAGTAGTTGTGATTGATGAAGCTGCCGCCATCCCCCTCCCTTGGTGAAGAGCCTACTTGGCCCCACCTTG
TTTTCATGGCATCCACCATCAATGGCTATGAGGGCACTGGCCGGTCACTGTCCCTCAAGCTAATTACAGCAGCTCC
GTCAACAGAGCGCCAGAGCCAGGTACAGCACCCTGCTGAGAATAAGACCACGACGACAGCCAGATTGGCATCAG
CGCGGACACTGCATGAGGTTTCCCTCCAGGAGTCAATCCGATACGCCCCCTGGGGATGCAGTGGAGAAGTGCTGA
ATGACTTGCTGTGCCTGGATTGCCTCAACATCACTCGGATAGTCTCAGGCTGCCCCCTTGCCCTGAAGCTTGTGAAC
TGTACTATGTTAATAGAGATAACCCTCTTTTGCTACCACAAGGCCTCTGAAGTTTTCTCCACGGCTTATGGCCC
TCTACGTGGCTTCTCACTACAAGAACTCTCCCAATGATCTCCAGATGCTCTCCGATGCACCTGCTCACCATCTCT
TCTGCCCTCTGCCTCTGTGCCCCCACCAGAAATGCCCTTCCAGAAGTGCTTGTGTTATCCAGGTGTGCCCTTG
AAGGGGAGATTTCTCGCCAGTCCATCTTGAACAGTCTGTCTCGAGGCAAGAAGGCTTCAGGGGACCTGATTCCAT
GGACAGTGTGAGAACAGTTCCAAGATCCAGACTTTGGTGGTCTGTCTGGTGGAAAGGCTGCTTCGCATTGCTGTTT
ACCCAGATTATCAAGGGATGGGCTATGGCAGCCGTGCTCTGCAGCTGCTGCAGATGTACTATGAAGCAGGTTTC
CTTGCTCGGAGGAAAAGGTCTTTGAGACACCACAGGAAATTCACACCGTAAGCAGCGAGGCTGTCAGCTTGTGG
AAGAGTCACTACTCCCCGAAGGACCTGCCTCTTTACTCTCAAATTGAATGAGAGGCCTGCCGAACGCTGG
ATTACCTGGGTGTTTCTATGGCTTGACCCCAAGGCTCTCAAGTCTTGAAACGAGCTGGATTGTTCTCTGTTT
ATCTGAGACAGACCCCAATGACCTGACCGGAGAGCACTCGTGCATCATGCTGAAGACGCTCACTGATGAGGATG
AGGCTGACCAGGGAGGCTGGCTTGACGCTTCTGGAAAGATTTCCGACGGCGGTTCTAGCCTTGCTCTCTTACC
AGTTCAGTACCTTCTCTCTTCCCTGGCTCTGAACATCAATCAGAACAGGAACATGGGGAAGCCAGCCAGCCTG
CCCTGAGCCGGGAGGAGCTGGAAGCACTCTTCTCCCTATGACCTGAAGCGGCTGGAGATGTATTACGGAATA
TGGTGGACTATACCTCATCATGGACATGATCCCGGCCATCTCTCGCATCTATTTCTGAACCAGCTGGGGGACC
TGGCCCTGTCTGCGGCTCAGTCGGCTCTTCTCTTGGGATTGGCCTGCAGCATAAGTCTGTGGACCGGCTGGAAA
AGGAGATTGAGCTGCCCTCGGGCCAGTTGATGGGACTTTTCAACCGGATCATCCGCAAAGTTGTGAAGCTATTTA
ATGAAGTTCAGGAAAAGGCCATTGAGGAGCAGATGGTGGCAGCGAAGGATGTGGTCATGGAGCCACGATGAAGA
CCCTCAGTGACGACCTAGATGAAGCAGCAAAGGAATTCAGGAGAAACACAAGAAGGAAGTAGGGAAGCTGAAGA
GCATGGACCTCTCTGAATACATAATCCGTGGGGACGATGAAGAGTGAATGAAGTTTTGAACAAAGCTGGGCCGA
ACGCCTCGATCATCAGCCTGAAAAGTGACAAGAAAAGGAAGTTAGAGGCCAAACAAGAACCCAAACAGAGCAAGA
AGTTGAAGAACAGAGAGACAAAGAACAAAAAGATATGAACTGAAGCGGAAGAAATAGTGAAGAGAACTCGGG
CATCTGTGTTTGATCATGGGAAGATACTCTCACTAACTGAACCCCTCTCTGGCTGGACTGTTAAAAGCAACGAGAG
GCCCCGGCACACCTGGAAGCTGGCCGCGAATTCGGCCTCTGGGCCTGTGTGTCTGTGAGCTCAACCTGGCTAAAG
GCAGAGTCACTCCCAAATGGGTCTCTTTAGAAGTTGATGGCTGGGCCTGCCATCTCTAGAATTGCCACGAGTCT
CTCTCTTCTGCCCAGTCCAGGGCCCTCTTTCTATAAGTTTCATATTTTGCTTTGAGCCAGCTTTTGTAGTCTCA

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FIGURE 217B

TTCCCACACATGTGGAAGCCACGTTGCCTCTCGACCGCCTGAGGCCCTTAAGTACATCGCTTTCTGGTGGTGCCC
AGGAGGCTGCTGCTGGGCCGCTGGGTCTCTCTTTGTGGACTTGTACCTGGAGCAGGAGGAAGTCCAGTCCGTCCC
GGCATCCATGGCAGCCCCGCGGTTAGGTGCGCCAGGGTTTGCTGATGTTGTCTTGTGCTGTTCCACTCTTGGCTCC
AGCAGACCCACTGTCCCAGAAAAGCCTGATCCTGTAGTTTATGTAGAATGCCACATCTGCGTCCTCAAGACCTGT
TTCATCCATTTGGGAAAAGATGTTGGGAAAGGCCACTTTGCTCGCAGGGGTGAGGGGAAGGATAGAGAATCTATT
TTTAATAAATAACATTCTAGAAAGATC

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FIGURE 218

MHRKKVDNRIRILIENGVAERQSRSLFVVVGDRGKDQVVILHHMLSKATVKARPSVLWCYKKELGFSSHRKKRMRO
LQKKIKNGTLNIKQDDPFELFIAATNIRYCYYNETHKILGNTFGMCVLQDFEALTPNLLARTVETVEGGGLVVIL
LRTMNSLKQLYTVMVHSRYRTEAHQDVVGRFNERFILSLASCKKCLVIDDQLNILPISSHVATMEALPPQTPD
ESLGPSDLELRELKESLQDTQPVGVLVDCCKTLDQAKAVLKFIEGISEKTLRSTVALTAARGRGKSAALGLAIAG
AVAFGYSNIFVTSPCPDNLHTLFEFVFKGFDALQYQEHLDYEIIQSLNPEFNKAVIRVNVFREHRQTIQYIHPAD
AVKLGQAELVVIDEAAAIPLELVKSLLGPLYLVFMASINGYEGTGRSLSLKLIQQLRQSSAQSQVSTTAENKTTT
TARLASARTLHEVSLQESIRYAPGDAVEKWLNDLLCLDCLNITRIVSGCPLPEACELYVNRDTLFCYHKASEVF
LQRLMALYVASHYKNSPNDLQMLSDAPAHHLFCLLPVPPTQNALPEVLAVIQVCLEGEISRQSIILNSLSRGKKA
SGDLIPWTVSEQFQDPDFGGLSGGRVVRIAVHPDYQGMGYGSRALQLLQMYEGRFPCLEEKVLETPQEIHVSS
EAVSLLEEVITPRKDLPPLLKLNERPAERLDYLGVSYGLTPRLLKFWKRAGFVPVYLRQTPNDLTGEHSCIMLK
TLTDEDEADQGGWLAAFWKDFRRRFLALLSYQFSTFSPSLALNIIQNRNMGKPAQPALSREELEALFLPYDLKRL
EMYSRNMVDYHLIMDMIPASRIYFLNQLGDLALSAAQSALLLGIGLQHKSVDRLEKEIELPSGQLMGLFNRIIR
KVVKLFNEVQEKAIEEQMVAAKDVMEPTMKTLSDDLDEAAKEFQEKHKKEVGKLKSMDLSEYIIRGDDEEWNEV
LNKAGPNASIIISLKSDDKKRLEAKQEPKQSKKLKNRETKNKKDMKLKRRK

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FIGURE 219A

TATAAATTGCTTTTTAACTTCGTTGAACAAAACATGAAAATAGAGAGACTGGTTGAAGTAAAGCCTTCCTTAGTT
ATTGACTATTTAAAGACAGAAAAGAAGCTATTCTGGCCAAAGATAAAGAAGGTAAATGTGCAGGTAAGTTTCAAT
CCTGAGAACAAAACAAAAGGCATTTTACTAACTGGCTCAAAGACCGAAGTACTGAAGGCAGTGGACATTGTCAAG
CAAGTCTGGGATTCACTGTGTGTTAAAGTGTCCATACTGATAAGCCAGGAGCCAAGCAGTTCTTCCAGGATAAA
GCACGGTTTTATCAAAGTGAGATCAAACGGTTGTTTGGTTGTTACATTGAACTACAGGAGAATGAAGTAATGAAG
GAGGGAGGCAGCCCCGCTGGGCAGAAGTGCTTCTCTCGGACAGTCTTGGCCCTGGCGTTGTGCTGATTGTGCAG
CAGGGTGACTTGGCAGCGCTTCCTGTGATGTGGTGGTGAATGCATCTAATGAGGACCTTAAGCATTATGGTGGC
CTGGCCGCTGCGCTCTCAAAGCAGCTGGCCCTGAGCTCCAGGCCGACTGTGACCAGATAGTGAAGAGAGAGGGC
AGACTCCTACCGGGCAATGCCACCATCTCCAAGCAGGAAAGCTGCCCTACCACCACGTGATCCATGCAGTGGGG
CCCCGCTGGAGCGGATATGAGGCCCGAGGTGTGTGTACCTATTAAGGAGAGCTGTGCAACTCAGTCTCTGTCTA
TGCGTGGAGACCATTGTTTCTGCCATCAAGGAAAACCTCCAATTCAAGAAGGATGGACACTGCTTGAAAGAAATC
TACCTTGTGGATGTATCTGAGAAGACTGTTGAGGCCTTTCAGAAAGCTGTGAAAACGTGATTTTAAAGCCACCCTG
CCAGATACAGCTGCCCCGCCAGGTTTACCACCAGCAGCAGCGGGGCTGGGAAAACATCATGGGAAAAGGAAGC
CTGGTGTCCCCGGGAGGCCTGCAGATGCTGTTGGTGAAGAGGGTGTGCAGAATGCTAAGACCGATGTTGTTGTC
AACTCCGTTCCCTTGGATCTCGTGCTTAGTAGAGGGCCTCTTCTAAGTCCCTCTTGGAAAAGCTGGACCAGAG
CTCCAGGAGGAATTGGACACAGTTGGACAAGGGGTGGCTGTGAGCATGGGCACAGTGCTCAAAACCAGCAGCTGG
AATCTGGACTGTGCTATGTGCTTCACGTGGTAGCTCCGGAGTGGAGAAATGGTAGCACATCTTCACTCAAGATA
ATGGAAGACATAATCAGAGAATGTATGGAGATCACTGAGAGCTTGTCTTAAATCAATTGCATTTCAGCAATA
GGAACAGGAAACTTGGGATTTCTTAAACATATTGCTGAATTAATCATTTCAGAGGTGTTCAAATTTAGTAGC
AAGAATCAGCTGAAAACCTTTACAAGAGGTTCACTTCTGCTGCACCCGAGTGATCATGAAAATATTCAAGCATT
TCAGATGAATTTGCCAGAAGGGCTAATGGAAATCTCGTCAGTGACAAAATTCGAAGGCTAAAGATACACAAGGT
TTTTATGGGACTGTTTCTAGCCCTGATTCAGGTGTGTATGAAATGAAGATTGGCTCCATCATCTCCAGGTGGCT
TCTGGAGATATCACGAAAGAAGAGGCAGATGTGATTGTAAATTCAACATCAAACCTCATTCAATCTCAAAGCAGGG
GTCTCCAAAGCAATTTTAGAATGTGCTGGACAAAATGTAGAAAGGGAATGTTCTCAGCAAGCTCAGCAGCGCAAA
AATGATTATATAATACCGGAGGTGGATTTTGGAGGTGCAAGAATATCATTGTAATTGGTGGAAATGATGTC
AAGAGTTCAGTTTCTCTGTTTTGCAGGAGTGTGAAAAAAAATTACTCATCCATTTGCCTCCCAGCCATTGGG
ACAGGAAATGCCAAACAACACCCAGATAAGGTTGCTGAAGCCATAATTGATGCCATTGAAGACTTTGTCCAGAAA
GGATCAGCCCAGTCTGTGAAAAAGTTAAAGTTGTTATCTTTCTGCGTCAAGTACTGGATGTGTTTTATGCCAAC
ATGAAGAAAAGAGAAGGGACTCAGCTTTCTCCCAACAGTCTGTGATGTCTAAACTTGATCATTTTTTGGGCTTT
TCAAAGCAATCTCCCCAAAAAAGAATCATTGGT TTTGGAAAAGAAAACAGAATCAGCAACTTTTCGGGTGTGT
GGTGAATATGTACAGTGTGTGGAATACGCTATCTCTGGCTACAAGACCTGATTGAAAAAGAACAGTGTCTTAC
ACCAGTGAAGATGAGTGCATCAAAGACTTTGATGAAAAGGAGTATCAGGAGTTGAATGAGCTGCAGAAGAAGTTA
AATATTAACATTTCCCTGGACCATAAGAGACCTTTGATTAAGGTTTTGGGAATTAGCAGAGATGTGATGCAGGCT
AGAGATGAAATTGAGGCGATGATCAAGAGAGTTGATTGGCCAAAGAACAGGAATCCCGGGCAGATTGTATCAGT
GAGTTTATAGAATGGCAGTATAATGACAATAACACTTCTCATTGTTTTAACAAAATGACCAATCTGAAATTAGAG
GATGCAAGGAGAGAAAAAGAAAAAACAGTTGATGTCAAATTAATCATCGGCACTACACAGTGAACCTGAACACA
TACACTGCCACAGACACAAAGGGCCACAGTTTATCTGTTTCAGCGCCTCACGAAATCCAAAGTTGACATCCCTGCA
CACTGGAGTGATATGAAGCAGCAGAAATTTCTGTGTGGTGGAGCTGCTGCTAGTGATCCTGAGTACAACACGGTG
GCAAGCAAGTTTAAATCAGACCTGCTCACACTTCAGAATAGAGAAGGTAAGCCTTCTGCTAGAATGCAGTTTCTGG
ATGGTGGAAATAAGTTCTGTGATGGTCTATATAAAATCCATTTTCACTTCTCTATCACATTTTTTTAAACC
CAGAATTAGAATTTGTATGGTAATTAGTAGTTCTAGATTCTACTCATGTGACCATAATTACTGAGGCATTAAGAT
TCTTGTGTGATGATTACAATATTTGATTGTAATATGATAGAACACTAAAGACATATATTTACTTTGTGAAGCAA
GCTAATACAAATTCAAAGATATGGCTTTAAATTTGATTTGATAGCTAGCAAATTCACAGAGGCCATGCAGAG
GCTCCTTAGATCAGGACCATGTTACTCTGCCCCATTATTCACAGATCAACAGTGTCTCCTTGATAAAGCCAGCAG
GCCTTTTCTCGTTTATCATAATTATTTTGGGCAGGTGAATGTGATGATTGCTGCCTGTAGTCCCAGCTATTGGGA
GGCTGAGGTGGAAGGATTGCATGAGCCAGGAGTTTGACGCCAGTCTGGGTAAACATAGTGAGATCCTGCTCTCAA
ATAAAAACAACCAATTATTTTGGCATCTTCTTCCATTTTTTAAACATTTTGTATTTGCTGTTTGAATTTATATTT

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FIGURE 219B

TCCTTGACTTCTCTAGCAAAATTATTATGATTTTTTTTTTCCTTGACTAATTTCTTTTCATTTTTGCAGGCACG
CTGTTTCTCTTCCAAACCCCTAATTCTAGCTTTATTCAGCCATTTATGCTTAAACGGTCTTTTGTCTCTGTACC
TCACCAGGGAATATATTTACCCTTCTTGGATTCAACTATTAGTTCAATGTCGATAGCTCCCAAATCAACATTACC
AACCTGGGTCTTTGACTCAAGCTCTAGAACATACTCCCAGTGGCCTAAAAAATCTCCACTTGAGGCTGGGCACA
GTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGTGGATCACGAGGTCAAGGGTTCAAGACCAT
CCTGGTGAAGATGGTGAAACCACGTCTCTACTAAACTACAAAAATTAGCCGGGCATGTTGGCAGGTGCCTATAA
TCCCACCTACTTGGGAGGCTGAGGCAGGATAATTGCTTGAACATGGGCGGCAGAGATTGCAGTGAGCCAAGATCA
CGCCACTGCACTCCAGCCTGGTCGACAGAGTGAGACTCCGTCTCAAAAAAAAAAATCTCCACTTGAATATCTAAC
TGCAAAATCAACTTCTCTAAATCTAATGCATCATACGTAAGTAATTCTCTTTCCCTTTCCTTCCTCATTCTGT
TTTTGGTTCTACCACTTTCTGAGTAAAGCCGGAGATCTTTGATCCACCATAAGTCTGCCAGTAAGACCTACATTT
TCTTTGCAAATTTTTCTTACTCTCTATTTGAACTGCCAACACTGTTTATTTCATGTTGTTAAGTACATCATAATTT
AAAAAGATTCAAAGTGGCCTACAAAGATATAAACTATACCTTCAGATAAAATAAATATACAAAGAAAAATGGTTA
AAGAGAAAAGAATGGCAGGGAAAATAAGATAATACAGACGAAGTCTAGTTCTCAAAAATATATAACATGAGGTT
ACCAATTTGTCCCTGAGCTTCCCTAGTAGACAAAGCAAGAAGTAAACATTCAGGTACAAGACTCATAATGTCCGTA
AATCAAAAAGCAAACCATTTGATAAGGAGGCTCACAGCTCCTCACAATACTGAGACTGACTCCTGAGAGATTTCT
CTTGTGGATCAAGTACTAGAGAATATCCTCAACGTATCCTCACAATAAATTAAATATCAACTTTTATATCACTG
TTTTTTTTTAATGTAAACTGGTTGAACAAAACCGATGCCTGATTGAATGAAAACAATTCTATGAGGCACCAAGA
CAATATGATTCAAGTATGCAGCTCTATGATGGTCTATTTCTGAGATAACAAGTAAGTCTCACTCCAAGTACCAAT
TACTACTAACTGGTAGTGGCTGATTGGCACATTGTGATGAGATGCTAAGTTTAGATTGAGCAGGAATGAATGTTT
TGCTTGACCAGCAATATCTACAGTGGGCCCTGTGGATGCCTGCTGTGTATTGGCAGACCCTGGCCAGAGAATTGA
TTTCAACACTTTTTTGCAGTGAAACCTTTTTTTTCAATAAAATCTTATGTGAAATCCCAGTGTATGAACCAGATA
AAAGCAGAGGTGTGGGTAGTACTTAAGGTGCCTCCATGGAGGTCCCTAGAATTGTG

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FIGURE 220

YKLLFNVEQNMKIERLVEVKPSLVIDYLKTEKKLFWPKIKKVNQVVSFNPENKQKGILLTGSKTEVLKAVDIVK
QVWDSVCVKS VHTDKPGAKQFFQDKARFYQSEIKRLFGCYIELQENEVMKEGGSPAGQKCF SRTVLAPGVVLIVQ
QGD LARLPVDVVVNASNEDLKHYGG LAAALSKAAGPELQADCDQIVKREGRLLPGNATISKAGKLPYHHVIHVG
PRWSGYEAPRCVYLLRRAVQLSLCLAEKYKYRSIAIPAISSGVFGFPLGRCVETIVSAIKENFQFKDGHCLKEI
YLVDVSEKTVEAFAEAVKTVFKATLPDTAAPPGLPPAAAGPGKTSWEKGS LVSPGGLQMLLVKEGVQNAKTDVVV
NSVPLDLVLSRGPLSKSLLEKAGPELQEELDTVGQGVAVSMGTVLKTSSWNLD CRYVLHVVAPEWRNGSTSSLKI
MEDI IRECMEITESLSLSKSIAPPAIGTGNLGF PKNIFAELI ISEVFKFSSKNQLKTLQEVHFLHPSDHENIQAF
SDEFARRANGNLVSDKIPKAKDTQGFYGT VSSPD SGVYEMKIGSII FQVASGDITKEEADVIVNSTSNSFNLKAG
VSKAILECAGQNVVEREC SQQAQQRKNDYIITGGGFLRCKNIIHVIGGNDVKSSVSSVLQECEKKNYSSICLPAIG
TGNAKQHPDKVAEAIIDAIEDFVQKGS AQSVKKVKVVIFLPQVLDVFYANMKKREGTQLSSQQSVMSKLASFLGF
SKQSPQKKNHLVLEKKTESATFRVCGENVTCVEYAI SWLQDLIEKEQCPYSEDEC IKDFDEKEYQELNELQKKL
NINISLDHKRPLIKVLGISRDVMQARDEIEAMIKRVRLAKEQESRADCISEFIEWQYNDNNTSHCFNKMTNLKLE
DARREKKKTVDVKINHRHYTVNLNTYTATDTKGHSLSVQRLTKSKVDIPAHWSDMKQQNF CVVELLPSPDPEYNTV
ASKFNQTC SHFRIEKVSLLECSFWMVEISSVMVLYKIH FHS LPITFF

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FIGURE 221

GCCTCGGGGGAGGACAACAAAGGGCCGCGGGCGGGCAGTGGTGTCCAGTCTCCCGGTGCTTCCCTGAGGCT
GAGGCGCCCGGCTCCCGCCCGCGCTCCAGATGAAGTGTGAGCACTGCACGCGCAAGGAATGTAGTAAGAAA
ACAAAAACTGATGACCAAGAGAAATGTGTGAGCCGATGCACCGAGTCCAGCCCAGGAAAAATGGAGAGAAGGGAGAA
TTCCACAAGTTGGCTGATGCCAAGATATTTTTGAGCGACTGCCTGGCATGTGACAGCTGTATGACTGCAGAGGAA
GGAGTCCAACCTTTCCAGCAAAATGCCAAGGACTTCTTCCGCGTTCTGAACCTTAACAAGAAATGTGATACCTCA
AAGCACAAGTGCTGGTAGTGTCTGTGTGTCCTCAATCTTTGCCTTATTTTGCTGCTAAATTCAACCTCAGTGTA
ACTGATGCATCCAGAAGACTCTGTGGTTTCTCAAAAGTCTTGGGGTGCAGTATGTATTTGATACGACGATAGCT
GCGGATTTTAGTATCCTGGAGAGTCAAAAAGAATTCTGTGCGTGCCTATCGCCAGCACAGTGAGGAGGAACGCACC
CTGCCCATGCTGACCTCTGCCTGTCTGGCTGGGTCCGATACGCCGAGCGGGTGCTGGGTGCGCCCCATCACTGCC
CACCTCTGCACCGCCAAGTCCCCCAGCAGGTCATGGGCTCTTTGGTGAAGGATTATTTGCGCCAGACAGCAGAAC
CTGTCTCCAGAGAAGATTTTCCACGTCATTGTGGCCCTTGTTATGACAAGAAGCTGGAGGCTCTTCAGGAAAGC
CTTCCCCCTGCTTTGCATGGCTCCCGGGCGCTGACTGCGTGTTAACATCAGAAATTAGCCAGGCGTGGTGGTG
ACACCTGTGATCACAGCTACTCGGGAGGCTGCGGCAAGAGAATCACTTGAACCCGGGAGGCAGAGGTTACAGCGA
GACAAGATTGCACCACTGGACTCCAGCCTGGGCGGCGGAGGTGAAATTGCTCAAATAATGGAGCAAGGTGACCTC
TCAGTGAGAGATGCTGCCGTCGACACTCTGTTTGGAGACTTGAAGGAGGACAAAGTGACGCGTCATGATGGAGCC
AGCTCAGACGGGCACCTGGCACACATCTTCAGACATGCGGCCAAGGAGCTGTTCAACGAGGATGTGGAGGAGGTC
ACTTACCGAGCCCTGAGAAACAAAGACTTCCAAGAGGTCACCTTGAGAAGAACGGAGAGGTGGTGTTACGCTTT
GCTGCAGCCTATGGCTTTTCAAACATCCAGAACATGATCCTGAAGCTTAAGAAGGGCAAGTCCCATTCCACTTT
GTGGAGGTCTCGCCTGTGCTGGAGGATGCTTAAATGGCAGAGGCCAAGCCCAGACTCCAGACGGACATGCGGAT
AAGGCCCTGCTGCGGCAGATGGAAGGCATTTACGCTGACATCCCTGTGCGGCGTCCGGAGTCCAGTGACACGTC
CAGGAGCTGTACCAGGAGTGGCTGGAGGGGATCAACTCCCCAAGGCCCGAGAGGTGCTGCATACCACGTACCAG
AGCCAGGAGCGTGGCACACACAGCCTGGACATCAAGTGGTGAAGTCAGGCCAGGGCCTTCCAGCTGCTCTTGGGG
CCAGAGCCAAGAGCCTCTCAGTAGAGGGAGGGGCTGCCCTGAGTGGAGTATTAAAGACACTTAAGAAAACCGCTC
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 222

MKCEHCTRKECSKKTCTDDQENVVSADAPSPAQENGEKGEFHKLADAKIFLSDCLACDSCMTAEEGVQLSQONAKD
FFRVLNLNKKCDTSKHKVLVSVCPQSLPYFAAKFNLSVTDASRRLCGFLKSLGVHYVFDTTIAADFSILESQKE
FVRRYRQHSEEERTLPMLTSACPGWVRYAERVLGRPITAHLC TAKSPQQVMGSLVKDYFARQQNLSPEKIFHVIV
APCYDKKLEALQESLPPALHGSRGADCVL TSEISQAWWCTPVITATREAAAARESLPGRQRLQRDKIAPLDSSLG
GGGEIAQIMEQGDLSVRDAAVDTLFGDLKEDKVTRHDGASSDGH LAHIFRHA AKELFNEDVEEV TYRALRNKDFQ
EVTLEKNGEVVLRFAAAYGFRNIQNMILKLKKGKFPFH FVEVLACAGGCLNGRGQAQTPDGHADKALLRQMEGIY
ADIPVRRPESSAHVQELYQEWLEGINSPKAREVLHTTYQSQERGTHSLDIKW

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FIGURE 223

TTTCACCTCAGCAAGGCCAGGGGATCTGCACGTTGTGTTAGACATGGCTAAAGTAGCTGATACCATCCTGTTCCCT
CCTTGATCCACTAGAAGGCTGGGACAGCACCGGTGATTACTGTCTTTCCTGCCTCTTTGCTCAGGGCCTTCCGAC
CTATACACTAGCTGTCCAGGGGATTTCTGGCCTCCCACTGAAGAAACAAATAGATAACCAGGAAGAAGCTAAGTAA
AGCAGTGGAGAAGCGCTTTCCGCATGACAACTCCTCTTGTGTTAGACACTCAACAGGAGGCAGGGATGCTGCTTAG
GCAGTTGGCTAACCAGAAGCAACAGCATCTTGCTTTTCGAGATCGGCGGGCCTACCTATTTGCCCATGCTGTTGA
TTTTGTTCCCTAGTGAAGAGAATAAATTGGTGGGCACCTTGAAAAATTCAGGCTATGTTTCGAGGGCAGACTCTGAA
TGTCATAGGTTGCTGCATATCGTTGGATATGGTGATTTCCAGATGAAACAGATAGATGCCCCGGAGACCCTTT
CCCTTTAAATCCTAGAGGAATTAAACCCCAAAGGACCCAGACATGGCAATGGAGATTTGTGCTACGGATGCTGT
AGATGATATGGAAGAAGGTCTTAAAGTCCTAATGAAGGCAGACCCTTGATAGACAGGAATCCTTGCAAGCAGAGGT
TATCCAGATCCAATGGAGGGAGAGCAAACCTGGCCCACTGAGGAGGAGCTGAGCGAGGCAAAGGATTTCTTGAA
GGAAAGTTCTAAGGTGGTAAAGAAGGTCCCCAAAGGAACATCCAGTTACCAAGCTGAATGGATTTTGGATGGTGG
CAGCCAAAGTGGTGGGGAAGGAGATGAATATGAATATGATGATATGGAACATGAGGATTTTATGGAGGAGGAATC
TCAGGATGAGAGTAGTGAAGAAGAGGAAGAATATGAACTATGACTATTGGGGAGTCTGTGCATGATGATCTGTA
TGATAAGAAAAGTAGATGAAGAAGCTGAGGCAAAAATGTTGGAGAAAATATAAACAAGAAAGACTGGAAGAGATGTT
TCCAGATGAAGTGGACACGCCCCGTGATGTGGCTGCTCGAATTCGATTTCAGAAATACAGAGGCCCTTAAGAGCTT
CCGGACATCTCCATGGGATCCTAAGGAAAACCTTCCTCAAGATTATGCTCGAATATTTTCAGTTTCAGAACTTTAC
TAACACTAGGAAAAGCATCTTTAAAGAGGTTGAAGAAAAAGAGGTTGAAGGAGCTGAGGTTGGCTGGTATGTCAC
ACTTCATGTCCTCTGAAGTCCCCGTCTCAGTGGTCGAGTGCTTCAGGCAAGGAACACCCTTGATTGCATTTTCTTT
ACTACCTCATGAACAGAAGATGTCAGTATTGAATATGGTGGTGAGGCGTGACCCTGGCAACACTGAACCTGTGAA
AGCCAAGGAGGAGCTCATATTTCACTGTGGATTGAGGCGCTCCGAGCCTCACCTTTATTCTCTCAGCACACTGC
AGCGGACAAACATAAATTGCAGAGATTCTGACTGCTGACATGGCCCTGGTGGCGACAGTCTATGCGCCAATCAC
TTTTCTCCTGCATCTGTGCTGCTTTTCAAGCAGAAAAGCAATGGAATGCACAGCCTCATTGCTACAGGCCATCT
TATGTCAGTAGATCCAGACAGAATGGTCATCAAGAGAGTTGTTCTGAGTGGTCATCCTTTCAAAATTTTACTAA
GATGGCAGTAGTACGTTACATGTTCTTCAACAGAGAGGATGTGCTGTGGTTTAAACCAGTGGAAGTGAAGACGAA
GTGGGGCCGGAGAGGACATATCAAGGAACCTTTAGGTACCCATGGCCACATGAAATGCAGCTTTGATGGGAAGCT
AAAAATCTCAAGACACAGTACTGATGAACCTGTATAAACGAGTCTTCCCCAAATGGACTTATGATCCATATGTACC
AGAACCAGTACCCTGGCTGAAAAGTGAGATTTCTTCAACAGTGCCTCAAGGGGGCATGGAGTAATGGATTCAAAG
AGATTCTGTCTACCGGTGCCAGTCAGTACTCCAGGGATGGGAGGCACAAGTTGTGATTGGGCAAAGTTTATTTT
CTATGTCAGCCTGTCTAGTCCACTGCCCCATTTTGAAGACTTTTTTTTAGCCTTGACAAAATGTCTCAGTTAAGT
ATAAAAGTTTTTCCACTACTTAGTCCAAAAAAACATTAAATCTTAATGAAAT

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FIGURE 224

MAKVADTILFLDDPLEGWDSTGDYCLSCLEFAQGLPTYTLAVQGISGLPLKKQIDTRKKLSKAVEKRFPDHLKLLLL
DTQQEAGMLLRQLANQKQHLAFRRRAYLFAHAVDFVPSENNLVGTLKISGYVRGQTLNVNRLHLHIVGYGDFQ
MKQIDAPGDPFPLNFRGIKPQKDPDMAMEICATDAVDDMEGLKVLKADPCRQESLQAEVIPDPMEGEQTWPTE
EELSEAKDFLKESKVVKKVPKGTSSYQAEWILDGGSQSGGEGDEYEYDDMEHEDFMEEESQDESSEEEEEYEYTM
TIGESVHDDLKVDKKEAEAKMLEKYKQERLEEMFPDEVDTPRDVAARIRFQKYRGLKSFRTPSPWDPKENLPQD
YARIFQFQNFNTNRKSIKKEVEEKEVEGAEVGWYVTLHVSEVPVSVVECFRQGTPLIAFSLLPHEQKMSVLNMVV
RRDPGNTEPVKAKEELIFHCGFRFRASPLFSQHTAADKHLQRFALTADMALVATVYAPITFPPASVLLFKQKSN
GMHSLIATGHLMSVDPDRMVIKRVLSGHPFKIFTKMAVVRYMFFNRDVLWFKPVELRTKWGRGRGHIKEPLGTH
GHMKCSFDGKLKSQD TVLMNLYKRVFPKWTYDPYVPEPVPWLKSEISSTVPQGGME

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FIGURE 225A

CCGGTTCCCGCGGTTCGACGCTCCAGCCGCTCCTCCGCGCAGCCGCGCCTCAGCTGCTCGCTCTGTGGGTCCGT
CCTCTCCGGCACTTGGGCTCCAGTTCGCGCCCTCCAAGCCCTTCAGGCCGCCCCAGTGTCTCTCTCTCTCCGGC
CAGACCCAGCCCCGCGAAGATCGTGGACCGCGAGCAACTGGTGCAGAAAGCCCGGCTGGCCGAGCAGGCGGAGCG
CTACGACGACATGGCCGCGCCATGAAGAACGTGACAGAGCTGAATGAGCCACTGTGCAATGAGGAACGAAACCT
TCTGTCTGTGGCTTACAAGAACGTTGTGGGGGCACGCCGCTCTTCTGAGGGTCATCAGTAGCATTGAGCAGAA
GACATCTGCAGACGGCAATGAGAAGAAGATTGAGATGGTCCGTGCGTACCGGGAGAAGATAGAGAAGGAGTTGGA
GGCTGTGTGCCAGGATGTGCTGAGCCTGCTGGATAACTACCTGATCAAGAATTGCAGCGAGACCCAGTACGAGAG
CAAAGTGTCTTACCTGAAGATGAAAGGGGACTACTACCGCTACCTGGCTGAAGTGGCCACCGGAGAGAAAAGGGC
GACGGTGGTGGAGTCTCCGAGAAGGCCTACAGCGAAGCCCACGAGATCAGCAAAGAGCACATGCAGCCCACCCA
CCCCATCCGATTAGGCTTGCTCTTAATACTACTCCGTCTTCTACTATGAGATCCAGAACGCCCCAGAGCAAGCGTG
CCACTTGGCCAAGACCGCGTTCGACGACGCCATCGCCGAGCTTGACACCCCTCAACGAGGACTCCTACAAGGACTC
CACGCTCATATGCAGTCTCTCCGCGACAACCTCACGCTCTGGACGAGCGACCAGCAGGACGACGATGGCGGCGA
AGGCAACAATTAAGGCCCCAGGGAACTGGCAGCGCACGCGGATGCTACTACTGCAGTCTTTATTTTTTCCCAT
GAGTTGGGGGTTCGGGTGGGGGAGGGAAAGGGAGGGATGACCTTCCAGGGAGAAACCCACGACCTGTCTGTCTT
TGATCGCCTCTTTGACATTTTGCAGAAATACCAC TAGTGGAAGTCAGGCTAGCTGTGCTGGTATTGGAATAGC
AGCCTCACACTGGCGTCTGGACTGTTCTGTAGATT CATGCAAGTGGAGCTGTCTGTCTCTAATTTAACTTATTGC
TAGATAATAGGGTTTTAGATGAAAAGAAAACCTTAAAGAGGAATGGCCCTCATTAGTAAGTTCTGTGGTTCCAG
TAAGGATTTTTATGTACATACGCTCTCGTCTCTCGTTTTGGGTACTTTCTATCTCATCTGTCTCGGCTCTGCATG
TTTTCCAGGGTGTAGCCTACAGACATGGAACAGTGTAATCCCAGACTGACAGACTTAGAACCTGAGGTCTCATT
CATCCTTATGGTTTAGGCTTGCCAGTTTTCCGAAGTCTCTGATTAGTTGACAGTATTAACACTAAATTGCAGTT
TACAGTATTTCTACATTACAGCCATATGTAACATCAAGCCATCGATTGTGTACTTTTCCTTTGCTAGTTGTTTGG
GCTTTAACATCCTTATTACGCTTATCCAGGTTGGTTTTGCTGTTGATCGGTCTCCTAGGCTAAATGAGAATGAA
AGCGACTTCAGGTTTTTGGTTCATAGGTGCTCGGCAGGTGGCTGTGGGATTTTTTTTTTGGTCTTCTTTCTCTC
TTAACGTAAATCCACCACCAAAATTATTAATCCTCTTGAGAGAAACGTGAAACGCCACAAAAATAGAGAAATTC
AGGTCTGTATGTCATGGATCGTGTGGTATTTTCAGAGAACATCCCGCTTCTGAAGCTGCTGCAGCTCCCTCCTC
AGGGATCACACTGCCGTACCCACTCTGCACTGGGGCGTTTTCTACTGCGCCTCGTCTGGCGGACGCAGCTGGG
TGCAGAAGCTGTGGGTTCGGAGAGGCGTTTGGAGAAGGTCTGTGGTGCAGTGTGTGAAAATTCAGGTGCTAGAAG
CCTACTGGTAGAAAACCCAAAAGGAAGAGCTATATCCTTAACCATCTGTCCAATTCGGGAGCCTTGTGAGTG
TGTGAGTTTTTCTCTCCCGAAGACACTCCTTCCCCAAGTAATTGTAGGAAGATAAAAAAACTGTTACCAGATAAC
AAACACTTAACCTCTATTTGACCAGAACTTTTTCTCTCGAGATAGTTTTTTCTTTTAAATGAAAAAGCATAGG
AATTGGAGATTGGCTTGTCTCACGCAGCCAGTGCAATTTGGAATTGACGGAACAACGTTGCTATTTCCACCCA
TTTGTTTTTCGGCAGCCTTAAGGCCCTCATTCTCATTTCCGGTGAATCTGTCTATCTGTGAACGTGGCCCGCATGT
GCATTCTTTTTTTTTATATATATAAAAGTCAGTGACGAGGCACTCCCGAGACGTGTAATGACACCACACTTGTTTTC
TTTGTCTCTTTGTTTTATTAGGCAAGAAGAGGTGTGAGTAATTGAGGAAAACTGACAGATGCTTTTGCTAATA
CCAAAATTGAGCTTACAATTAGGAAGTGAATGTGTAACAGGATACAGGTGACAGTGAAGATAGAAGAACCACG
ATGACCACAGACTCAATGTGCTCTGTAACATCGCACAGTTTACCCAGCATGACTTTCCTTAGGAGGCCCTCCT
CACGCTAGAGTAAAAGTCCAGTTAAGTGAAGCCTACCAGAAGAACTAGTAGAAGAAGCTTTGCCGCTTTTGTGC
CTCTCACAGGCGCTAAAGTCATTGCCATGGGAGGAAGACGATTTGGGGGGGAGGGGGGGGAGGGTAGGTGG
GGCTTTCCCTAATTTATCTTCATGTCCAGTGAGCAGTGTTGCGTTTTTCTTGTAGCATTGGAATGATTTACT
GGAATTACAAAACCTATTTTTCTTTAAATTTAGCTTTGGCTCTGGCTGCTTTTTAGAAATGCAAGATAAAA
ATCACACCTGAGGGCTGAAAACGGAGAGGGAATGGGAGACTTGATATTTAAGCAGCTTGAATGGTTTTCTTTTC
TTTATTTTTTAAAGAAATGCACTTGCCATGATACTGTCTCTCCAGTGAATGATTACTCTCCTCATTACTCTATTG
ATACAATATTGTGCAIGCTAGTGTTGTATTTCTATACAGTAGCTTGAAATTGATTAACCTTATACTGTAGGTGTTA
TGTATTCTATGACAAAAAAATTAAGTCTTCAAAATTTTTTAAAGGTTTTTTTTTTTAAATTTAATTTTTCTTTT
TGGGGGTAAAGTTTGTCTTACCAATAGTGATTGTAAACAAATTGATCTGTTTTGGATGTTGCTATAGTGACATGC
AGTTATATATTTTTGTTTTTAAAGGGGGGAGCAAAAGAAACACCAGTGTTAGCTTAATCTTAATGTCTGGTGTT
TGTGATGGTGAATTTATACTATTACAGTGTTGGAGAACAACAATATGTTCTCTGAATGAGCCTTTGTGCTTTT
TGTGATGTTATGCAGTGAATTTTTTAAGGTCTAATCAGTGATTATTTTTCCAGCTCCGTGTTCTCTAAGGAA

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FIGURE 225B

TTATTTACACACGGACCATCTTTAGCAGTTTCCTCAGTGATGGAATATCATGAATGTGAGTCATTATGTAGCTG
TCGTACATTGAGCAAATAAACTTACAGATCTGACGCC

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FIGURE 226

MVDREQLVQKARLAEQAERYDDMAAAMKNVTELNEPLSNEERNLLSVAYKNVVGARRSSWRVISSIEQKTSADGN
EKKIEMVRAYREKIEKELEAVCQDVLSLLDNYLIKNCSETQYESKV FYLKMKG DYRYLA EVATGEKRATV VESS
EKAYSEAHEISKEHMQP THPIRLGLALNYSVFYIEIQNAPEQACHLAKTAFDDAIAELDTLNEDSYKDSTLIMQL
LRDNLTLWTS DQQDDDGEGNN

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FIGURE 227A

ATCCAGTTCACGCAGTCGTCATTCCAGTATCTCACCTGTGTCAGGCTTCCACTTAATTCCAGTCTGGGAGCTGAACT
CAGTAGGAAAAAGAAGGAAAGAGCAGCTGCTGCTGCTGCAGCAAAGATGGATGGAAAGGAGTCCAGCTACGAAAG
AAGTGGCTCTTACAGCGGGCGATCGCCAGTCCCTATGGTCGAAGGCGGTCCAGCAGCCCTTTCTGAGCAAGCG
GTCTCTGAGTCGGAGTCCACTCCCCAGTAGGAAATCCATGAAGTCCAGAAGTAGAAGTCTGCATATTCAAGACA
TTCATCTTCTCATAGTAAAAAGAAGAGATCCAGTTCACGCAGTCGTCATTCCAGTATCTCACCTGTGTCAGGCTTCC
ACTTAATTCCAGTCTGGGAGCTGAACTCAGTAGGAAAAAGAAGGAAAGAGCAGCTGCTGCTGCTGCAGCAAAGAT
GGATGGAAAGGAGTCCAAGGGTTCACCTGTATTTTTGCTTAGAAAAAGAGAACAGTTCAGTAGAGGCTAAGGATT
AGGTTTGGAGTCTAAAAAGTTACCCAGAAGTGTAATAATTGGAAAAATCTGCCCCAGATACTGAACTGGTGAATGT
AACACATCTAAACACAGAGGTAAAAATCTTCAGATACAGGGAAGTAAAGTTGGATGAGAAGTCCGAGAAGCA
TCTTGTTAAAGATTTGAAAGCACAGGGAACAAGAGACTCTAAACCCATAGCACTGAAAGAGGAGATTGTTACTCC
AAAGGAGACAGAAACATCAGAAAAGGAGACCCCTCCACCTCTTCCACAATTGCTTCTCCCCACCCCTCTACC
AACTACTACCCCTCCACCTCAGACACCCCTTTGCCACCTTTGCCCTCCAATACCAGCTCTTCCACAGCAACCACC
TCTGCCTCCTTCTCAGCCAGCATTAGTCAGGTTCCTGCTTCCAGTACTTCAACTTTGCCCCCTTCTACTCACTC
AAAGACATCTGCTGTGCTCTCAGGCAAATTTCTCAGCCCCCTGTACAGGTTCCTGTGAAGACTCAAGTATCTGT
AACAGCTGCTATTCCACACCTGAAACTTCAACGTGCTCCTTTGCCCTCCCACCTTATTACCTGGAGATGA
TGACATGGATAGTCCAAAAGAACTCTTCTTCAAAACCTGTGAAGAAAGAGAAGGAACAGAGGACACGTCACTT
ACTCAGACCTTCTCTCCCTCCAGAGCTCCCTGGTGGAGATCTGTCTCCCCCAGACTCTCCAGAACCAGGCG
AATCAGACACCTCAGCAACCATATAAAAAGAGACAAAAATTTGTTGCTCCTCGTTATGGAGAAAGAAGACAAAC
AGAAAGCGACTGGGGGAAACGCTGTGTGGACAAGTTGACATTATTGGGATTATTGGAGAAGGAACCTATGGCCA
AGTATATAAAGCCAAGGACAAAGACACAGGAGAAC TAGTGGCTCTGAAGAAGGTGAGACTAGACAATGAGAAAGA
GGGCTTCCCAATCAGAGCATTCTGTGAAATCAAAATCCTTCGTGAGTTAATCCACCGAAGTGTGTTAATCATGAA
GGAAATTGTACAGATAAACAAGATGCACTGGATTCAAGAAGGACAAAGGTGCCTTTTACCTTGTATTGAGTA
TATGGACCATGACTTAATGGGACTGCTAGAATCTGGTTTGGTGCACTTTTCTGAGGACCATATCAAGTCGTTTCA
GAAACAGCTAATGGAAGGATTGGAATACTGTACAAAAAGAATTTCTGCATCGGGATATTAAGTGTCTTAACAT
TTTGCTGAATAACAGTGGGCAAATCAAACTAGCAGATTTTGGACTTGCTCGGCTCTATAACTCTGAAGAGAGTCG
CCCTTACACAAACAAAGTCATTACTTTGTGGTACCGACCTCCAGAACTACTGCTAGGAGAGGAACGTTACACACC
AGCCATAGATGTTTGGAGCTGTGGATGTATTCTTGGGGAACATTACAAAGAAGCCTATTTTCAAGCCAATCT
GGAAGTGGCTCAGCTAGAACTGATCAGCCGACTTTGTGGTAGCCCTGTCCAGCTGTGTGGCCTGATGTTATCAA
ACTGCCCTACTTCAACACCATGAAACCGAAGAAGCAATATCGAAGGCGTCTACGAGAAGAATCTCTTTTATTCC
TTCTGCAGCACTTGATTTATTGGACCACATGCTGACACTAGATCCTAGTAAGCGGTGCACAGCTGAACAGACCCT
ACAGAGCGACTTCCTTAAAGATGTGAACTCAGCAAAATGGCTCCTCCAGACCTCCCCACTGGCAGGATTGCCA
TGAGTTGTGGAGTAAGAAACGGCGACGTGAGCGACAAAGTGGTGTGTAGTGAAGAGCCACCTCCATCCAAAAC
TTCTCGAAAAGAACTACCTCAGGGACAAGTACTGAGCCTGTGAAGAACAGCAGCCAGCACCACCTCAGCCTGC
TCCTGGCAAGGTGGAGTCTGGGGCTGGGGATGCAATAGGCCTTGCTGACATCACACAACAGCTGAATCAAAGTGA
ATTGGCAGTGTTATTAAACCTGCTGCAGAGCCAAACCGACCTGAGCATCCCTCAAATGGCACAGCTGCTTAACAT
CCACTCCAACCCAGAGATGCAGCAGCAGCTGGAAGCCCTGAACCAATCCATCAGTGCCCTGACGGAAGCTACTTC
CCAGCAGCAGGACTCAGAGACCATGGCCCCAGAGGAGTCTTTGAAGGAAGCACCCCTCTGCCCCAGTGATCCTGCC
TTCAGCAGAACAGACGACCCTTGAAGCTTCAAGCACACCAGCTGACATGCAGAATATATTGGCAGTTCTCTTGAG
TCAGCTGATGAAAACCCAAGAGCCAGCAGGCAGTCTGGAGGAAAAACAACAGTGACAAGAACAGTGGGCCACAGGG
GCCCCGAAGAACTCCCAATGCCACAGGAGGAGGCAGCAGGTAGGAGCAACGGTGGGAATGCCCTCTGAGGAAT
GCAGTGATGTCCATCAGTCACCTCTCAGCCAGAGCCTGGCAAATTCAGTCTCTTTACAGAACCTAAAGCCAAGC
CAGGTTTCACTGGGAAATCCACCTGTCCAAACACTGTGTGAGACACCAGAATTAGAGGCCTGCAAGCCTGCTTCC
TTCATCCCCAATGCCAGATGGGACAGGTACACAGCCTCCTGTGTCTACCCCCACCTTTCTTGCTTGCTGGCCTC
CTCTCTCTCAGTGCCTCTCTCATCCCTGCAATCCAGACAGCACATGCAGCAGCTCAACCAATTCCATTCTTGGC
TACCTCATCCCTCCAGTCTGAAAGGACGTGTGAATGCCACCAGGATCTGAACCCAAGATTCCAGCCTCGGTCA
CACCCTGACCTGAGAATGCCACTGGGATGGGGAGAAGTTGTGAGTCTTCATCCTTCCCCACAAGTATACTGAAG
CCAGGACAGCACCTGCCTTAGAGAGCTCTTAGAGGGATTATCCGAGCCTGAAGAAAGAAGGTTACAAGTGAAG
AGAACTTCTGAACAGGGAAGAGTGAAGAAAAGACTGCAGCTCAGCTCCAGAAGCAGACCCAGAATGGCATCCTT

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FIGURE 227B

CTCTGAGACCCAGACCCCAGCCCCTTTTCATGGAAGACCAGCACAAAGGAGGAAGTAGGTTAGGGAATGGTAAGG
CTCCATGTGATGGGACTAATGTGGAGAGGCCTGGGGCCTTTCCCTGAGGACTGGATGGCTGGAGTTTGGGAGCCT
GAGTTGACAGAGGAGGCTAAGCCCGGGCAGCTACTTTGTTCCAGAAATCTAAGGTCCCTGGAGGGAGGCTCTGCT
TTGGGAGGGGGAAGGGAGCTAACATTGCAGAGCACCAACTGTGAACCAGGTACAATGGCAGAGCCTTTCCATACC
TGTA CTCACA ACTAGCGGGTGAGGAGTCAAGGCAAATAGGTGTCTCATAGCTCCCCATATCTCGGCAGTCGACCA
CCTCCTCTTTTGATTCTCTGATGTCACTGCCAGTTCTCCTCCTATTGCTCTGACCTGTCTTTCTCTGTGTCCTTT
GCAA ACTCATTCTCAACTCCTTAGACTCAGTCAAGTCCCCCAGTTACACACTTCCATGGTACTATATATCATTCC
TTCAGAGCACTTAACACAGTTATTTCTATGTATTTGTCCAGTCATTTGAATAATGATCCTAGTTTCATTGGATG
GAAAGTTCCACAAGGTCAGTGACCATTTCTATCTGTGTTACCAATGTGTTCCAGTGCCCAGAAACAATGCCTA
GCATAAAGCAGCTGTTTTGTAAATACTTGTTCAATGAATGAATAAATGACAAAAGAACATC

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FIGURE 228

SSSRSRHSSISPVRPLNSSLGAELSRKKKERAAAAAAKMDGKESYERSGSGRSPSPYGRRRSSPFLSKR
SLSRSPLP SRKSMKSRSPAYSRHSSSHSKKKRS SSSSRHSSISPVRPLNSSLGAELSRKKKERAAAAAAKMDGKESKGS
PVFLPRKENSSVEAKDSGLESKKLPRSVKLEKSAPDTELNVNTHLNTTEVKNSSDTGKVKLDENSEKH
LVKDLKAQGTRDSKPIALKEEIVTPKETETSEKETPPPLPTIASPPPLPTTTTPPPQTPPLPPLPPIPALPQQPP
LPSPQAFSQVPASSTSTLPPSTHSTSAVSSQANSQPPVQVSVKTQVSVTAAIPHLKTSTLPPPLPPLPPLPGDD
DMDSPKETLPSKPVKKEKEQTRHLLTDLPPLPELPGGDLSPDSPEPKAITPPQQPYKKRPKICCPRYGERRQT
ESDWGKRCVDKFDIIGIIGEGTYGQVYKAKDKDTGELVALKKVRLDNEKEGFPITAIKILRQLIHRSVVNMK
EIVTDKQDALDFKKDKGAFYLVFEYMDHDLMLLESGLVHFSEDHIKSFMKQLMEGLECHKKNFLHRDIKCSNI
LLNNSGQIKLADFGIARLYNSEESRPYTNKVITLWYRPELLLGEERYTPAIDVWSCGCILGELFTKKPIFQANL
ELAQLELISRLCGSPCPAVWPDVIKLPYFNTMKPKKQYRRRLREEFSFIPSAALDLDHMLTLDPSKRCTAEQTL
QSDFLKDVELSKMAPPDLPHWQDCHELWSKKRRRQQRQSGVVVEEPPPSKTSRKETTSGTSTEPVKNSSPAPPQPA
PGKVESGAGDAIGLADITQQLNQSELAVLLNLLQSQTDL SIPQMAQLLNHSNPEMQQLEALNQSISALTEATS
QQQDSETMAPEESLKEAPSAPVILPSAEQTLEASSTPADMQNILAVLLSQLMKTQEPAGSLEENNSDKNSGPQG
PRRTPTMPQEEAAGRSNGGNAL

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FIGURE 229

AATCGCGAAACCCGGCGAGCGGCGCGCTGGCTATCGAGCGAGCGGGGCGGAACCGGGAGTTGCGCCGCCGCTCGG
GCGCCGGGCTCCGTCGCGGGCCGAGCCCCGCGGGTCCGCTCCCGTGCCCTGCCCCGCGGACACCCTGGCCGTGGA
CACCCTGGCCGTGGGCACCCGCGGGGCGCGGCGGGCGCTGCGCGGGCGGCGGGCGGCATGAAGGTCACGTCG
CTCGACGGGCGCCAGCTGCGCAAGATGCTCCGCAAGGAGGCGGCGGCGCGCTGCGTGGTGCTCGACTGCCGGCCC
TATCTGGCCTTCGCTGCCTCGAACGTGCGCGGCTCGCTCAACGTCAACCTCAACTCGGTGGTGCTGCGGCGGGCC
CGGGGCGGCGCGGTGTGCGGCGGCTACGTGCTGCCCGACGAGGCGGCGCGCGCGCGGCTCCTGCAGGAGGGCGGC
GGCGGCGTGC GGCGCGGTGGTGGTGCTGGACCAGGGCAGCCGCCACTGGCAGAAGCTGCGAGAGGAGAGCGCCGCG
CGTGTCGTCCTCACCTCGCTACTCGCTTGCCCTACCCGCGGCGCGCGGGTCTACTTCCTCAAAGGGGGATATGAG
ACTTTCTACTCGGAATATCTGAGTGTTGCGTGGA TGTAACCCATTTCACAAGAGAAGATTGAGAGTGAGAGA
GCCCTCATCAGCCAGTGTGGAACCCAGTGGTAAATGTCAGCTACAGGCCAGCTTATGACCAGGGTGGCCAGTT
GAAATCCTTCCCTTCTCTACCTTGGAAGTGCTACCATGCATCCAAGTGCAGTTCCTCGCCAACCTTGCACATC
ACAGCCCTGCTGAATGTCTCCGACGGACCTCCGAGGCTGCATGACCCACCTACACTACAAATGGATCCCTGTG
GAAGACAGCCACACGGCTGACATTAGCTCCCACTTCAAGAAGCAATAGACTTCATTGACTGTGTGAGGAAAAAG
GGAGGCAAGGTCTGGTCCACTGTGAGGCTGGGATCTCCCGTTACCCACCCTGTCATGGCTTACCTTATGAAG
ACCAAGCAGTTCGCGCTGAAGGAGGCTTCGATTACATCAAGCAGAGGAGGAGCATGGTCTCGCCCAACTTTGGC
TTCATGGGCCAGCTCCTGCAGTACGAATCTGAGATCCTGCCCTCCACGCCCAACCCCGAGCTCCCTCCTGCCAA
GGGGAGGACAGCAGGCTCTTCACTGATAGGCCATTTGCAGACACTGAGCCCTGACATGCAGGGTGCCTACTGCACA
TTCCCTGCCTCGGTGCTGGCACCGGTGCCTACCCACTCAACAGTCTCAGAGCTCAGCAGAAGCCCTGTGGCAACG
GCCACATCCTGCTAAAACCTGGGATGGAGGAATCGGCCCAGCCCCAAGAGCAACTGTGATTTTTGTTTTTAAGACT
CATGGACATTTTATACCTGTGCAATACTGAAGACCTCATTCTGTGTCATGCTGCCCCAGTGAGATAGTGAGTGGTCA
CCAGGCTTGCAAATGAACCTCAGACGGACCTCAGGGTAGGTTCTCGGGACTGAAGGAAGGCCAAGCCATTACGGG
AGCACAGCATGTGCTGACTACTGTACTTCCAGACCCCTGCCCTCTTGGGACTGCCAGTCCTTGACCTCAGAGT
TCGCCTTTTCATTTCAAGCATAAGCCAATAAATACCTGCAGCAACGTGGGAGAAAGAAGTTGCTGGACCAGGAGA
AAAGGCAGTTATGAAGCCAATTCATTTGAAGGAAGCACAATTTCCACCTTATTTTTGAACCTTGGCAGTTTCA
ATGCTGTGCTCTGTTGCTTCGGGGCATAAGCTGATCACCGTCTAGTTGGGAAAGTCACCCCTACAGGGTTTGTAGG
GACATGATCAGCATCCTGATTTGAACCCCTGAAATGTTGTGTAGACACCCTCTTGGGTCCAATGAGGTAGTTGGTT
GAAGTAGCAAGATGTTGGCTTTTCTGGATTTTTTTTGCCATGGGTTCTTCACTGACCTTGGACTTTGGCATGATT
CTTAGTCATACTTGAACCTGTCTCATTCCACCTCTTCTCAGAGCAACTCTTCTTTGGGAAAAGAGTTCTTCAGA
TCATAGACCAAAAAAGTCATACCTTCGAGGTGGTAGCAGTAGATTCCAGGAGGAGAAGGGTACTTGCTAGGTATC
CTGGGTCAGTGGCGGTGCAAACCTGGTTTCTCAGCTGCCTGTCTTCTGTGTGCTTATGTCTCTTGTGACAATTG
TTTTCTCCCTGCCCTGGAGGTGTCTTCAACTGTGGACTTCTGGGATTGTCAGATTTTGCAACGTGGTACTAC
TTTTTTTTCTTTTTGTCTGTTAGTTATTTCTCCAGGGGAAAAGGCAATAATTTCTAAGACCCGTGTGAATGTGA
AGAAAAGCAGTATGTTACTGGTTGTGTTGTTGTTCTTGTTTTTTATATGTAAAATAAAAATAGTGAAAGGAG

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FIGURE 230

MKVTSLDGRQLRKMLRKEAAARCVVLD CRPYLAFAASNVRGSLNVNLNSVVLRRARGGAVSARYVLPDEAARARL
LQEGGGGVAAVVVLDQGSRHWQKLREESAARVVLTSLLACLPAGPRVYFLKGGYETFYSEYPECCVDVKPISQEK
IESERALISQCGKPVVNVSYRPAIDQGGPVEILPFLYLGSAYHASKCEFLANLHITALLNVSRRITSEACMTHLY
KWIPVEDSHTADISSHFQEAIDFIDCVREKGGKVLVHCEAGISRSPTICMAYLMKTKQFRLKEAFDYIKQRRSMV
SPNFGFMGQLLQYESEILPSTPNPQPPSCQGEAAGSSLIGHLQTLSPDMQAYCTFFASVLAPVPTHSTVSELSR
SPVATATSC

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FIGURE 231

GCAGCCCAGCCAAGCACTGTCAGGAATCCTGTGAAGCAGCTCCAGCTATGTGTGAAGAAGAGGACAGCACTGCCT
TGGTGTGTGACAATGGCTCTGGGCTCTGTAAGGCCGGCTTTGCTGGGGACGATGCTCCCAGGGCTGTTTTCCCAT
CCATTGTGGGACGTCCCAGACATCAGGGGTGATGGTGGGAATGGGACAAAAAGACAGCTACGTGGGTGACGAAG
CACAGAGCAAAAGAGGAATCCTGACCCTGAAGTACCCGATAGAACATGGCATCATCACCAACTGGGACGACATGG
AAAAGATCTGGCACCACCTCTTTCTACAATGAGCTTCGTGTTGCCCCTGAAGAGCATCCCACCCTGCTCACGGAGG
CACCCCTGAACCCCAAGGCCAACCGGGAGAAAATGACTCAAATTATGTTTGAGACTTTCAATGTCCCAGCCATGT
ATGTGGCTATCCAGGCGGTGCTGTCTCTCTATGCCTCTGGACGCACAACCTGGCATCGTGCTGGACTCTGGAGATG
GTGTCACCCACAATGTCCCCATCTATGAGGGCTATGCCTTGCCCCATGCCATCATGCGTCTGGATCTGGCTGGCC
GAGATCTCACTGACTACCTCATGAAGATCCTGACTGAGCGTGGCTATTCTTCGTTACTACTGCTGAGCGTGAGA
TTGTCCGGGACATCAAGGAGAACTGTGTTATGTAGCTCTGGACTTTGAAAATGAGATGGCCACTGCCGCATCCT
CATCCTCCCTTGAGAAGAGTTACGAGTTGCCTGATGGGCAAGTGATCACCATCGGAAATGAACGTTTCCGCTGCC
CAGAGACCCTGTTCAGCCATCCTTCATCGGGATGGAGTCTGCTGGCATCCATGAAACCACCTACAACAGCATCA
TGAAGTGTGATATTGACATCAGGAAGGACCTCTATGCTAACAATGTCTTATCAGGGGGCACCCTATGTACCCTG
GCATTGCCGACCGAATGCAGAAGGAGATCACGGCCCTAGCACCCAGCACCATGAAGATCAAGATCATTGCCCTC
CGGAGCGCAAATACTCTGTCTGGATCGGTGGCTCCATCCTGGCCTCTCTGTCCACCTTCCAGCAGATGTGGATCA
GCAAACAGGAATACGATGAAGCCGGGCCTTCCATTGTCCACCGCAAATGCTTCTTAAAACACTTTCTGCTCCTCT
CTGTCTCTAGCACACAACGTGAATGTCTGTGGAATTATGCCTTCAGTTCTTTTCCAAATCATTCTAGCCAAA
GCTCTGACTCGTTACCTATGTGTTTTTAATAAATCTGAAATAGGCTACTGGTAA

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FIGURE 232

MCEEEDSTALVCDNGSGLCKAGFAGDDAPRAVFPSIVGRFRHQGVVMVGMGQKDSYVGDEAQSKRGILTLYPIEH
GIITNWDDMEKIWHHSFYNELRVAPEEHPTLLTEAPLNPKANREKMTQIMFETFNVPAMYVAIQAVLSLYASGRT
TGIVLDSGDGVTHNVEIYEGYALPHAIMRLDLAGRDLTDYLMKILTERGYSFVTTAEREIVRDIKEKLCYVALDF
ENEMATAASSSSLEKSYELPDGQVITIGNERFRCPETLFQPSFIGMESAGIHETTYSIMKCDIDIRKDLYANNV
LSGGTTMYPGIADRMQKEITALAPSTMKIKIIAPPERKYSVWIGGSILASLSTFQQMWISKQEYDEAGPSIVHRK
CF

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FIGURE 233

CGGGAAGCGCGGCGGGGCTCCAGACCGGGGCGGGCTTAAGGGTGACATCTGCGCTTTAAAGGGTCCGGGTCAGC
TGA CTCCCCGACTCTGTGGAGTCTAGCTGCCAGGGTCGCGGCAGTGCGGGGAGAGATGACTGGGGAGCGACCCAGC
ACGGCGCTCCCGGACAGACGCTGGGGGCGCGGATTCTGGGCTTCTGGGGAGGCTGTAGGGTTTGGGTGTTTGCC
GCGATCTTCTGTCTGTCTCTGGCAGCCTCCTGGTCCAAGGCTGAGAACGACTTCGGTCTGGTGACGCCGCTG
GTGACCATGGAGCAACTGCTGTGGGTGAGCGGGAGACAGATCGGCTCAGTGGACACCTTCCGCATCCCCGCTCATC
ACAGCCACTCCGCGGGGCACTCTTCTCGCCTTTGCTGAGGCGAGGAAAATGTCTCATCCGATGAGGGGGCCAAG
TTCATCGCCCTGCGGAGGTCCATGGACCAGGGCAGCACATGGTCTCCTACAGCGTTCATTGTCAATGATGGGGAT
GTCCCCGATGGGCTGAACCTTGGGGCAGTAGTGAGCGATGTTGAGACAGGAGTAGTATTTCTTTCTACTCCCTT
TGTGCTCACAAGGCCGGCTGCCAGGTGGCCTCTACCATGTTGGTATGGAGCAAGGATGATGGTGTTCCTGGAGC
ACACCCCGGAATCTCTCCCTGGATATTGGCACTGAAGTGTGCCCCCTGGACCGGGCTCTGGTATTCAGAAACAG
CGGGAGCCACGGAAGGGCGCCTCATCGTGTGTGGCCATGGGACGCTGGAGCGGGACGGAGTCTTCTGTCTCCTC
AGCGATGATCATGGTGCCTCCTGGCGCTACGGAAGTGGGGTCAGCGGCATCCCCTACGGTCAGCCCAAGCAGGAA
AATGATTTCAATCCTGATGAATGCCAGCCCTATGAGCTCCCAGATGGCTCAGTCGTCAATGCCCGAAACCAG
AACA ACTACCACTGCCACTGCCGAATTGTCTCCGCAGCTATGATGCCTGTGATACACTAAGGCCCCGTGATGTG
ACCTTCGACCCCTGAGCTCGTGGACCCCTGTGGTAGCTGCAGGAGCTGTAGTCACCAGCTCCGGCATTGTCTTCTTC
TCCAACCCAGCACATCCAGAGTTCCGAGTGAACCTGACCCTGCGATGGAGCTTCAGCAATGGTACCTCATGGCGG
AAAGAGACAGTCCAGCTATGGCCAGGCCCCAGTGGCTATTCATCCCTGGCAACCCTGGAGGGCAGCATGGATGGA
GAGGAGCAGGCCCCCAGCTCTACGTCTGTATGAGAAAGGCCGGAACCACTACACAGAGAGCATCTCCGTGGCC
AAAATCAGTGTCTATGGGACACTCTGAGCTGTGCCACTGCCACAGGGGTATTCTGCCTTCAGGACTCTGCCTTCA
GGAACACGGGTCTGTAGAGGGTCTGCTGGAGACGCCTGAAAGACAGTTCATCTTCCTTTAGACTCCAGCCTTGG
CAAAATCACCTTCCCTTTACCAGGGAAATCACTTCCTTTAGGACTGAAAGCTAGGCGTCCTCTCCCACAAAAAAG
TCCTGCCCTCATCTGAGAATACTGTCTTTCCATATGGCTAAGTGTGGCCCCACCACCTCTCTGCCTCCCGGGAC
ATTGATTGGTCTCTTGGGCAGGTCTAGTGAGCTGTAGAATTGAATCAATGTGAACTCAGGGA ACTGGGAAG
GCTGAGCCTCCTCTTTGGTGTGCGGTAAGATAACCGACAGGGCTGGTGAAAGTCCCCAGATGGCAGGATATTTG
GTTTCAGAGTAAGGACTAGGTGCACCACCATGACTGACTATCAATCAAAATGTTTGTAACCTAAAAATTTTAAATG
AAGGATAATGAATATTTTA

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FIGURE 234

MTGERPSTALPDRRWGPRILGFWGGCRVWVFAAIFLLLSLAASWSKAENDFGLVQPLVTMEQLLWVSGRQIGSVD
TFRIPILITATPRGTLIAFAEARKMSSSDEGAKFIALRRSMDQGSTWSPTAFIVNDGDVPDGLNLGAVVSDVETGV
VFLFYSLCAHKAGCQVASTMLVWSKDDGVSWSSTPRNLSLDIGTEVFAPGPGSGIQKQREPRKGRLIVCGHGTLE
DGVFCLLSDDHGASWRYGSGVSGIPYGQPKQENDFNDECQPYELPDGSSVINARNQNNYHCHCRIVLRSYDADC
TLRPRDVTDFPELVDPVVAAGAVVTSSGIVFFSNPAHPEFRVNLTLRWSFSNGTSWRKETVQLWPGPSGYSSLAT
LEGSMDGEEQAPQLYVLYEKGRNHYTESISVAKISVYGT

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FIGURE 235

GCTCGTGGGTTTTCCGTGAAGTCGCGGTGCAGCGGTGGGCGGCATGCTGTGGCCGGTGGGGAGATTTCGTGGGGA
CACGGGGGGAGAGGACACTGCTGCTCCCGCCGGTTCAGCTTCAGCCCGGAGCCACGCTCGAGGACATCCGCCG
CCTCCATGCTGAGTTTGCTGCGGAACGAGACTGGGAACAGTTCCATCAGCCTCGGAATCTCCTCCTGGCCTTGGT
TGGGGAAGTGGGGGAGCTGGCAGAACTCTTTCAGTGGAAAACCGATGGGGAACCTGGCCCCCAAGGCTGGTCCCC
CAGGGAACGGGCAGCCCTTCAAGAGGAGCTTAGTGACGTCTCATCTACCTGGTGGCATTAGCAGCCCGCTGCCG
TGTGGATCTGCCGCTAGCAGTGCTCTCCAAAATGGACATCAACCGGCGACGCTACCCAGCCCATCTGGCCCGCAG
CTCTTCCCGCAAGTATACAGAATTGCCCCATGGGGCCATCTCTGAAGACCAGGCTGTGGGGCCTGCGGACATTCC
CTGTGACTCCACAGGCCAGACCTCAACCTAGAAAGATGGCCACAGGACTTGCAACTCAGGGTGGTGTCTGAAGAG
CAGAGAGTGGCCTGGCCCTGGAGCCTTTTTCTAGTCTTTTCAGAATAGATCATGGGCCTGAGGCCTCCACTTCTT
GAGGTCTGAGGCCCAGCAGCCTCTAGAAGGTAGCTCCTGGTGTGTTGTTCTCCAGTAAAATGGTTTTGGGCGAT
AACTTCTAGATTATTCCITGGATGGCCAGGGAGGCTCTCTGTCTCAGCAGGTGATGACGGGGGTACCAGGGGTGCC
TCTGAGACCCATTCTCGTGTGTTCCCTGTTGTACCTTTTGCCCTGCAGGGCAGAGAGATCTGGTTTCTAGCAAATTC
CCAGTAGGATGTGATGTAAGTTCCTTCCCCCTCTTAGAGATTGAAGGCTGTAAGAGTCCAGATGGTGGAGCCAGG
CTGTCTGGGTTCAAATGCCATCTTTGACACTTGCAAGCTAAATGACATTACTCAAATTAATCGTTCTGCACTTCA
GCTTCCTTGTCTATCAAATAAAAAGAATAGTACCTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAA

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FIGURE 236

MSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRRLHAEFAAERDWEQFHQPRNLLLALVGEVGE LAELFQWKT
DGEPPQGWSRERAAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDINRRRYPAHLARSSSRKYTELPHGAIS
EDQAVGFADIPCDSTGQTST

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FIGURE 237

GTGGAATTCA**ATGG**CATCTACTTCGTATGACTATTGCAGAGTGCCCATGGAAGACGGGGATAAGCGCTGTAAGCTT
CTGCTGGGGATAGGAATTCTGGTGCTCCTGATCATCGTGATTCTGGGGGTGCCCTTGATTATCTTCACCATCAAG
GCCAACAGCGAGGCCTGCCGGGACGGCCTTCGGGCAGTGATGGAGTGTGCGCAATGTCACCCATCTCCTGCAACAA
GAGCTGACCGAGGCCCAGAAGGGCTTTCAGGATGTGGAGGCCCAGGCCGCCACCTGCAACCACACTGTGATGGCC
CTAATGGCTTCCCTGGATGCAGAGAAGGCCCAAGGACAAAAGAAAGTGGAGGAGCTTGAGGGAGAGATCACTACA
TTAAACCATAAGCTTCAGGACGCGTCTGCAGAGGTGGAGCGACTGAGAAGAGAAAACCAGGTCTTAAGCGTGAGA
ATCGCGGACAAGAAGTACTACCCAGCTCCAGGACTCCAGCTCCGCTGCGGCGCCCCAGCTGCTGATTGTGCTG
CTGGGCCTCAGCGCTCTGCTGCAG**TGAG**ATCCCAGGAAGCTGGCACATCTTGAAGGTCCGTCTGCTCGGCTTT
TCGCTTGAACATTCCCTTGATCTCATCAGTTCTGAGCGGGTCATGGGGCAACACGGTTAGCGGGGAGAGCACGGG
GTAGCCGGAGAAGGGCCTCTGGAGCAGGTCTGGAGGGGCCATGGGGCAGTCCTGGGTGTGGGGACACAGTCGGGT
TGACCCAGGGCTGTCTCCCTCCAGAGCCTCCCTCCGGACAATGAGTCCCCCTCTTGCTCTCCACCCTGAGATTG
GGCATGGGGTGCGGTGTGGGGGGCATGTGCTGCCTGTTGTTATGGGTTTTTTTTTTCGGGGGGGGTGTGCTTTTTTC
TGGGGTCTTTGAGCTCCAAAAATAAACACTTCCTTTGAGGGAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAA

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FIGURE 238

MASTSYDYCRVPMEDGDKRCKLLLGIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAVMECRNVTHLLQQEELT
EAQKGFQDVEAQAATCNHTVMALMASLDAEKAQGQKKVEELEGEITTLNHKLQDASAEVERLRRENQVLSVRIAD
KKYYPSSQDSSSAAAPQLLIVLLGLSALLQ

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FIGURE 239

ATGGCGGCCTCAGCAGCGCGAGGTGCTGCGGCGCTGCGTAGAAGTATCAATCAGCCGGTTGCTTTTGTGAGAAGA
ATTCTTGGACTGCGGCGTCGAGTCAGCTGAAAGAACACTTTGCACAGTTCGGCCATGTCAGAAGGTGCATTTTA
CCTTTTGACAAGGAGACTGGCTTTCACAGAGGTTTGGGTTGGGTTTCAGTTTCTTCAGAAGAAGGACTTCGGAAT
GCACTACAACAGGAAAATCATATTATAGATGGAGTAAAGGTCCAGGTTTCACTAGAAAGGCCAAAACCTTCGCAA
ACATCTGATGATGAAAAGAAAGATTTTTGA

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FIGURE 240

MAASAARGAAALRRSINQPVAFVRRIPWTAASSQLKEHFAQFGHVRCILPFDKETGFHRGLGWVQFSSEEGLRN
ALQQENHIIDGVKVQVHTRRPKLPQTSDDDEKKDF

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FIGURE 241

GGCTCTTTTAAATGACCCAGGCGTCGTGATTGAATCCTAGACTCACGTCCGTCTCGCCGGCGCCCGAGCCAGT
CCGCGCGCACCGCGTCTGCGTCCCCGAAAGCCCCGCCCCGCAAGGGCTGCCCTGCCCTACCTGGTCTCCGACGTGCT
CGTCTGGAGGGCGGTGCGAGGGGCCGAGCCGACGAGATGTTCTTGCTGCCCTCTCCGGCTGCGGGGCGAGTAGTC
GTCCGACGTCTGGCCGTAGTACGTTCTGGGAGCCGGAGTCTCTCCACCGCAGACATGACGAAGGGCCTTGTTTTTA
GGAATCTATTCCAAAGAAAAAGAAGATGATGTGCCACAGTTCACAAGTGCAGGAGAGAATTTTGATAAATTGTTA
GCTGGAAAGCTGAGAGAGACTTTGAACATATCTGGACCACCTCTGAAGGCAGGGAAGACTCGAACCTTTTATGGT
CTGCATCAGGACTTCCCCAGCGTGGTGCTAGTTGGCCTCGGCAAAAAGGCAGCTGGAATCGACGAACAGGAAAAC
TGGCATGAAGGCAAAGAAAACATCAGAGCTGCTGTGTCAGCGGGGTGCAGGCAGATTCAAGACCTGGAGCTCTCG
TCTGTGGAGGTGGATCCCTGTGGAGACGCTCAGGCTGCTGCGGAGGGAGCGGTGCTTGGTCTCTATGAATACGAT
GACCTAAAGCAAAAAAGAAGATGGCTGTGTCGGCAAAAGCTCTATGGAAGTGGGGATCAGGAGGCCTGGCAGAAA
GGAGTCCTGTTTGCTTCTGGGCAGAACTTGGCACGCCAATTGATGGAGACGCCAGCCAATGAGATGACGCCAACC
AGATTTGCCGAAATTATTGAGAAGAATCTCAAAAGTGCTAGTAGTAAACCGAGGTCCATATCAGACCCAAGTCT
TGGATTGAGGAACAGGCAATGGGATCATTCCCTCAGTGTGGCCAAAGGATCTGACGAGCCCCCAGTCTTCTTGAA
ATTCACTACAAAGGCAGCCCCAATGCAAACGAACCAACCCCTGGTGTGTTGTTGGGAAAGGAATTACCTTTGACAGT
GGTGGTATCTCCATCAAGGCTTCTGCAAAATATGGACCTCATGAGGGCTGACATGGGAGGAGCTGCAACTATATGC
TCAGCCATCGTGTCTGCTGCAAAAGTTAAATTTGCCCATTAATATTATAGGTCTGGCCCCCTCTTTGTGAAAATATG
CCCAGCGGCAAGGCCAACAAGCCGGGGGATGTTGT TAGAGCCAAAAACGGGAAGACCATCCAGGTTGATAACACT
GATGCTGAGGGGAGGCTCATACTGGCTGATGCGCTCTGTTACGCACACACGTTTAACCCGAAGGTCATCCTCAAT
GCCGCCACCTTAACAGGTGCCATGGATGTAGCTTTGGGATCAGGTGCCACTGGGGTCTTTACCAATTATCCTGG
CTCTGGAACAAACTCTTCGAGGCCAGCATTGAAACAGGGGACCGTGTCTGGAGGATGCCTCTCTTCGAACATTAT
ACAAGACAGGTTGTAGATTGCCAGCTTGCTGATGTAAACAACATTGGAAAATACAGATCTGCAGGAGCATGTACA
GCTGCAGCATTCTGAAAGAATTGTAACCTCATCTAAGTGGGCACATTTAGACATAGCAGGCGTGATGACCAAC
AAAGATGAAGTTCCCTATCTACGGAAAGGCATGACTGGGAGGCCACAAAGGACTCTCATTGAGTTCTTACTTCGT
TTCAGTCAAGACAATGCTTAGTTTCAGATACTCAAAAATGCTTCACTCTGTCTTAAATTGGACAGTTGAACCTTAA
AAGGTTTTTGAATAAATGGATGAAAATCTTTTAACGGAGACAAAGGATGGTATTTAAAAATGTAGAACACAATGA
AATTTGTATGCCTTGATTTTTTTTTTCATTTACACACAAAGATTTATAAAGGTAAAGTTAATATCTTACTTGATAAG
GATTTTAAAGATACTCTATAAATGATTAAATTTT TAGAACTTCCTAATCACTTTTCAGAGTATATGTTTTTCAT
TGAGAAGCAAAATTGTAACCTCAGATTGTGATGCTAGGAACATGAGCAAACTGAAAATTACTATGCACTTGTGAG
AAACAATAAATGCAACTTGTTGTGAAAAAAAAAAAAAAAAAAAAA

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FIGURE 242

MFLPLPAAGRVVRRRLAVVRSGSRSLSTADMTKGLVLGIYSKEKEDDVPQFTSAGENFDKLLAGKLRETINISG
PPLKAGKTRTFYGLHQDFPSVVLVGLGKKAAGIDEQENWHEGKENIRAABAAGCRQIQDLELSSVEVDPCGDAQA
AAEGAVLGLYEYDDLKQKKKMAVSAKLYGSGDQEAQKGVLFASGQNLARQLMETPANEMTPTRFAEIEKNLKS
ASSKTEVHIRPKSWIEEQAMGSFLSVAKGSDEPPVFLEIHYKGSPPNANEPPLVFVGKGITFDSSGGISIKASANMD
LMRADMGGAATICSIVSAAKLNLPINIIIGLAPLCENMPSGKANKPGDVVRAKNGKTIQVDNTDAEGRLLILADAL
CYAHTFNPKVILNAATLTGAMDVALGSGATGVFTNSSLWNKLFEASLETGDRVWRMPLFEHYTRQVDCQLADV
NNIGKYRSAGACTAAAFLEFVTHPKWAHLDIAGVMTNKDEVYLRKGMTGRPTRTLIEFLLRFSQDNA

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FIGURE 243

CCGCTGTTATACGTCACCTCCACGGCTCAGCGTCAGGGAGGAGAGAGAATGTCTTTTCGAGGCGGAGGTTCGTGGA
GGCTTTTAATCGAGGTGGTGGAGGTGGCGGCTTCAACCGAGGCGGCAGCAGCAACCACTTCCGAGGTGGAGGCGGC
GGTGGAGGCGGCGGCAATTTTCAGAGGCGGCGGCAGGGGAGGATTTGGACGAGGGGGTGGCCGCGGAGGCTTTAAC
AAAGGCCAAGACCAAGGACCTCCAGAACGTGTAGTCTTATTAGGAGAGTTCCTGCATCCCTGTGAAGATGACATA
GTTTGTAATGTACCACAGATGAAAAAAGGTGCCTTATTTCAATGCTCCTGTTTACTTAGAAAACAAAGAACAA
ATTGAAAAGTGATGAAATATTTGGACAACCTCAGAGATTTTTATTTTTTCAGTTAAGTTGTCAGAAAACATGAAG
GCTTCATCCTTTAAAAAACTACAGAAGTTTTATATAGACCCATATAAGCTGCTGCCACTGCAGAGGTTTTTACCT
CGACCTCCAGGTGAGAAAGGACCTCCAAGAGGTGGTGGCAGGGGAGGCCGAGGAGGAGGAAGAGGAGGAGGTGGC
AGAGGTGGTGGCAGAGGCGGTGGTTTTAGAGGTGGAAGAGGAGGTGGAGGTGGGGGCTTCAGAGGAGGAAGAGGT
GGTGGTTTTCAGAGGGAGAGGACATTAAGTGAAACAGTTGACAGACATCACCAGTTGACTTCTGCATTAACCTGCA
TGATCTGTTTCTACTATGGATTGGAAACTTGTTCCTGAACAAGTCTTGAAGATCTTGGTCATTTTATGACAATG
GATCTAAAATGTCAGCATCATGCAAAGTGCAACGGAATAGTGAATTTTGCTCTAAAAGAGCATGAACAAGTCTTT
CTAATGTTTTGTACAGTGCCTGGCACTCTGTGGGTGCTCAATAAATGGATAGGAGTTTTTCATTTGAAGCATATTT
GAATTTTTAAATAAAGTGTTTTATTCCTTAAAAAAAAAAAAAAAAA

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FIGURE 244

MSFRGGGRGGFNRRGGGGGNRRGGSSNHFRGGGGGGGGNFRGGGRGGFGRGGGRGGFNKGQDQGPPERVVLLGE
FLHPCEDDIVCKCTTDENKVPYFNAPVYLENKEQIGKVDIEIFGQLRDFYFSVKLSENMKASSFKKLQKFIIDPYK
LLPLQRFLPRPPGEKGPPRRGGGRGGGRGGGGRRGGGRGGGFRGGRRGGGGGFRGGRRGGGFRGRGH

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FIGURE 245

CTGGAAGGAGTCATGGCGGATGGTCAGGTGGCGGAAGTCTGCTCCGGCGGCTGGAGGCGTCTGATGGCGGCCTG
GACAGCGCCGAGTTGGCGGCTGAGCTGGGCATGGAGCACCAGGCGGTGGTGGGCGCCGTGAAGAGCCTTCAGGCG
CTGGGCGAGGTCATCGAGGCTGAACTTCGGTCCACCAAGCACTGGGAGCTTACTGCGGAGGGCGAGGAGATTGCC
CGGGAGGGCAGCCATGAGGCCCCGTGTGTTTTCGAAGCATTCCTCCAGAGGGCCTGGCCCAGAGCGAGCTTATGCCA
CTGCCCAGTGGCAAAGTGGGCTTCAGCAAGGCCATGTCCAACAAGTGGATTTCGGGTGGACAAGAGTGC GGCTGAC
GGGCCCCGGGTGTTCGAGTGGTGGACAGCATGGAGGATGAGGTGCAGCGGCGGCTCCAGCTGGTCCGGGGGGGA
CAGGCTGAGAAGCTGGGGGAGAAGGAGAGGAGCGAGCTGAGGAAGAGGAAGCTGTTGGCTGAAGTGA CTCTGAAG
ACCTACTGGGTGAGCAAAGGCAGTGCCTTTAGTACCAGCATCTCCAAGCAAGAGACAGAGCTGAGCCCAGAGATG
ATCTCCAGTGGCTCTTGGCGGGACCGGCCCTTCAAGCCCTACAACCTCTTGGCCCACGGTGTCTCCCCGACAGC
GGCCACCTTCACCCGCTGCTCAAGGTCCGCTCCCAGTTCGACAGATCTTCTGGAGATGGGGTTCACCGAGATG
CCGACTGATAACTTCATTGAGAGCTCCTTCTGGAACTTTGACGCCCTCTTCCAGCCCCAGCAGCACCAGCCCGT
GACCAGCACGACACCTTCTTCTTCGAGATCCAGCGGAGGCCCTGCAGCTCCCAATGGACTATGTCCAGCGGGTC
AAGCGGACCCACTCTCAGGGCGGCTACGGCTCACAGGGGTACAAGTATAACTGGAAGCTGGACGAGGCCCCGAAA
AACCTACTGCGAACCACACACATCAGCCAGCGCCCGTGCCTCTACCGCCTTGCCCAGAAGAAGCCCTTCACT
CCGGTCAAGTACTTCTCCATCGACCGGTATTCCGGAATGAGACCCTGGACGCCACGCACCTGGCTGAGTTCCAC
CAGATCGAGGGCGTGGTGGCGGATCATGGTCTCACCTTGGGCCACCTCATGGGCGTTCTGCGGGAGTTCTTCACC
AAGCTGGGTATCACGCAACTCCGCTTCAAGCCAGCCTACAACCCATACACAGAGCCCAGCATGGAGGTGTTTCAGC
TACCACCAAGGCCCTGAAGAAGTGGGTGGAGGTCGGAACCTCGGGGGTCTTCCGTCCAGAGATGCTGCTGCCCATG
GGGCTTCCCGAGAACGTGTCGGTCATTGCCTGGGGCCTCTCCCTGGAGCGCCCAACGATGATCAAATATGGCATC
ACAATATCCGGGAGCTGGTGGGCCACAAGGTGAACCTGCAGATGGTGTATGACAGTCCCTGTGCCGCTGGAT
GCCGAGCCGAGGCCCCCTCCACACAGGAGGCTGCGTGACATGGGCCACTCTAGGACAGGTCATCTCCCCGAGT
CCCTGCTGCTGCGCTCCTTTGCATCCCTGGCCAGTGACCTTGATTTATGAGGCTCTGTGAGGCCAGCCCCACC
TTCTCTTTCCACCTGTCCCAGGACCAGAATCCCAGGGACAGAGGACTGGGTAGCAGGTTCTTCTGTTGTCTCT
GTGTGGTGTGTCTACTGTGAGGGTGGGCCCTGAGGAGACCTGTGGGCCACCTATTGTCTAATAAAGTGGGCAGTT
GCCCCCA

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FIGURE 246

MADGQVAELLLRRLEASDGGLDSAELAAELGMEHQAVVGAVKSLQALGEVIEAELRSTKHWELTAEGEEIAREGS
HEARVFRSIPPEGLAQSELMRLPSGKVGFSKAMSNKWIRVDKSAADGPRVFRVDSMEDEVQRRQLVRGGQAEK
LGEKERSELKRKLLAEVTLKTYWVSKGSFSTSI SKQETELSPEMISSGSWRDRPFKPYNFLAHGVLDPDSGHLH
PLLKVR SQFRQIFLEMGTTEMPD NFI ESSFWNFDA LFQPQQHPARDQHDTFFLRDPAEALQLPMDYVQVRKRTH
SQGGYGSQGYKYNWKLDEARKNLLRTHHTTSASARALYRLAQKKPFTPVKYFSIDRVFRNETLDATHLAEFHQIEG
VVADHGLTLGHLMGVLREFFTKLGITQLRFKPAYNPYTEPSMEVFSYHQGLKKWVEVGNSGVFRPEMLLPMGLPE
NVSVIAWGLSLERPTMIKYGINNIRELVGHKVNLMVYDSPLCRLDAEPRPPPTQEAA

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FIGURE 247

CTATCTGAAATGCAGAGATTAAGCCAAATACCTGATGTATTGTGAAAGCCACTGATTTTAAGAATGGAGAGAAAG
GGATTTTTTACTGCATCCCTCTGTATGAATATGAAATCAGAGACCAGGGCATGATGTTGCTAGGATTAGAGCCTC
TCAGTCTGGCCTCTTCACCCAAGTGCAAGAACTCAGTCTCTTACTGTTCAAAGAAAGAATCTTAACAGTTGAATT
ATGGAGGGAAATTCCCTTTTGCCCCAAGCGTTTCTATATTTAAAGCAATATCCCAGGAGAATATGTCAGACTTAG
GATGATACCTTCAGCCACTTGAAGAAGAAATAGAAGGCGCTCATTCCAATATAGTCTTTATTCCCATTGAGATA
CAGGTTGAGCATCCCTAATCTGAACAGTTAAAACCCCAAATGCCCCAAAATCCAAACCTTCCTGAACGCTATGA
CACCATGAGTGGAAAATTCCACACCTAACAAACACATTTGCTTTCTTATGGTTCAATGTACACAACTGTTTTAT
ATAGAAAATGATTTCAAATATCATAAAATTACCTTCAGGCTATGTGCATAAAGTATATATGAGCCATAAATGAAT
TTTGTGTTTAGACTTTGTGTCCATCCCCAAGATCTCTCATTATATATATA

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FIGURE 248

MNFVFRLCVHPQDLSLY

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FIGURE 249

CGAAAAAAGAGGGGAAGAGTATTAAAGACCATTTC TGGCTGGGCAGGGCACTCTCAGCAGCTCAACTGCCCAGCG
TGACCAAGTGGCCACCTCTGCAGTGTCTTCCACAACCTGGTCTTGACTCGTCTGCTGAACAAATCCTCTGACCTCA
GGCCGGCTGTGAACGTAGTTCCCTGAGAGATAGCAAACATGCCCCAACAGTGAGCCCGCATCTCTGCTGGAGCTGTT
CAACAGCATCGCCACACAAGGGGAGCTCGTAAGGTCCCTCAAAGCGGGAAATGCGTCAAAGGATGAAATTGATTCT
TGCAGTAAAGATGTTGGTGTCTATTAAAAATGAGCTACAAAGCTGCCGCGGGGAGGATTACAAGGCTGACTGTCC
TCCAGGGAACCCAGCACCTACCAGTAATCATGGCCAGATGCCACAGAAGCTGAAGAGGATTTTGTGGACCCATG
GACAGTACAGACAAGCAGTGCAAAAGGCATAGACTACGATAAGCTCATTGTTTCGGTTTGAAGTAGTAAAATTGA
CAAAGAGCTAATAAACCGAATAGAGAGAGCCACCGGCCAAAGACCACACCACTTCCTGCGCAGAGGCATCTTCTT
CTCACACAGAGATATGAATCAGGTTCTTGATGCCTATGAAAATAAGAAGCCATTTTATCTGTACACGGGCCGGGG
CCCCCTCTTCTGAAGCAATGCATGTAGGTACCTCATTCATTTATTTTACAAAGTGGCTCCAGGATGTATTTAA
CGTGCCCTTGGTCATCCAGATGACGGATGACGAGAAGTATCTGTGAAGGACCTGACCCTGGACCAGGCCTATGG
CGATGCTGTTGAGAATGCCAAGGACATCATCGCCTGTGGCTTTGACATCAACAAGACTTTTCATATTCTCTGACCT
GGACTACATGGGGATGAGCTCAGGTTTCTACAAAAATGTGGTGAAGATTCAAAGCATGTTACCTTCAACCAAGT
GAAAGGCATTTTCGGCTTCACTGACAGCGACTGCATTGGGAAGATCAGTTTTCTGCCATCCAGGCTGCTCCCTC
CTTCAGCAACTCATTCCCACAGATCTTCCGAGACAGGACGGATATCCAGTGCCTTATCCCATGTGCCATTGACCA
GGATCCTTACTTTAGAATGACAAGGGACGTCGCCCCCAGGATCGGCTATCCTAAACCAGCCCTGTTGCACTCCAC
CTTCTTCCCAGCCCTGCAGGGCGCCAGACCAAAATGAGTGCCAGCGACCCAACTCCTCCATCTTCTCACCAG
CACGGCCAAGCAGATCAAACCAAGGTCAATAAGCATGCGTTTTCTGGAGGGAGAGACACCATCGAGGAGCACAG
GCAGTTTGGGGGCAACTGTGATGTGGACGTGTCTTTCATGTACCTGACCTTCTTCTCGAGGACGACGACAAGCT
CGAGCAGATCAGGAAGGATTACACCAGCGGAGCCA TGCTCACCGGTGAGCTCAAGAAGGCACTCATAGAGGTTCT
GCAGCCCTTGATCGCAGAGCACCAGGCCCGCGCAAGGAGGTACGGATGAGATAGTGAAAGAGTTCATGACTCC
CCGGAAGCTGTCCTTCGACTTTCAGTAGCACTCGTTTTACATATGCTTATAAAAGAAGTGATGTATCAGTAATGT
ATCAATAATCCCAGCCAGTCAAAGCACCGCCACCTGTAGGCTTCTGTCTCATGGTAATTACTGGGCCTGGCCTC
TGTAAGCCTGTGTATGTTATCAATACTGTTTCTTCTGTGAGTTCCATTATTTCTATCTCTTATGGGCAAAGCAT
TGTGGGTAATTGGTGTGGCTAACATTGCATGGTGGATAGAGAAGTCCAGCTGTGAGTCTCTCCCCAAAGCAGC
CCCACAGTGGAGCCTTCGGCTGGAAGTCCATGGGCCACCCTGTTCTTGTCCATGGAGGACTTCCGAGGGTTCCAA
GTATACTCTTAAGACCCACTCTGTTTAAAAATATATATTCTATGTATGCGTATATGGAATTGAAATGTCATTATT
GTAACCTAGAAAGTGCTTTGAAATATTGATGTGGGGAGGTTTATTGAGCACAAAGATGTATTTAGCCCATGCCCC
CTCCCCAAAAGAAATTGATAAGTAAAAGCTTCGTTATACATTTGACTAAGAAATCACCCAGCTTTAAAGCTGCTT
TTAACAATGAAGATTGAACAGAGTTCAGCAATTTTGATTAAATTAAGACTTGGGGTGAAACTTTCCAGTTTACT
GAACTCCAGACCATGCATGTAGTCCACTCCAGAAATCATGCTCGCTTCCCTTGGCACACCAGTGTTCTCTGCCA
AATGACCCTAGACCCTCTGTCTGCAGAGTCAGGGTGGCTTTTCCCTGACTGTGTCCGATGCCAAGGAGTCTGTG
GCCTCCGACAGATGCTTCATTTTGACCCCTGGCTGCAGTGGAAGTCAGCACAGAGCAGTGCCCTGGCTGTGTCTG
GACGGGTGGACTTAGCTAGGGAGAAAGTCGAGGCAGCAGCCCTCGAGGCCCTCACAGATGTCTAGGCAGGCCTCA
TTTCATCACGCAGCATGTGCAGGCCTGGAAGAGCAAAGCCAAATCTCAGGGAAGTCCTTGGTTGATGTATCTGGG
TCTCCTCTGGAGCACTCTGCCCTCCTGTACCCAGTAGAGTAAATAAACTTCCTTGGCTCCTAAAAA

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FIGURE 250

MPNSEPASLLELFNSIATQGELVRSCLKAGNASKDEIDSAVKMLVSLKMSYKAAAGEDYKADCPPGNPAPTSNHGP
DATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIFFSHRDMNQVLDAY
ENKKPFYLYTGRGPSSEAMHVGHLPFI FT KWLQDVFNVLVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIAC
GFDINKTFIFSDLDYMGMSGGFYKNVVKIQKHVTFNQVKGIFGFTDSDCIGKISFPQAIQAAPSFNSFPQIFRDR
TDIQCLIPCAIDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTD TAKQIKTKVKNH
AFSGGRDTIEEHRQFGGNCVDVVSFMYLTFFLEDDDKLEQIRKDYTS GAMLTGELKKALIEVLQPLIAEHQARRK
EVTDEIVKEFMTPRKLSFDFQ

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FIGURE 251

CACCGCGCAAGCGCATCCTGGCCTTTCTTCAGTCCACAGTGCGATCCTTCCCGGCAACTTTTTCGAGAAAAATG
CCCAAATTCAAGGCGGCCCGTGGGGTGGGGGTCAGGAAAAACATGCGCCCTGGCCGATCAGATCCTGGCTGGG
AATGCGGTGCGGGCGGGGTCCGGGAGAAGCGGCGGGTTCGCGGGACAGGAGAAGCGGAGGAAGAGTATGTGGG
CCCCGGCTGAGCCGACGGATTTTGAGCAAGCACGGCAGCAACAGGAGGAACCTGAGGCCGAGCATGGGACTGGG
GACAAGCCCGCGGCGCCGCGGGAACGCACCACGCGGCTGGGTCCAAGAATGCCTCAGGATGGATCAGATGACGAG
GACGAGGAGTGGCCACCCTGGAGAAGGCTGCCACAATGACAGCAGCGGGCCATCATGCAGAGGTGGTTGTGGAC
CCTGAGGATGAGCGTGCCATAGAGATGTTCAATGAACAAGAACCCTCCTGCCAGGCGCACCCCTGGCTGACATCATC
ATGGAGAAGCTGACTGAGAAGCAGACAGAGGTTGAGACAGTCAATGTCAGAGGTGTCGGGCTTCCCTATGCCCCAG
CTGGACCCCGGGTCTAGAAAGTGTACAGGGGGTCCGGGAGGTATTATCTAAGTACCGCAGTGGAAGAACTGCCC
AAGGCATTTAAGATCATCCCTGCACTCTCCAAGTGGGAGCAATCCTCTACGTCACAGAGCCGGAGGCCTGGACT
GCAGCTGCCATGTACCAGGCCACCAGGATTTTTGCGCTCTAACCTGAAGGAACGCATGGCCAGCGCTTCTACAAC
CTTGTCTCTGCTCCCTCGAGTACGAGATGACGTTGCTGAATACAAACGACTCAACTTCCATCTCTACATGGCTCTC
AAGAAGGCCCTTTTCAAACCTGGAGCCTGGTTCAAAGGGATCCTGATTCCACTGTGCGAGTCTGGCACTTGTACC
CTCCGGGAAGCCATCATTGTGGGTAGCATCATCACCAGTGCTCCATCCCTGTGTTGCACTCCAGTGCGGCCATG
CTGAAAATTGCTGAGATGGAATACAGCGGTGCCAACAGCATCTTCCTGCGACTGCTGCTGGATAAGAAGTATGCA
CTGCCTTACCGGGTGTGGATGCCCTAGTCTTCACTTCCTGGGGTTCGGACAGAGAAGCGTGAAGTGCCTGTG
CTGTGGCACCAGTGCTCCTGACTTTGGTCCAGCGCTACAAGGCCGACTTGGCCACAGACCAGAAAGAGGCCCTC
TTAGAACTGCTCCGGCTGCAGCCCCATCCACAGCTATCGCCGAAATCAGGCGTGAGCTTCAGAGTGCAGTCCCC
CGCGATGTGGAAGATGTTCCCATCACCCTGGAGTGAAGAAAACAGTCAGCTGTCTGGCCAAAGGGGTTTGGAAG
GACACCAAGACCCCCGTTGGTGACTGAAGATGACACTGAGCTTTAATGGCTGAAGACCCAGATCAGGGCAGTGAC
AGATCACAGGGACATCTGTGGCTCCAGTCCAGGACAGGAAGGACTGAGGGTCTGGCTGGTTCCCTCTTCCATTC
TAGGCCCTTATCCCTGTTTAGTTCTGAGAGCCAACCTTGAGATACCATATGCTAGCATTCCAGTCCCCAGCTGGG
GCTTGGTGTGAGTACTTTTTCTATGGCTATTGTGTGAGGTCACTGTGGATAAAGGCAAAGACAGATATTTATTGA
AAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 252

MNKNPPARRTLADIIMEKLTEKQTEVETVMSEVSGFMPQLDPRVLEVYRGVREVL SKYRSGKLPKAFKIIPALS
NWEQIILYVTEPEAWTAAAMYQATRIFASNLKERMAQRFYNLVLLPRVRDDVAEYKRLNFHLYMALKKALFKPGAW
FKGILIPLCESGTCTLREAIIVGSIITKCSIPVLHSSAAMLKIAEMEYSGANSIFLRLLLDKKYALPYRVLDALV
FHFLGFRTEKRELPVLWHQCLLTLVQRYKADLATDQKEALLELLRLQPHPLSPEIRRELQSAVPRDVEDVPITV
E

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FIGURE 253

TGGAGACTCACCAATCTATCTCCCTACATCAAGGTCTCTTAGAAGTCACCTTTCTGCTGTATAATACAGCGTAA
CCCTACTTGAGACATTTCCATTTAAATTGCTCTGTTCACATGTTTCATCCTGTCTTGCTGTAAGTGTGTAGGT
GGGTGACAACATTTTCGAACTGTATATTTGTCACCTCTGTAGTCTATCTCTAAGAACACAGCCAATAAGACATC
ACTTGACAAGCCATTACCTTATTGACCAAGACTATTTTGTGAATCAAATGCAATGTGACTTGAAAATCAAATCGT
TTCAATGGTCATTTAAGTTGTTAATTTTAAAAAATGGTCATTTTCAGCTTGATGCATAAGAGCGTTCTTTGCAGGA
ACTTCATTTTTGACTACAAAGGCTTTGAATTTTATTTTGCTGCTTGACAGTAATTTTGTTTTCTTTTCTTCCAG
GGTATATGAGAAAATATTGACTCCTATCTGGCCTTCATCAACTGACCTCGAAAAGCCTCATGAGATGCTTTTTCT
TAATGTGATTTTGTTCAGCCTCACTGTTTTTACCTTAATTTCAACTGCCCACACACTTGACCGTGCAGTCAGGAG
TGACTGGCTTCTCCTTGTCCTCATTATGCATGTTTGAGGAGCTGATTCCCTGAACTCATATTTAAACTCTACTG
CCAGGGAAATGCTACATTATTTTTCTAATTGGAAGTATAATTAGAGTGATGTTGGTAGGGTAGAAAAAGAGGGAG
TCACTTGATGCTTTTCAGGTTAATCAGAGCTATGGGTGCTACAGGCTTGTCTTTCTAAGTGACATATTCTTATCTA
ATTCTCAGATCAGGTTTTGAAAGCTTTGGGGGTCTTTTATAGATTTTAAATCCCTACTTTCTTTATGGTACAAATAT
GTACAAAAGAAAAGGTCTTATATTCTTTTACACAAATTTATAAATAAATTTTGAACCTCTTCTGTAAAAAA

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FIGURE 254

MHKSVLCRNFI FDYKGFEFYFAACSNFCFLFLPGYMRKY

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FIGURE 255

ATGAGTGAGAAACAATAAGAATTCCTTGGAGAGCAGCCTACGGCAACTAAAATGCCATTTACCTGGAACCTTGATG
GAGGGAGAAAACTCCTTGGATGATTTTGAAGACAAAGTATTTTACCGGACTGAGTTTCAGAAATCGTGAATTCAAA
GCCACAATGTGCAACCTACTGGCCTATCTAAAGCACCTCAAAGGGCAAAACGAGGCAGCCCTGGAATGCTTACGT
AAAGCTGAAGAGTTAATCCAGCAAGAGCATGCTGACCAGGCAGAAATCAGAAGTCTGGTCACCTGGGGAAACTAT
GCCTGGGTCTACTATCACATGGGCCGACTCTCAGACGTTTCAAGTTTATGTAGACAAGGTGAAACATGTCTGTGAG
AAGTTTCCAGTCCCTATAGAATTGAGAGTCCAGAGCTTGACTGTGAGGAAGGGTGGACACGGTTAAAGTGTGGA
GGAAACCAAAATGAAAGAGCGAAGGTGTGCTTTGAGAAGGCTCTGGAAAAGAAGCCAAAGAACCCAGAATTCACC
TCTGGACTGGCAATAGCAAGCTACCGTCTGGACAACTGGCCACCATCTCAGAACGCCATTGACCCTCTGAGGCAA
GCCATTCGGCTGAATCCTGACAACCAGTACCTTAAAGTCCTCTGGCTCTGAAGCTTCATAAGATGCGTGAAGAA
GGTGAAGAGGAAGGTGAAGGAGAGAAGTTAGTTGAAGAAGCCTTGGAGAAAGCCCCAGGTGTAACAGATGTTCTT
CGCAGTGCAGCCAAGTTTTATCGAAGAAAAGATGAGCCAGACAAAGCGATTGAACTGCTTAAAAAGGCTTTAGAA
TACATACCAAAACAATGCCTACCTGCATTGCCAAATTGGGTGCTGCTATAGGGCAAAAGTCTTCCAAGTAATGAAT
CTAAGAGAGAATGGAATGTATGGGAAAAGAAAGTTACTGGAACATAATAGGACACGCTGTGGCTCATCTGAAGAAA
GCTGATGAGGCCAATGATAATCTCTTCCGTGTCTGTTCCATTCTTGCCAGCCTCCATGCTCTAGCAGATCAGTAT
GAAGACGCAGAGTATTACTTCCAAAAGGAATTCAGTAAAGAGCTTACTCCTGTAGCGAAACAACCTGCTCCATCTG
CGGTATGGCAACTTTCAGCTGTACCAATGAAGTGTGAAGACAAGGCCATCCACCCTTTATAGAGGGTGTA
ATAAACCAGAAATCAAGGGAGAAAGAAAAGATGAAAGACAACTGCAAAAAATTGCCAAATGCGACTTTCTAAA
AATGGAGCAGATTCTGAGGCTTTGCATGTCTTGGCATTCTTCAGGAGCTGAATGAAAAATGCAACAAGCAGAT
GAAGACTCTGAGAGGGGTTTGGAGTCTGGAAGCCTCATCCCTTCAGCATCAAGCTGGAATGGGGAATGA

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FIGURE 256

MSENNKNSLESSLRQLKCHFTWNLMEGENSLDDFEDKVFYRTEFQNRFEKATMCNLLAYLKHLKGQNEAALECLR
KAEELIQQEHADQAEIRSLVTWGN YAWVYYHMGRLSDVQIYVDKVKHVCEKFSSPYRIESPELDCEEGWTRLKCG
GNQNERAKVCFEKALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPDNQYLKVL LALKLHKMREE
GEEEGEGEKLVEEAEKAPGVTDLRSAAKFYRRKDEPDKAIELLKKALEYIPNNAYLHCQIGCCYRAKVFQVMN
LRENGMYGKRKLLELIGHAVAHLLKKADEANDNLFRCVCSILASLHALADQYEDA EYFQKEFSKELTPVAKQLLHL
RYGNFQLYQMKCEDKAIHHFIEGVKINQKSREKEKMKDKLQKIAKMRLSKNGADSEALHVLAF LQELNEKMQQAD
EDSERGLESGSLIPSASSWNGE

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FIGURE 257

TGAACTGAGCGGCCCTGAGCTGACAGATACACTGCGCAGTGGAAACGGCGAGCGAGCCGACGGGCGAGTGAGGGG
CGCACATGATCACCTCGGCCCTGGAATTATTTCTCTTCTGGATGAAGATGAACCACAGCTTAAGGAATTTGCAC
TACACAAATTGAATGCAGTTGTTAATGACTTCTGGGCAGAAATTTCCGAGTCCGTAGACAAAATAGAGGTTTTAT
ACGAAGATGAAGTTTTCCGGAGTCGGCAGTTTGCAGCCTTAGTGGCATCTAAAGTATTTTATCACCTGGGGGCTT
TTGAGGAGTCTCTGAATTATGCTCTTGGAGCAAGGGACCTCTTCAATGTCAATGATAACTCTGAATATGTGGAAA
CTATTATAGCAAAATGCATTGATCACTACACCAACAATGTGTGGAAAATGCAGATTTGCCTGAAGGAGAAAAAA
AACCAATTGACCAGAGATTGGAAGGCATCGTAAATAAAATGTTCCAGCGATGTCTAGATGATCACAAGTATAAAC
AGGCTATTGGCATTGCTCTGGAGACACGAAGACTGGACGTCTTTGAAAAGACCATACTGGAGTCGAATGATGTCC
CAGGAATGTTAGCTTATAGCCTTAAGCTCTGCATGTCTTTAATGCAGAATAAACAGTTTCGGAATAAAGTACTAA
GAGTTCTAGTTAAATCTACATGAACTTGGAGAAAACCTGATTTTCATCAATGTTTGTCTAGTGCTTAATTTTCTTAG
ATGATCCTCAGGCTGTGAGTGATATCTTAGAGAAAACCTGGTAAAGGAAGACAACCTCCTGATGGCATATCAGATTT
GTTTTGATTTGTATGAAAGTGCTAGCCAGCAGTTTTTGTCTATCTGTAATCCAGAATCTTCGAACTGTTGGCACCC
CTATTGCTTCTGTGCCTGGATCCACTAATACGGGTACTGTTCCGGGATCAGAGAAAAGACAGTGACTCGATGGAAA
CAGAAGAAAAGACAAGCAGTGCATTGTAGGAAAGACACCAGAAGCCAGTCCAGAGCCTAAGGACCAGACTTTGA
AAATGATTAAATTTTAAAGTGGTGAAATGGCTATTGAGTTACATCTGCAGTTCTTAATACGAAACAATAATACAG
ACCTCATGATTCTAAAAACACAAGGATGCAGTACGGAATTCTGTATGTCTACTGCAACCGTTATAGCAAACCT
CTTTTATGCACTGTGGGACAACCAAGTGACCAAGTTTCTTAGAGATAAATTGGAATGGTTAGCCAGAGCCACTAACT
GGGCAAAATTTACTGCTACAGCCAGTTTGGGTGTAATTCATAAGGGTCATGAAAAGAAGCATTACAGTTAATGG
CAACATACCTTCCCAAGGATACTTCTCCAGGATCAGCCTATCAGGAAGGTGGAGGTCTCTATGCACTAGGTCTTA
TTCATGCCAATCATGGTGGTGATATAATTGACTATCTGCTTAATCAGCTTAAGAACGCCAGCAATGATATCGTTA
GACACGGTGGCAGTCTGGGCCCTTGGTTTGGCAGCCATGGGAACTGCACGTCAAGATGTTTATGATTTGCTAAAAA
CAAACCTTTATCAGGATGATGCAGTAACAGGGGAAGCAGCTGGCCCTAGGTTTGGTTATGTTGGGCTCTA
AAAATGCTCAGGCTATTGAGGACATGGTTGGTTATGCACAAGAACTCAACATGAGAAGATTCTGCGTGGTCTTG
CAGTTGGCATAGCTTTAGTAATGTATGGGAGGATGGAAGAGGCTGATGCTCTCATTGAATCTCTCTGTCTGAC
AGGACCCAATTCTTCGAAGGTCTGGAATGTATACTGTAGCCATGGCTTAATTGTGGCTCTGGTAACAACAAAGCAA
TTCGACGCCTGCTACATGTGGCTGTAAGTGATGTGAATGATGATGTCAGGAGTGCAGCAGTAGAATCACTTGGGT
TCATTCTATTTCAGAACCCCTGAACAGTGCCCAAGTGTGTCTCTTTGTTGTCTAGAGAGTTACAACCCCTCAIGTGC
GCTACGGAGCTGCAATGGCCTTGGGGATATGCTGTGCTGGTACAGGAACAAGGAAGCCATTAATTTGCTAGAAC
CAATGACAAACGACCCCGTGAACACTACGTGAGGCAAGGGGCACCTCATAGCTTCAGCTCTCATCATGATCCAGCAGA
CTGAAATCACTTGTCCAAAGGTGAATCAGTTCAGACAGCTGTATTCCAAAGTCATCAATGATAAGCATGATGATG
TCATGGCCAAGTTTGGCGCTATTCTGGCCAGGGCATACTGGATGCAGGTGGTCATAATGTCACAATCTCCTTGC
AGTCCAGGACTGGGCATACTCATATGCCTTCTGTGGTTGGCGTCTTGTATTTACCCAGTTTTGGTTCTGGTTTC
CTCTTTACACTTTCCTGTCTATTGGCTTATACCCCTACCTGTGTCTATTGGCCTTAACAAGGACTTAAAGATGCCGA
AAGTTTCAGTATAAATCGAACTGTAAACCATCCACATTTGCATATCCTGCCCTCTGGAAGTACCAAAAGAAAAAG
AAAAGGAAAAGGTTTCTACTGCTGTATTATCTATAACTGCCAAGGCTAAAAAGAAGGAAAAAGAAAAAGAAAAA
AGGAGGAGGAGAAAATGGAAGTGATGAGGCAGAGAAAAGGAGGAAAAAGAGAAGAAAAAGAACCTGAGCCAA
ACTTCCAGTTATTGGATAACCCAGCCCGAGTTATGCCTGCCAGCTTAAGGTCCTAACCATGCCGAGACCTGTA
GATACCAGCCTTTCAAACCACTCTCTATTGGAGGCATCATATTCTGAAGGATACCAGTGAAGACATTGAGGAGC
TGGTGGAACTGTGGCAGCACATGGCCAAAAATCGAGGAGGAGGAACAAGAGCCAGAACCCCAAGAACCTTTG
AGTATATTGATGATTAAGGACCAGAGGATCTCACTTGCTTATCTGAAGAAGATTGTCCAGGCTCATATTGGGAAT
GCTTATGAGGAAATTCATGCCGAGACCTGCTATTCAATGCATGTATCGTTGCCTCTGCACTGACCTGAAGAACCC
TGTCTCCAAGTCTTTGGTTGAAGAGAAGATATGACTGTTGAGTGTGCTCTTTCACAGAAGTGGTTTTCAAT
AAATATAAGATCTCCAGATGGACAAG

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FIGURE 259

CGCAAAGAGTAGTCAGTCCCTTCTTGGCTCTGCTGACACTCGAGCCCACATTCCATCACCTGCTCCCAATC**ATGC**
AGGTCTCCACTGCTGCCCTTGCCGTCCCTCTGCAACCATGGCTCTCTGCAACCAGGTCCCTCTGCAACCACGTG
AGTCCATGTTGTTGTTGTTGGGTATCACCACCTCTCTGGCCATGGTTAGACCACATCAGTCTTTTTTTCGGGCTGA
GAGCCCCGAAGAGAAAAGAAGGAAGTTCTTAAAGCGCTGCCAAACACCTTGGTCTTTTTCTTCACAACTTTTATT
TTTATCTCTAGAAGGGGTCTTAGCCCTCCTAGTCTCCAGTTGCTGCTGACACGCCGACCGCCTGCTGCTTCAGCT
ACACCTCCCGACAGATTCCACAGAATTCATAGCTGACTACTTTGAGACGAGCAGCCAGTGCTCCAAGCCCAGTG
TCATCTTCCTAACCAAGAGAGGGCCGGCAGGTCTGTGCTGACCCAGTGAGGAGTGGGTCCAGAAATACGTCAGTG
ACCTGGAGCTGAGTGCC**TGAG**GGGTCCAGAAGCTTCGAGGCCAGCGACCTCAGTGGGCCCAGTGGGGAGGAGCA
GGAGCCTGAGCCTTGGAACATGCGTGTGACCTCTACAGCTACCTCTTCTATGGACTGGTTATTGCCAAACAGCC
ACACTGTGGGACTCTTCTTAACCTAAATTTTAATTATTTATACTATTTAGTTTTTATAATTTATTTTTGATTC
ACAGTGTTTTGTGATTGTTTGCTCTGAGAGTTCCCCCTGTCCCCTCCACCTCCCCTCACAGTGCTGTGCTGGTGAC
AACCGAGTGGCTGTATCGGCCTGTGTAGGCAGTGATGGACCAAAGCCACCAGACTGACAAATGTGTGATCAGA
TGCTTTTGTTTCAGGGCTGTGATCGGCCTGGGGAATAATAAAGATGTTCTTTTAAACGGT

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FIGURE 260

MQVSTAALAVLLCTMALCNQVLSAPLAADTPTACCFSYTSRQIPQNFADYFETSSQCSKPSVIFLTRGRQVCA
DPSEEWVQKYVSDLELSA

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FIGURE 261

GAGAGAGAAGGAGAAGATAATACTGAAAAGAAGAGGAGGAGAGAGCGACGGGACGGGACGGGAGCGGGAGCG
 CAGCCGCCCTCTCGGCTCCGCGGCGGCGCCTCGCAAGTCCGGGAGGCGAGGGGGGCCCCAGGGGAGACGCCGTGA
 CAACTTTCGTTTCCCTCTGAGGGAATTGGGAGGTGCGCGGCCCCAAAAGCTTTCAGTCCAGTGTAAAGCTGTTGG
 AGCGCGGGAGCAAAGGTAAAGAATGATGTAATGCACTGGCTGCTCCAAAGCATCTTTTGTGTGGAATGGTTATT
 CCAGTCATCTCTTTATGAATCAAATGTGAGGGGCTGCTTGTGGACGGAGTCCTTTGCAAGAGCACATCAACGGG
 AAAGAGAAAGAGACATTCATTGGAGGGCTCTTGCTGAAAATGGGTTTAACTCTCCTTTTGCCAGTCACCACCAG
 CCTGACCTCATACACTTTTAGTACAATGGAGTGGCTGAGCCTTTGAGCACACCACCATTACATCATCGTGGCAAA
 TTAAAGAAGGAGGTGGGAAAAGAGGACTTATTGTTGTCATGGCCCCATGAGATGATTGGAACCTCAAATTGTTACTG
 AGAGGTTGGTGGCTCTGCTGGAAGTGGAAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCATTTGTGGAATACA
 ATACATCCACATTTTGGAAAGCCATTAATATCAACTGCTCCAAGCTTATGAAGCGAAGGTTGCAACAGGACAAAAG
 TGTTAATTACAGAGCTCATCCAGCATTACGCGAAACATAAGGTTGACATTGATTGCAGTCAGAAGGTTGTAGTTT
 ACGATCAAAGCTCCCAAGATGTTGCCTCTCTCTCTTCAGACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGA
 AGAGCTTCAACTCTGTTACCTGCTTGCAAGTGGGTTTGTGAGTTCTCTCGTTGTTTCCCTGGCCTCTGTGAAG
 GAAAATCCACTCTAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCTGTTGCCAACATTGGGCCAACCCGAATTC
 TTCCAATCTTTATCTTGGCTGCCAGCGAGATGTCTCAACAAGGAGCTGATGCAGCAGAATGGGATTGGTTATG
 TGTTAAATGCCAGCAATACCTGTCCAAAGCCTGACTTTATCCCCGAGTCTCATTTCCTGCGTGTGCCTGTGAATG
 ACAGCTTTTGTGAGAAAATTTTGGCGTGGTTGGACAAATCAGTAGATTTTATTGAGAAAGCAAAAGCCTCCAATG
 GATGTGTTCTAGTGCATGTTTAGCTGGGATCTCCCGCTCCGCCACCATCGCTATCGCCTACATCATGAAGAGGA
 TGGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAGACCTACTATATCTCCAACTTCAATTTTC
 TGGGCCAACTCCTGGACTATGAGAAGAAGATTAAGAACCAGACTGGAGCATCAGGGCCAAAGAGCAAACCTCAAGC
 TGCTGCACCTGGAGAAGCCAAATGAACCTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCCCTCA
 GTCCACCCTGTGCCGACTCTGCTACCTCAGAGGCGAGGACAAAGGCCCGTGCATCCCGCCAGCGTGCCAGCG
 TGCCAGCGTGAGCGCTCGCTGTTAGAGGACAGCCCGCTGGTACAGGCGCTCAGTGGGCTGCACCTGTCCGAG
 ACAGGCTGGAAGACAGCAATAAGCTCAAGCGTTCCCTTCTCTCTGGATATCAAATCAGTTTTCATATTACGCCAGCA
 TGGCAGCATCCTTACATGGCTTCTCCTCATCAGAAGATGCTTTTGAATACTACAAACCTTCCACTACTCTGGATG
 GGACCAACAAGCTATGCCAGTTCTCCCTGTTTCAGGAACCTATCGGAGCAGACTCCCGAAACCAGTCCGTGATAAGG
 AGGAAGCCAGCATCCCCAAGAAGCTGCAGACCGCCAGGCCTTCAGACAGCCAGAGCAAGCGATTGCATTCCGTCA
 GAACCAGCAGCAGTGGCACCGCCAGAGGTCCTTTTATCTCCACTGCATCGAAGTGGGAGCGTGGAGGACAATT
 ACCACACCAGCTTCCCTTTTGGCCCTTTCACCAGCCAGCAGCACCTCACGAAGTCTGCTGGCCTGGGCCTTAAGG
 GCTGGCACTCGGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACCAGCAGCTGGTATTTTGCCACAGAGT
 CCTCACACTTCTACTCTGCCTCAGCCATCTACGGAGGCGAGTGCCAGTTACTCTGCCTACAGCTGCAGCCAGCTGC
 CCACTTGGCGAGACCAAGTCTATTCTGTGCGCAGGCGGCAGAAGCCAAGTGAAGAGCTGACTCGCGGCGGAGCT
 GGCATGAAGAGAGCCCTTTGAAAAGCAGTTTAAACGCAGAAGCTGCCAAATGGAATTTGGAGAGAGCATCATGT
 CAGAGAACAGGTACGGGAAGAGCTGGGGAAAGTGGGCAGTCAGTCTAGCTTTTCGGGCAGCATGGAAATCATTG
 AGGTCTCCTGAGAAGAAAGACACTTGTGACTTCTATAGACAATTTTTTTTTTCTTGTTCACAAAAAATTCCTGT
 AAATCTGAAATATATATATGTACATACATATATATTTTTGGAAAATGGAGCTATGGTGTAAAGCAACAGGTGGA
 TCAACCCAGTTGGTTACTCTCTTAACATCTGCATTTGAGAGATCAGCTAATACTTCTCTCAACAAAAATGGAAGG
 GCAGATGCTAGAATCCCCCTAGACGGAGGAAAACCATTTTATTAGTGAATTACACATCCTCTGTCTTAAAA
 AAGCAAGTGTCTTTGGTGTGGAGGACAAAATCCCCTACCATTTTACGTTGTGCTACTAAGAGATCTCAAATAT
 TAGTCTTTGTCCGACCTTCCATAGTACACCTTAGCGCTGAGACTGAGCCAGCTTGGGGGTCAGGTAGGTAGAC
 CCTGTTAGGGACAGAGCCTAGTGGTAAATCCAAGAGAAATGATCCTATCCAAAGCTGATTACAAACCCACGCTC
 ACCTGACAGCCGAGGGACACGAGCATCACTCTGCTGGACGGACATTAGGGGCCTTGCCAAGGTCTACCTTAGAG
 CAAACCCAGTACCTCAGACAGGAAAGTCGGGGCTTTGACCACTACCATATCTGGTAGCCATTTTCTAGGCATTG
 TGAATAGGTAGGTAGCTAGTCACACTTTTCAGACCAATTCAAAGTGTCTATGCACAAAATTCCTGGGGCCTAGA
 TGGAGATAATTTTTTTTTTCTTCTCAGCTTTATGAAGAGAAGGGAAACTGTCTAGGATTACGTGAACACCAGGA
 ACCTGGCAACATCACGATTTAAGCTAAGGTTGGGAGGCTAACGAGTCTACCTCCCTCTTTGTAATCAAAGAATT
 GTTTAAATGGGATTGTCAATCCTTTAAATAAAGATGAACCTGGTTTCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 262

MAHEMIGTQIVTERLVALLESQTEKVLIDSRPFVEYNTSHILEAININCSKLMKRRLOQDKVLITELIQHSAKH
KVDIDCSQKVVVYDQSSQDVASLSSDCFLTIVLLGKLEKSFNSVHLLAGGFAEFSRCFPGLCCEGSTLVPTCISQP
CLPVANIGPTRILPNLYLGCQRDVNLKELMQQNGIGYVLNASNTCPKPDFIPESHFLRVPVNDSECEKILPWLDK
SVDFFIEKAKASNGCVLVHCLAGISRSATIAIAYIMKRMDMSLDEAYRFVKEKRPTTISPNNFLGQLLDYEKKIKN
QTGASGPKSKLKLHLEKPNPVPVAVSEGGQKSETPLSPPCADSATSEAGQRPVHPASVPSVPSVQPSLLEDSP
LVQALSGLHLSADRLEDSENKLRFSLDIKSVSYSASMAASLHGFSSSEDALEYKPSSTLDGTNKLCCQFSPVQE
LSEQTPETSPDKEEASIPKKLQTARPSDSQSKRLHSVRTSSSGTAQRSLLSPLHRSGSVEDNYHTSFLFGLSTSQ
QHLTKSAGLGLKGWHS DILAPQTSTPSLTSSWYFATESSHFYASAIYGGASYSAYSQSCQLPTCGDQVYSVRRR
QKPSDRADSRRSWHEESPFEKQFKRRSCQMEFGESIMSENRSREELGKVGSSFSGSMEIIEVS

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FIGURE 263

AGCTGAAGTTGAGGATCTCTTACTCTCTAAGCCACGGAATTAACCCGAGCAGGCATGGAGGCCTCTGCTCTCACC
TCATCAGCAGTGACCAGTGTGGCCAAAGTGGTCAGGGTGGCCTCTGGCTCTGCCGTAGTTTTGCCCCTGGCCAGG
ATTGCTACAGTTGTGATTGGAGGAGTTGTGGCCATGGCGGCTGTGCCCATGGTGCTCAGTGCCATGGGCTTCACT
GCGGCGGGAATCGCCTCGTCCTCCATAGCAGCCAAGATGATGTCCGCGGCGGCCATTGCCAATGGGGGTGGAGTT
GCCTCGGGCAGCCTTGTGGGTACTCTGCAGTCACTGGGAGCAACTGGACTCTCCGGATTGACCAAGTTCATCCTG
GGCTCCATTGGGTCTGCCATTGCGGCTGTCATTGCGAGGTTCTACTAGCTCCCTGCCCCTCGCCCTGCAGAGAAG
AGAACCATGCCAGGGGAGAAGGCACCCAGCCATCTGACCCAGCGAGGAGCCAACCTATCCCAAATATACCTGGGT
GAAATATACCAAATTCTGCATCTCCAGAGGAAAATAAGAAATAAGATGAATTGTTGCAACTCTTAAAAAAA

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FIGURE 264

MEASALTSSAVTSVAKVVRVASGSAVVLPLARIATVVIGGVVMAAAVPMVLSAMGFTAAGIASSSIAAKMMSAAA
IANGGGVASGSILVGTLQSLGATGLSGLTKFILGSIGSAIAAVIARFY

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FIGURE 265

ATGGGGCTTGGGGCTGGGCGGCCAGACGCTAACTCGGATGCTCCCAGGCTACGCCTTGGCCATGACCCGTGCGGC
CGCGCGCCCCCGCCTTCACCTTCGGCGCGCGCTTCCCCACGCAGCAGACGACGTGCGGCCCCGGGCCAGGCCACC
TGGTGCCCGCTCGCAT**TGA**CCGTGCGCGGCACCGACGGCGCCCCCGCCTACTCCATCTACGGCCGCCCACGCCGCT
CAGCGCCCTTCTCTACTCCGGGACCTGGTCAGGACCCCCGGGCCCTGGCCACCCCAACGCCGAAGTGCCTCCAG
GGAGGCCCCACCTGGGAACCCCGACCTGAACCCCGAGTCCCCCTCGGATACCCCTAACACGATATTCCGGTACCCCC
ATATCCGGATCTCAAATCCCAAACCCCGAACCCACGGGGCTTTGATAAATCGTGGCTCAGACTCCCCACTAGTCC
CAGGACCCCATCTCGGGTACCCACCAGGCTCCACGCAGTTCTAGCCCCCACACCCTTGATCCGCCCCGAGGC
AGGTACTTCCCGGAGCGAGCGGGGAACGCGACGTACCCAGTGCCTCGGCACACCAATTGCTCCCCGAAACTGG
GGTGTCAGGCGGAACAGCAGAGCCAGGTCCCGCGGCCTATACGGTGCCCTCGCTCTTGGGTCCGCGCGTCATC
GGCAAAGTCTCCGCCCCAACTTGCTCCATCTACGGCCGCAGAGCGGCTGGCAGTTTCTTCGAGGACCTCAGCAAG
GTCGTGAGTCCAGGGGTCTACAAGTCCCGGGCCCCCAGTTACGATTCTGGCGCGGACTTCGCTCCCCCAAGAC
AACACTCGGAAGCCAGGGCCCCGCGGCCTACAACGTGGATCAGCACCGGAAGCCCCGCGGCTGGAGTTTCGGGATC
CGGCACTCGGACTACCTGGCCCCGCTGGTGACCGACGCGGACAAGTACCCCGCCAGGCGGGAGCGGCCCCACACG
TGTTTGCTTAAAGTCTGCGAGTCCGCATCGTGTCCGCCTCTCTCTCTCTCTCTCTGCGCGTCTTGGCGCAAGGCC
TGGGGTGGAGCCACGGCTGGGGCCGTGTCCCAACTCCGAACCCAGCGGGCGGGGCCCGAGCGTGGGGCGAGGCC
GGGACCCAGCGCTGCGCCGCGTCCGAACGTGAGACCCACCGAGGGCGGGAGGGGACTCTCGGGAGCCACAG
ACGCCCCAGACCCACGCCGGGCGGGACCGGCCAGGGATACCCCGCCGACGCCCCGGGCCCCGACGGCCCGGA
AGTTCGCGTGTCCGGGGGACCGGGGGATTGGCCGGGGCGCGCGTGCAAGGCTTCCCGGGGGCGGCGACTGCC
GAGTCCGCCCCTCAGGCGGCCCCACCCGCTGCCGTCTTGGGGCGCCGCCGCCCGCCCGCCGCGGCACTGGACCGC
TGTGCGGAACCTGAACCTACGGTCCCGACCCGCGGGCGAGGCCGGGTACCTGGGCTGGGATCCGGAGCAAGC
GGGCGAGGGCAGCGCCCTAAGCAGGTACGGGCGGGGCTCAAGTCGCGAGGCGGGGAAGCGGGAGGCAGACACGGA
CGAGGGCGACACAGACACGGGACCGAGGGGCGGACACCGGAGAGACACGGGAAAGGGGTGGGGACAGGAGCACGT
GGCTCAGACACCGACGCCGGGAGGCCGAGACCCCGGACGTGTCAGGCATCCCCGACGGCCCCGAGCG

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FIGURE 266

MGLGAGRPDANS DAPRLRLGHDP CGRAPPPSP SARASPRSRRAAPGQATWCPLA

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FIGURE 267

AGACTGACCACTAGCCGACGCGGGCGAGAGGGACAGGAGCGTGACCTCCCCATCCCGAGGGGCGGACGCTCGGG
CGCCTCCCCGCTCCCCCACTCGGAGGCCGCGCGCGCCGTTAGCCCCCTTCCTCGCTCCCCCGCCCCAGTCCCGCA
GTCCGGGAGGCGGGGTCGGCAGCCGGCTGAGTGGAACCGCGCGGTGTCTGAGGAGGCAGTCGGCGACCGGTTT
CCACTTCAAGCGTGACCCTTTTGCCTGTGGGATGAGCTCCAGCATGGGGTGAGGTACAGAAGAGAGACTTGAAGA
GCGTGCCCTTGGGACTCAAGCGCCAAACCTGTACCCTAGCGAGTGTCTACTCCGCATCCGTAATGGAAGGAAATG
CACATCTTACTCCAGAGGCACAAGAGGAGGACATCCCATGCGGCTACTCTGCCAGCGTGGTGGGGCAGCAGAA
GCTCCAGAGCCCAGACTTGCAGGCTCACGGTGCAGGGTGAACCTGGCCACAGCTCACCTTGAACAGCCACAATG
TCTGCCCTTAGAGAAGAACCCTGAAATCAGACCAGTTTTTGGCGCTCCCCCTTCTCTCTGTACAGTGCCC
TTTCCAGGCCTTAAGAGAAGTAAACTTAGCTGCAGCGCCAGGAGGTGGACCCAGAGTGTGAGTGGCAGCTTC
CCTGTGAACCCGTCCTCACCATGTTTGCCACATCTGGGGCAGTGGCAGCGGGGAAGCCTTACTCGTGACGCAAT
GTGGCAAGAGCTTCTGCTACAGCTCAGTGCTGCTGCGACATGAACGAGCTCACGGCGGTGACGGCGCTTCCGTT
GCCTAGAATGCGGTGAGCGCTGTGCACGGGCTGCTGACCTCCGAGCGCACAGGCGCACGCATGCTGGCCAGACCC
TCTACATCTGCAGTGAGTGGGACAAAGCTTCCGCCACAGCGGCCGTCTTGACCTACACTTGGGCGCACACCGGC
AGCGATGCCGCACTTGCCCTGCCGCACATGCGGCCGCGCTTCCCGCACCTCCCGGCGCTGCTGCTACACCGGC
GCCGCCAGCATCTGCCAGAGCGGCCCGCGCTGCCGCTGTGCGCCGCACCTTCCGGCAGAGCGCGCTGCTCT
TCCACCAGGCGCGGGCGCACCCCTTGGGGACAACCTCTGACCCTGCTGCCCCACCCACCGCTGCGCGCAGTGCC
CGCGAGCCTTCCGAAGCGGCGCCGGGCTGCGGAGTCACGCGCGCATCCAGTGTCCCGAGCCCCACGCGACCC
GTGTCTCAGACGCCCACCAGTGTGGCGTGTGCGGAAGTGCTTTGGCAAGAGCTCTACGCTGACGCGACACCTGC
AGACGCACTCGGGGGAGAAACCCCTCAAGTGCCCGAGTGCGGCAAGGGCTTCTGGAGAGTGCCACGCTGGTGC
GCCACCAGCGCACACACAGGGCGAGAAGCCGTACGCATGTGGCGACTGTGGACGCTGCTTACGCGAGAGTTCCA
CGCTGCTGCGCCATCGGCGCAGCCATCAGGGCGAGCGGCCACATGCGTGCGCCACTTGCGGCAAGGGTTTCGGGC
AGCGCTCCGACCTGGTGGTGCACCAGCGCATCCACACGGGCGAGAAGCCCTTCGCGTGCCCCGAGTGCGGCGGCC
GCTTCAGCGACCGCTCGGACCTCACCAAGCACCGGCGCACGCACAGGGCGAGAAGCCCTACCGCTGCGAACTGT
GCGGCAAGCGGTTACGTCGCTGTCCAATCTCAACGTGCATCGGCGCAACCATGCCGGCCACAAGCCACACAAAT
GCCCCGAGTGCGCAAGGCCCTTACGCTCGCCTCCAAGCTTGCCTGACCCGCAAGACGCACCTGGGCGAACGGC
CAGCGGAGTGCGCAGAGTGCGGCAAGTGCTTCAGCCACAGCCGCTCGCTGTACAGCATCAGCGGGCCACACGC
GCGCCCGCACCGCTGCCGCCGTTGCCATCCAGTCCGCGAGTGGGCACTGCCCTCGTCTTTGAGGGGCGCGCTGAAC
AGGAAAAGCCAGGGTTCTCTGTGTCCTAGTTGAGGGAGGCTTGCTGAGGCTTCTCTAAAGGTGGTTGGGCAAGCA
CCTATATAGTATCACGGGGACAGTTGAGGCAACTCGTAGATGGAGATTTGGGAAAAGACGATGTGGCCTCCTACC
TTTCCAGTTTTCTGTGGCAGCCCTTACGTAGCCTCCTGCCTCGCCTCTACACCTACTACCTGTGCGCCCTTTT
GCCATGCTGTCTCTGTATAACTCGGATTCTCTCCTCAGGTGTAGGTGCAGGGAGTCAGGGAACCCCTTAGACTCCC
CTGTGTGCAAGAGCCCAGGTGTGGTGTGTCCCTTTAATGCTACTGTGCTCTCTGGTGTCTCTGATTTTCTGCTG
TTTATTCTGTCTTCTCTTGTCTATCTCATTCCAGCCACATCTTCTCCTTTCCTGATTACTTTTGTGTCTGCTG
CTCTTCAGGTAATGGTCACAGATTTGGCTGTAGGCACGTTACCAGCCCTGTGGCTTCTTGACTCTTGGTTCCCTG
TTAACTCTGTTTTCTGAGAAATGTGGGTATGGAGGTGGGTGGGAAAGCTCACTTCCATGAAGGATGTCTCCATGCT
AGGAGCTGCCTGCACCTTGGCAGAGGTGGCCAGTCACGTGAAGGTGGGCAGGGCCCTTAGCATGGCCACACATGT
CCCCAGGGCAGATCAAGGGGCCCTCTCAGAACCATGTTCCCCAGCCAGGTGAGGACCATTTTCACTGGGACCCAGG
CCAAAACCATGTGGGTGCACAAAGCCAGGCACTGCCAAGTGGAACATGAGGTATTTCCAAATCATGGGAGCCAC
CAGCAGGGAGAGGGCAGGATGAAAAATCCCCTGGAGCCGGTCAACTTTTTGCTCATGGCTAGTGAAATAAAGTTG
TTTGAGTACTAAAAAAA

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FIGURE 268

MFATSGAVAAGKPYSCECGKSF CYSSVLLRHERAHGGDGRFRCLECGERCARAADLRAHRRTHAGQTL YICSEC
GQSFRHSGRLDLHLGAHRQRCRTCPCRTCGRRFPHLPALLHRRRQHLPERPRRCPLCARTFRQSALLFHQARAH
PLGTTS DPAAPP HRCAQCPRAFRSGAGLRSHARIHVSRSPTRPRVSDAHQCGVCGKCFGKSSTLTRHLQTHSGEK
PFKCPECGKG FLESATLVRHQRTHTGEKPYACGDCGRCFSESSTLLRHRRSHQGERPHACATCGKGFGQRSDLV
HQR IHTGEKPFACPECGRRFSDRSDLT KHRRTHTGEKPYRCELCGKRFTCVSNLNVHRRNHAGHKPHKCPECSKA
FSVASKLALHRKTHLGERPAECAECGKCFSHSRSLSQHQR AHTRARTAAVAIQSAVGTALVFEGPAEQEKPGFS
VS

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FIGURE 269

GGCCGTGCCTTCTCTCGCTTCGGACTGCGCAACGCTGCGCTCTGGGCTGACAGGCGGATAAAACGGTCCCATCAA
GACTGAGAAAAAGCACACCAGCTATTGGCACAGCGTGGGCAGTGGGGCCTACAGGATGACTGACTTAGTCTACAG
AGATCCCGGCGTACTTAAGCAGATGAAGACTCTTAAGATGACAGAAGGTGATTTTCTGGTGATCGAGGACTTCC
GGGGTAATGACAGTGATGAAATGCAGGGGACCTGGTTGCCCCCAAGTTTCCTGGCAGTGTGTGATACTGAGGAGG
TGAGCTTGTTTCTGGAGCTGTGCTTTAAGATTCATGTTACATGTAAAGCTGTCCTCATTGTGACTATGGACCTA
TGGAGTTGGGACAATCTCTATGGGAAGCAGAAGGCAAGGACCCCGGTCATTTTAGGTAGAAACAACAGCATGCTA
ATGCAAAAAATTATGCAGTGTGCTACTGAACTTCAGAGGTGATCAATAAAAGAAGAATAAAAAGACTAATAAAAA
AA

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FIGURE 270

MQGTWLPPSFLAVCDTEEVSLFLELCFKIHVTCKAVLICDYGPMELGQSLWEAEGKDPGHFR

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FIGURE 271

GAGGAACATGATTTTATTGGTTCTTTCAGTTTACCACATCCGACTCGCGTCTCGGCCCTGGCCCCGCTTGCGGAC
CTTAAAGCAGTCAGTCCAGGGTTTGGGGGAAACGTGCTCACCCGACGGCAGCTCACAGGACCCCGGAGAGTCTTG
GCATGGTATCTCGGTCCGACTCTCCGCTGGGCCCCACGAAGGAGAAAGGCTGCCTCGGATTCTGCGCCCCAAGCC
AAGGTCCGGCGCCCCACGGAGGCAAGTCCGGTCTCACGGTGACCTCCCGCTGGCGCCGCTTTCGCCGCCAACCATC
CAGTTCTTCTCCAGGCCACGTTCTCTGCGTGGTTCGCTGCCTCTGAGAGTGGCCAGCAATAGCTGCTGGGTCT
CTGGCCGCTCTCTCCCTGCTCCTTGGGTCTGTCAGTGGCATCTCTGAGGGCAGGAAGGGGAGTTTCGAGGAGCT
CCAGTCCGGGGCTCTCCACCCGCCCCACCTTCTCGGGACTACCAGTTGCTTCTACCTTTAGCATTTCTGCTTC
CGCCGCTCTCCCGGGGTACGATAACGAGGAGCGCGTAGCCACGCCAGCCCTGCGCCAGCATTGCGACTGAG
ATCAGCATTTTCCGCAAGGAATCCATGGCCGCTGCACAGCCAGCGGAGCGCCACGGGAGCTCCCGCAGCCGC
AAGCTGTTGCCGCGCGGTCTCACTACCCCTTGGCGCAGGCTAGAGCGCCCTATAGCAGAAACCATAGATAAGCGG
CCGGCTAGAGAGGACCTGCTCGAGGAAACGTTTGAATCCGGAGCGCTTGGATCTCAGGTTTAGCTGAGGGGGTT
GAGGTGTCCAAGAAGTGTGTCACCAAGGGCTGAGCGCGGGGACCTGTGTCTCAATTCCGGGGTGGGATTGCT
AGGGGGAGAGTGCCTGTCTTTCATGGTTGCCGTGGGTTTTATGATTGCCCATTTTCTGTCTTCCGACGTTTCCCG
ATCAGTAGAGGCCCGAGCTGTGCTCTGTGGTTTCTGTCAGTACCCGCGAGTTTCAACACAGCGCATGGAGGGC
ATCTACACACATACATCCCTCTCCATCCCTCAACTCTGGAACAAACACTCAAAGTCAAGTATACTGGTTGGA
GAAATGGGTAAATAGTTACTTATCTTAAACATTTATTTTACAAACAACCTATTCCTTTCTCGTCATGGTACACAC
TTGGTATTGTTTGGGTTTTTTTTTGGTTTTGTTGTTGTTGTTGTTAGTGTGTGGGCGTGGTTTTGTTTGTGTTTGGAG
ACAAGGTCTCGCTCTGTGCGCCAGGGCTGGAGTGCAGTGGCGCATCATGGCTCACTGAAGCCTCGACTTCCAGG
GCCCCAAGCGATCCTCTGCTCAACCTCCCGGATAGCTGGGATTACAGGCGTGCACCACCACGCCGGCTGGTAT
TGCTTTTTGTTTTGCTTCGTTTTCTTTTTGCTTTTTGAGACAGAGTCTCACTCTGTTGCCAGCTGGAGTGCAG
TGGCGTGATCTCGGCTCACTGCAAGCTCTGCCTCCCGGGTTCACGCCATTCTCTGCTCAGCCTCCCGAGTAGC
TGGGACTACAGGCGCCCGCCACCACGGCCGGCTAAATTTTTGTTTTAGTAGAGAAAGAGTTTCACTATGTAG
GTCAGGCTGGTCTCGAACTCCTGACCTCGTGATCCGCCCAATCCGCCACCTCGGCCTCCCAAAGTGCTGGGATT
ACAGGTGTGAGCCACCGCGCCCGGCTGTTTTGCTTTGTTTTCAACCATAAAAGGCTGGATTTCGTGTAACATACT
GAATTCTGCTTTACAGAAGAAAACACCTCTTAGCTGTGTGACTGATTATAGGCAAGTCTTGTGCCCCGGTTTTCT
GCATCAGAAAATGAAGCTTATAACAACAGTACTTGTCTCACAGTTTTAGGATAATTAAATTAGTTATATGTAAAG
CAATTAACACAGCTCCTGCCAAAGAGTAAACACCATATAAATATTCATTAAATAACATACAAACATACCAGGTTG
GGAAAATCAGTAAGCATAGGAGTCAGGAAATTCGAAGTTGGTTATCACAACTCTTGGCCACAGGGCTTTAATC
CAGGTGCCCTTGTCTCCTACCCTTGTGTCATCCAGTGTCTCCAGGGAGTAAGTAGAAATAAAGATCCTATCTC
ACCTCTTGGGCATTTTCCCTGCGCTGAAAGCGTATAATCGCTTAGCACAGTCGGTGCTTAAGGGGCCAGGCTCC
AAAGAAGATTAAAGGAACAGTTTGTGGGGTGCACTGGGCAGCAGTACTCTCTCTGAGTTCAATCATCTTGCAT
CTAAGAATCACCACCATGGCCCTTGTGCCAGGGAGAAGCAAGGAGGATGGGCTTTGGACTAGAAATAGCCAGGC
TCCTCCAGCATCCAGAAAGTCCAGGCTGCCCAACCCTCTCTGGGACAGAGGAAAAATTGGCAAGGTTGAAGGT
CACCAGCACATTAGGATTTCTCTCAAAAGTCCCATCTGCCGTCTATTGTGGTGGAATCCAGTGAGGTGAATGAA
GAGAGTGGGGATCTCCATTTGCCCATGAGGAGCTGCTGCTGCTCACTGATGGTGAGGAAGAGGATGCTGAGGCC
TTCTTCCAAGACCAAAGTGAAGAGCCAGGCTGGGCTTGGAGCCACAGGACCCTAGAAGTCCTTTAAGAACATTT
AACGCTGGACTCAGCTGGGGGCAGGACCAGGATGAAGAAGATGCTTGTGATTCTTGAGGACACAGCATGTCTG
GAAGCCACCAACCCTGTCCCTTCTGGGACTCAACAGGCTCCCGTGTGTTAGAAAGTGGCTTTGTGGAATATTCC
CATCTCCTGCCTCCTAATAGCTTTGAGGGAGCTGAAGAAGAAGCTGTTCAAACGCCGGCGGGTGTGTAATCGGGA
GCGGCGTCTGAGGACCCGGGTGGTGGGGCTGTGATAGACCAAGGGCTGATCACGCGGCACCACCTCAAGAAGCG
GGCGTCCAGTGCAGTGCCAAACATTACACTGTGAGGGAAGAAGCGCAGAAACTCCTCCAGCAGATCCGGCTTGC
CCAGAAAGAGAAGACAGCCATGGAAGTGGAAGCCCCCTTCAAAGCCAGCCAGGACTAGTGAACCACAGCTCAAAAG
GCAAAAGAAGACAAAAGCCCCCAGGATGTAGAAATGAAGGACCTTGAAGATGAGAGCTAAACCTCTTCCACTAG
AAGATTCTCAACTGGAGCCAGCCTTCAGACTCAGTGGTTGTTTCAGAGGACTTTGACAAAAGCAAGGCCCTTTT
CACTCTCCAGATTTCTCTACCTAATGGCCTACTGACCTCCCTAGAGGGATGTCTTTGGGAGGGAAGAAGGTA
CAGAAGAAAGATTGGAGAAGGGCTCTCTAGCAGTCAACTCCATTTGTAATAAGCCCTAGCACTCTGAAAAAAA
AAAAAAAAAAAA

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FIGURE 272

MKKMLVGFLRTQHVKPPTTVPSGTQQAPVFVEVALWNIPISCLLIALRELKKKLFKRRRVLNRRRLRHRVVG
VIDQGLITRHHLLKKRASSARANITLSGKKRRKLLQQIRLAQKEKTAMEVEAPSKPARTSEPLKRQKKTKAPQDV
EMKDLEDES

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FIGURE 273

CTCACTGAATCTGCCTTAGTGAGAAATGTCACCTTATTGCTTATATTAATGCAGATGTCTTTCTCTGCCCTCC
TTGTTTCCAGATTGTACCATCATAATCAACCCTTCATAGGGCTTCCTATCAGAGCAGAGGTTCTAATGACTCTCT
ATTCCCTGCAGGATGAAGTGAAACTCTTTAGTATGGCCGTGTGTTTCCATGACTCGCCCCCTGCCTACATCCATG
GCTTCATCTACTACCTTTCCCCTCACAATGGTCTCTCCTTAGTAGATAGTGAAATATTAGTGTACTATTCTTTTT
ACATGAAAATGACATAGTGAAAGAGAAGGACTAGTTTAGCCTGTCTTGCAGAAAGAATGAAGAATAAATAATGA
CATACTTGAAAGTAACAGACATGGATTTGAACCCTAGATTTGCCATGAAATGTCTGAATGCCTTTGGTCAATTTA
CATAATGGCAGAAAGCCTTACAAATTCCTAGTGAAGATTAACTCAATAACGCGGGCAAAGTGCTTAACAAAATT
GCTGGAACATAGTACACCTCTACATGCTCAATAAATGGGAGTTAATTACCTTTTTTACCTCCCCTTCCCTTCCCA
AATAGTATGCATTACCTTTTAAATTTTAAATTGAGAAGTTTACAGTTGAATTAAAAAATGCAATGAATCACA

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FIGURE 274

LTESALVRMSLPYCLY

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FIGURE 275

AGGGGAGAGCGGCCCGCCGCTGCCGCTTCCACCACAGTTTGAAGAAAAACAGGTCTGAAACAAGGTCTTACCCC
CAGCTGCTTCTGAACACAGTGACTGCCAGATCTCCAAACATCAAGTCCAGCTTTGTCCGCCAACCTGTCTGACAT
GTCGGGACCCGTGCCAAGCAGGGCCAGAGTTTACACAGATGTTAATACACACAGACCTCGAGAATACTGGGATTA
CGAGTCACATGTGGTGAATGGGGAAATCAAGATGACTACCAGCTGGTTCGAAAATTAGGCCGAGGTAAATACAG
TGAAGTATTTGAAGCCATCAACATCACAATAATGAAAAAGTTGTTGTTAAAATTCTCAAGCCAGTAAAAAGAA
GAAAATTAAGCGTGAATAAAGATTTTGGAGAATTTGAGAGGAGGTCCCAACATCATCAGACTGGCAGACATTGT
AAAAGACCCTGTGTACGAACCCCGCCTTGGTTTTTGAACACGTAAACAACACAGACTTCAAGCAATTGTACCA
GACGTTAACAGACTATGATATTCGATTTTACATGTATGAGATTCTGAAGGCCCTGGATTATTGTCACAGCATGGG
AATTATGCACAGAGATGTCAAGCCCCATAATGTCATGATTGATCATGAGCACAGAAAGCTACGACTAATAGACTG
GGGTTTGGCTGAGTTTTATCATCCTGGCCAAGAATAATGTCCGAGTTGCTTCCCGATACTTCAAAGGTCCTGA
GCTACTTGTAGACTATCAGATGTACGATTATAGTTTGGATATGTGGAGTTTGGGTTGTATGCTGGCAAGTATGAT
CTTTTCGGAAGGAGCCATTTTCCATGGACATGACAATTATGATCAGTTGGTGAGGATAGCCAAGGTTCTGGGGAC
AGAAGATTTATATGACTATATTGACAAATACAACATTGAATTAGATCCACGTTTCAATGATATCTTGGGCAGACA
CTCTCGAAAGCGATGGGAACGCTTTGTCCACAGTGAATAATCAGCACCTTGTGAGCCCTGAGGCCTTGGATTTCCT
GGACAAACTGCTGCGATATGACCACCAGTCACGGCTTACTGCAAGAGAGGCAATGGAGCACCCCTATTTCTACAC
TGTTGTGAAGGACCAGGCTCGAATGGGTTTCATCTAGCATGCCAGGGGGCAGTACGCCCGTCAGCAGCGCCAATAT
GATGTCAGGGATTTCTCAGTGCCAACCCCTTACCCCTTGGACCTCTGGCAGGCTCACCAGTGATTGCTGCTGC
CAACCCCTTGGGATGCCTGTTCCAGCTGCCGCTGGCGCTCAGCAGTAAACGGCCCTATCTGTCTCCTGATGCCTG
AGCAGAGGTGGGGGAGTCCACCCCTCTCCTTGATGCAGCTTGCCTGGCGGGGAGGGGTGAAACACTTCAGAAGC
ACCGTGTCTGAACCGTTGCTTGTGGATTTATAGTAGTTCAGTCATAAAAAAAAAAATTATAATAGGCTGATTTCT
TTTTTCTTTTTTTTTTAACTCGAACTTTTCATAACTCAGGGGATTCCCTGAAAAATTACCTGCAGGTGGAATAT
TTCATGGACAAATTTTTTTTTCTCCCTCCCAAATTTAGTTCCCTCATCACAAAAGAACAAAGATAAACCAGCCTC
AATCCCGGCTGCTGCATTTAGGTGGAGACTTCTTCCCATTCACCATTGTTCTCCACCGTCCCACACTTTAGG
GGGTTGGTAICTCGTGCTCTTCTCCAGAGATTACAAAATGTAGCTTCTCAGGGGAGGCAGGAAGAAAGGAAGGA
AGGAAAGAAGGAAGGGAGGCCCAATCTATAGGAGCAGTGGACTGCTTGCTGGTCGCTTACATCACTTTACTCCA
TAAGCGCTTCAGTGGGGTTATCCTAGTGGCTCTTGTTGGAAGTGTGTCTTAGTTACATCAAGATGTTGAAAATCTA
CCCAAATGCAGACAGATACTAAAACTTCTGTTTCAGTAAGAATCATGTCTTACTGATCTAACCTAAATCCAAC
TCATTTATACTTTTATTTTGTAGTTTCAGTTTAAAATGTTGATACCTTCCCTCCAGGCTCCTTACCTTGGTCTTT
CCCTGTTTCATCTCCCAACATGCTGTGCTCCATAGCTGGTAGGAGAGGGAAGGCAAAATCTTCTTAGTTTTCTTT
GTCTTGGCCATTTTGAATTC

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FIGURE 276

MSGPVPSRARVYTDVNTHRPREYWDYESHVVEWGNQDDYQLVRKLGRGKYSEVFEAINITNNEKV VVKILKPVKK
KKIKREIKILENLRGGPNIITLADIVKDPVSRTPALVFEHVNNTDFKQLYQTLTDYDIRFYMYEILKALDYCHSM
GIMHRDVKPHNV MIDHEHRKRLRLIDWGLAEFYHPGQEYNVRVASRYFKGPPELLVDYQMYDYS LDMWSLGCLASM
IFRKEPFFHGHNDYDQLVRIAKVLGTEDLYDYIDKYNIELDP RFNDILGRHSRKRWERFVHSENQHLVSPEALDF
LDKLLRYDHQSRLTAREAMEHPYFYTVVKDQARMGSSSM PGGSTPVSSANMMSGISSVPTPSPLGFLAGSPVIAA
ANPLGMPVPAAAGAQQ

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FIGURE 277

AGGTTAATCTTAAAAGCCAGGTTACCCGCGGAAAATTTATGCTGTCCGGTCACCGTGACAATGCAGCTGAGGAAC
CCAGAACTACATCTGGGCTGCGCGCTTGCGCTTCGCTTCCTGGCCCTCGTTTCCTGGGACATCCCTGGGGCTAGA
GCACTGGACAATGGATTGGCAAGGACGCCTACCATGGGCTGGCTGCACTGGGAGCGCTTCATGTGCAACCTTGAC
TGCCAGGAAGAGCCAGATTCCCTGCATCAGTGAGAAGCTCTTCATGGAGATGGCAGAGCTCATGGTCTCAGAAGGC
TGGAAGGATGCAGGTTATGAGTACCTCTGCATTGATGACTGTTGGATGGCTCCCCAAAGAGATTGAGAAGGCAGA
CTTCAGGCAGACCCTCAGCGCTTTCCTCATGGGATTCGCCAGCTAGCTAATTATGTTACAGCAAAGGACTGAAG
CTAGGGATTTATGCAGATGTTGGAAATAAAACCTGCGCAGGCTTCCTGGGAGTTTTGGATACTACGACATTGAT
GCCCAGACCTTTGCTGACTGGGGAGTAGATCTGCTAAAATTTGATGGTTGTTACTGTGACAGTTTGGAAAATTTG
GCAGATGGTTATAAGCACATGTCCTTGGCCCTGAATAGGACTGGCAGAAGCATTGTGTACTCCTGTGAGTGGCCT
CTTTATATGTGGCCCTTTCAAAGCCCAATTATACAGAAATCCGACAGTACTGCAATCACTGGCGAAATTTTGCT
GACATTGATGATTCTTGAAAAGTATAAAGAGTATCTTGGACTGGACATCTTTAACCAGGAGAGAATTGTTGAT
GTTGCTGGACCAGGGGGTTGGAATGACCCAGATATGTTAGTGATTGGCAACTTTGGCCTCAGCTGGAATCAGCAA
GTAACTCAGATGGCCCTCTGGGCTATCATGGCTGCTCCTTTATTCATGTCTAATGACCTCCGACACATCAGCCCT
CAAGCCAAAGCTCTCCTTCAGGATAAGGACGTAATTGCCATCAATCAGGACCCCTTGGGCAAGCAAGGGTACCAG
CTTAGACAGGGAGACAACTTTGAAGTGTGGGAACGACCTCTCTCAGGCTTAGCCTGGGCTGTAGCTATGATAAAC
CGGCAGGAGATTGGTGGACCTCGCTCTTATACCATCGCAGTTGCTTCCCTGGGTAAAGGAGTGGCCTGTAATCCT
GCCTGCTTCATCACACAGCTCCTCCCTGTGAAAAGGAAGCTAGGGTTCTATGAATGGACTTCAAGGTTAAGAAGT
CACATAAATCCCACAGGCACTGTTTTGCTTCAGCTAGAAAATACAATGCAGATGTCATTAAAAGACTTACTTTAA

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FIGURE 278

MQLRNPELHLGCALALRFLALVSWDIPGARALDNGRLARTPTMGWLHWERFMCNLDCQEEPDCISEKLFMEMAEL
MVSEGWKDAGYEYLCIDDCWMAPOQDSEGRLOADPQRFPHGIRQLANYVHSGGLKGLGIYADVGNKTCAGFPGSFG
YYDIDAQTFADWGVDLLKFDGCYCDLENLADGYKHMSLALNRTGRSIVYSCEWPLYMWPFQKPNYTEIRQYCNH
WRNFADIDDSWKSISILDWTSFNQERIVDVAGPGGWNDPDMLVIGNFGLSWNQVQTQMALWAIMAAPLFMSNDL
RHISPAKALLQDKDVIAINQDPLGKQGYQLRQGDNFEVWERPLSGLAWAVAMINRQEIGGPRSYTIAVASLGKG
VACNPACFITQLLPVKKRLGFYEWTSLRSHINPTGTVLLQLENTMQMSLKDLL

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FIGURE 279

TGTTCACTCCCCGAGGTCCATGCAGGTTACAAGTGGCACCCCCAACAGCAACAGGATCGGGTGCTCTGCATAGT
GGCATCCGAACACAGGACTTCGAGGACATGAATGAAGAAAGTCCGCTGGAGCAGAGGAACTGAAATGACAAGGCG
AATGGGGACCCCCGAAACGAGTCTGCCAGCAGCAGAGATAAGGTCAAGTCCCTAAAGAGGTACTGATCAGTGCCGT
AAAGAGGTACTGGGAGCAGTGCTTTAAAGAAGTACTAGGAACAGGAAGTTTTCTGAATCAGGCTAACAAGGGGAA
GAATTTGTCTATTGAAGAAAAACATTATGTGCAGTTGCTTAAAGTTCTGTAGAGACAGTCTGGAGCTTAGGTTAA
TTCGCAGACACTAACCTCCTGCAGAAGCCACAAAAGGTTATTACGCATAACCCATGGTTCACAGGCAGGCATC
CTTGATATGGAAAATTGAGACAAAGCAGGAGAAGGATTAAAACAGGCTCATCAAAAAGGTCTTAGCTGATTCTTA
GTTGATTCTTCTGTTTTCTCCACTTGGAGTTTAGTTTGTACTGTACTTCTACCATTATCTCCTTATTATTCTGTG
GGACAACAGCCTGAATCTAAAAATCTGAAAGAATATGTTGTCCCACCCACAGCTCCAATTGAAAATAAAAAACAG
AGAGGATAAAAAATTGGCCTATACCGCCTCCTCCAATTGCAGAAACATCTGTACTGCCTCCTTCAGTAGCACAAAT
AGAAACCCCAATACAAAGAATTTTACGCTCTGCTGTCATAGCTGGAGAGCCCTTAGGACCTTGCCTGTTCCTGT
TTCCATAAGGCCTGATCCCAATAATCCACAGCAGTTTATTTCATGAACACACCCCACTAGAATTTTCAGTTGTTGAA
GGAATTAAAAACTAGTGTGGTCAATAATGGAGTACAAAGCCCATGGTTCCCAGAGGAAAGAACTAGATGTAGA
ACTCTGGGAACAAGTGGGGAGAAATCTTAAACAACATCAGGTGCAAAGGCATCAGGTCCCAGTAAAAATCTTTAAT
GTTATGGGCTTTAATTAGAGCAGCCCTGGCTCAGTTACACACAGAAGAGCCTAAAAAGAGGAAGGAGGAGAAAAAT
GTCACCTGCCTTATCACCTCCTCTTCCCTCAGTCCCAATATCACTGGGTCAAATAACAGGAAACGGAGGTCTCA
CCTAAGTCTCCTCCTCCAATAGATAGGAAAAAGGACAGAGGATATGCTATAGCCATCAGTGTGTAGATATGAGT
TCTAAATTTCTCTTTAAAGAATCAGTATGTCAGTATGTTCAATTCTTTGCCTTCTACTTCTAACTTAACTTCCT
CATAAAGCAACCTTTTTTCGATTACCTGCTCCATCTTGACTCATTCCGATTTCTGCTCTGCCATAACCATTTTTTC
CCGCCAAACCACTCACCTGTCACTCTCTTTAAATTAGCCAGTTGGAGTTAGTTTGGCCTGTGTGGTCTAACCTT
AGCCAATAGGGGAATGACACAGCAGCAGGGGCCATGTGCATCAGGGATAAGAACCCTTTCCCTCCCTTGTCAGG
TGTNCACTNAACCATTGCTCCATCTGTAAGGCGCACCTTCTGTAGAAGTACATTGACTTGCTGAGAATTAAAAA
GNACATTTTA

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FIGURE 280

MLSHPQLQLKIKNREDKNWPIPPPPIAETSVLPSSVAQIETPIQRILRS AVIAGEPLGPCAVPVSIRPD PNNPQQ
FIHEHTPLEFQLLKELKTSVVNNGVQSPWFPEERTLDVELWEQVGRNLKQH QVQRHQVPVKS LMLWALIRAALAQ
LHTEEPKKRKEEKMSPALSPPLPSVPI SLGQNNRKRRSHLSLLLQ

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FIGURE 281

ATGCCTAAATCAAAGGAACCTGTTTCTTCAAGCTCTTCTGGCAGTGATTCTGACAGTGAGGTTGACAAAAAGTTA
AAGAGGAAAAAGCAAGTTGCTCCAGAAAAACCTGTAAAGAAACAAAAGACAGGTGAGACTTCGAGAGCCCTGTCA
TCTTCTAAACAGAGCAGCAGCAGCAGAGATGATAACATGTTTCAGATTGGGAAAATGAGGTACGTTAGTGTTTCGC
GATTTTAAAGGCAAAGTGCTAATTGATATTAGAGAATATTGGATGGATCCTGAAGGTGAAATGAAACCAGGAAGA
AAAGGTATTTCTTTAAATCCAGAACAATGGAGCCAGCTGAAGGAACAGATTTCTGACATAGATGACGCAGTAAGA
AAGCTGTAA

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FIGURE 282

MPKSKELVSSSSSGSDSDSEVDKKLKRKKQVAPEKPVKKQKTGETSRALSSSKQSSSSRDDNMFQIGKMRYVSVR
DFKGKVLIDIREYWMDPEGEMKPGRKGISLNPEQWSQLKEQISDIDDAVRKL

FIGURE 283

[illegible]

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FIGURE 284

MPVAVGPGYQSQPSCFDRVKMGFVMGCAVGMAAGALFGTFSLRIGMRGRELMGGIGKTMMSGGTFGTMAIGM
GIRC

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FIGURE 285

GCGCCAGCCTGCCAGCCGCGCTGCTGCTCCTCCTGCTGTGGGACCGCTGACCGCGCGGCTGCTCCGCTCTC
CCCGCTCCAAGCGCCGATCTGGGCACCCGCCACCAGCATGGACGCTCGCCGCGTGCCGCAGAAAGATCTCAGAGT
AAAGAAGAACTTAAAGAAATTACAGATATGTGAAGTTGATTTCATGGAAACCTCGTCATCCTCTGATGACAGTTG
TGACAGCTTTGCTTCTGATAATTTTGCAAACACGAGGCTGCAGTCAGTTGCGGAAGGCTGTAGGACCCGCAGCCA
GTGCAGGCACTCTGGACCTCTCAGGGTGGCGATGAAGTTCCAGCGCGGAGTACCAGGGGAGCAACCAACAAAAA
AGCAGAGTCCC GCCAGCCCTCAGAGAATTCTGTGACTGATTCCAACCTCCGATTGAGAAGATGAAAGTGGAATGAA
TTTTTTGGAGAAAAGGGCTTTAAATATAAAGCAAAACAAAGCAATGCTTGCAAAACTCATGTCTGAATTAGAAAG
CTTCCCTGGCTCGTTCCGTGGAAGACATCCCTCCCAGGCTCCGACTCACAATCAAGGAGACCGCGAAGGCGTAC
ATTCCCGGGTGTGCTTCCAGGAGAAACCCTGAACGGAGAGCTCGTCCTCTTACCAGGTCAAGGTCCCGGATCCT
CGGGTCCCTTGACGCTCTACCCATGGAGGAGGAGGAGGAAGAGGATAAGTACATGTTGGTGAGAAAGAGGAAGAC
CGTGGATGGCTACATGAATGAAGATGACCTGCCCAGAAGCCGTCGCTCCAGATCATCCGTGACCCTTCCGCATAT
AATTGCCCCAGTGGAAGAAATTACAGAGGAGGAGTTGGAGAACGCTCTGCAGCAATTCTCGAGAGAAGATATATAA
CCGTTCACTGGGCTCTACTTGTCAATGCCGTCAGAAGACTATTGATACAAAACAACTGCAGAAACCCAGA
CTGCTGGGGCGTTTCGAGGCCAGTTCTGTGGCCCTGCCTTCGAAACCGTTATGGTGAAGAGGTGAGGGATGCTCT
GCTGGATCCGAACTGGCATTGCCCGCCTTGTGAGGAATCTGCAACTGCAGTTTCTGCCGCGAGCGAGATGGACG
GTGTGCGACTGGGGTCCTTGTGTATTTAGCCAAATATCATGGCTTTGGGAATGTGCATGCCTACTTGAAAAGCCT
GAAACAGGAATTTGAAATGCAAGCATAATACTGGAAAATTTGCTGCCTGCCTTCTACTTCTCAAATCTTTCTTG
TAAAAGTTTCCAATTTTTCCTGAAACCTGAGTTAAAAATCTTGATGATCAGCCTGTTTCATAAGAACTCCAA
TCAAGTTAATCTTAGCAGACATGTGTTTCTGGAGCATCACAGAAGGTATATTGCTAGTTACACTTTGCCCTCCTG
CAGTTTCTTCTGCTCCCAACCCCATCTCATAGCATCCCCCTCTATTTCGAATGCTCCTCTCCAACCGCTTAG
TTTCTGAATTTCTTTTAAATTACAGTTTTATGAAAGCATATTTTATTACTTGGTGTGAAATAGCCCTCATAAA
ACCTAAGCACTTGGAACACAATAATAGTATTAAC TAACTAGATCTATTGAATTTGAGAGAAGAGCCTTCTAACT
TGTTTACACAAAAACGAGTATGATTTAGCATTCTACTAGTTGAAATTTTAAATAGAATCAAGGCACAAAAGTCT
TAAAACCATGTGGAAAAATTAGGTAATTATTGCAGATTGATGTCTCTCAATCCCATGTATTGCGCTTATGTTACA
AGTTGTTGTACAGTTGAGACTTAATTTCTCCTAATTTCTTCTGCCCCGAAGGGTAAGTGGTGCCTCAGCTTACA
CAATCATAATTCAAAGGTTGGTGGGCAATGTAATACTTAATTAATAATGATGGAAGAGCTATCTGGAGATTAT
GAGTAAGCTGATTTGAATTTTTCAGTATAAACTTTAGTATAATTGTAGTTTGCAAAGTTTATTTAGTTTCACATG
TAAGGTATTGCAATAAATCTTGGACAATTTTGTATGGAACTTGATATTAAAAACTAGTCTGTGGTTCTTTGC
AGTTTCTTGTAATTTTATAAACCAGGCACAAGGTTCAAGTTTAGATTTTAAAGCACTTTTATAACAATGATAAGTG
CCTTTTGGAGATGTAACTTTTCAGAGTTTGTAAACCTGACATCTCTGCCAGTCTAGTTTCTGGGCAGGTTTCTT
GTGTCAGTATTCCCCCTCCTCTTTGCATTAATCAAGGTATTTGGTAGAGGTGGAATCTAAGTGTGTTGTATGTCCA
ATTTACTTGATATGTAAACCATTTGCTGTGCCATTCAATGTTTGTATGCATAATTGGACCTTGAATCGATAAGTGT
AAATACAGCTTTGATCTGTAATGCTTTTATACAAAAGTTTATTTAATAATAAAATGTTTGTCTAACTTGTCT
GCTTTTTTAAAAATAATCTTACTGTACTTAATTCTAATTTTTTCTCATATTTAAATAAAAGGCCATTTCCACCT
TTTCT

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FIGURE 286

MDARRVPQKDLRVKKNLKKFRYVKLISMETSSSSDDSCDSFASDNFANTRLQSVREGCRRSQCRRHSGPLRVAMK
FPARSTRGATNKKAESRQPSSENSVTDSNSDSEDESGMNFLEKRALNIKQNKAMLAKLMSELESFPGSFRGRHPLP
GSDSQSRRPRRRRTFPGVASRRNPFERRARPLTRSRSRILGSLDALPMEEEEEEDKYMLVRKRKTVDGYMNEDDLPR
SRRSRSSVTLPHIIRPVEEITEELENVCSNSREKIYNRSLGSTCHQCRQKTIDTKNCRNPDCWGVRGQFCGPC
LRNRYGEEVRDALLDPNWHCPPCRGICNCSFCRQRDGRCATGVLVYLAKYHGFGNVHAYLKSLSLKQEFEMQA

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FIGURE 287

GCTCCGGGAGACTTCCGGCAGGGCGGGCGCGGGGTCTTGGCGAACGGTCTTCGGAAGCGGGCGGCGCGGATGAC
CACGCTACGGGCCTTTACCTGCGACGACCTGTTCCGCTTCAACAACATTAACCTGGATCCACTTACAGAACTTA
TGGGATTCCCTTTCTACCTACAATACCTCGCCCACTGGCCAGAGTATTTTCATTGTTGCAGAGGCACCTGGTGGAGA
ATTAATGGGTATATATTATGGGTAAAGCAGAAGGCTCAGTAGCTAGGGAAGAATGGCACGGGCACGTCACAGCTCT
GTCTGTTGCCCCAGAATTTTCGACGCCTTGGTTTGGCTGCTAAACTTATGGAGTTACTAGAGGAGATTTTCAGAAAG
AAAGGGTGGATTTTTTGTGGATCTCTTTGTAAGAGTATCTAACCAAGTTGCAGTTAACATGTACAAGCAGTTGGG
CTACAGTGTATATAGGACGGTCATAGAGTACTATTTCGCCAGCAACGGGGAGCCTGATGAGGACGCTTATGATAT
GAGGAAAGCACTTTCCAGGGATACTGAGAAGAAATCCATCATACCATTACCTCATCTGTGAGGCCTGAAGACAT
TGAAATAACCTGGGCAGTGGTTCTTAGGCAGATACTCTAGATGCTTTATGGACAATATTATTTTCATTGGATGAT
TCTGGAGCTCTATTAGGAGAAAAGTAATCATTTTAGGTCTTAAAGACTTCAAGAAAATACAGGTTATCAATTTAT
TTTAAATCTCATTGTTTCCAGTTAGCAATATCATACCTATTAAAGCTGTTTCATTGTAACAAAATTCATCAAAAA
GGCAGCTAGGTCAGAAGGAAACATAACCACTCTCATGGTTCATAGTATTCACTGTATGTATGCTAGGGAAAAGACT
TGCTCCAGTCTCCTCCTCAGTTCTGTGCCTGAGAACCCTGCTGCATATATTTGTTTTTAAATTTTGATTGAAC
TGTTAATTGAAGCTTTAAAAGCATATATGAAATGTATAAATCTAAGATGTATAATACATTATTGACTCTAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 288

MTTLRAFTCDDLFRFNNINLDPLTETYGIPFYLAHWPEYFIVAEAPGGELMGYIMGKAEGSVAREEWHGHVT
ALSVAPEFRRLGLAAKLMELLEISERKGGFFVDLFVRVSNQVAVNMYKQLGYSVYRTVIEYYASNGEPDEDAY
DMRKALSRDTEKKSIIPLPHPVRPEDIE

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FIGURE 289

GTGCTCGGCGTTGAGCTCCTGCAGCCGCCGCCGCTGCAGTGGTCGTCCCTGCCCTCCCCGGCCCCGGGGTGCACC
CCGCAAGGCTCCCGCTGGTGTCCCTGGAGCATGGGAGGCTGCTGAGCGTGAGTGGCGGTGTCTGGCAGGAGCTGC
GTGGCAGGGAGGGCGTCCATGGGCTGCAGCCAACAAGGGCAACAAGCCCAGAGTCCGGGGTATCCGCTTTGCGGCA
GGCCACGATGCAGAAGGATCCCACAGCCACGTCCACTTTGATGAGAAGCTGCATGACTCGGTGGTCATGGTCACC
CAGGAGAGTGACAGCAGCTTTCTGGTCAAGGTTGGCTTCCTGAAGATCCTGCACAGGTATGAGATTACCTTCACT
CTGCCCCCAGTGCACAGGCTGAGCAAGGATGTCCGCGAGGCACCTGTCCCCAGCCTGCACCTCAAGCTCCTCAGC
GTGGTGCCCGTCCCTGAAGGTTATAGTGTCAAGTGTGAGTACTCGGCGCACAAAGAGGGCGTCCCTCAAAGAGGAG
ATACTGCTAGCCTGCGAAGGTGGCACTGGCACCTGTGTGCGCGTGACGGTGCAGGCCCCGCGTCATGGACCGGCAC
CACGGCACGCCCATGCTGCTGGATGGTGTCAAGTGTGTGGGCGCCGAGCTGGAATACGACTCAGAGCACAGCGAC
TGGCACGGCTTTGACTGAGGCCCCGAGGCCCCGCCTGCCCCGGGGCCCCCTCAGCCTTAAACCCCGCCTTGTCCTCCC
GACATGCTGCGTGATGGTGTGGCTTCCTCGCCCCCTCTCTGGGGTGGGTGTGGGGGTGGAGTGGCCTTGCCCACGC
CTCTCACCTCTGCCTTCATTTGTGCTGCCACCCTGCCCTCCCTCGTCCTCCTCTCCCACTTCCTCCTCTCTGTG
TGCCTCAGTCTCCTGCCGGAAGAAATGGGTTGATCCCGAAAGGAGGCTGTCTGAGGAAGGGAGAGGGAGGGCCTG
GGGTGGGTCCCCCACTCCCCACCCCAAGCCACAGGGACTCCCACCAGGGTCTGGGAGAGGACGGAGCTGGCTCTG
TGGCGTCGTGGCCCCATTACTGCTGCCTTGCTTCAGCCACCTCTCCTGCCCCCTCCCTAGTCCCCACTGCTGTCCA
CCATGAGTAGGAGGGAGGTGCAGTCCCCAGCCCCCACCCTCAGGTCTGTGTTACTTGGTTTTTTAAGCGACTGGT
TGGGATAGAACCCTAAAGAAATAAACTTCCAGTGGATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAA

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FIGURE 290

MAAANKGNKPRVRGIRFAAGHDAEGSHSHVHFDEKLHDSVVMVTQESDSSFLVKVGFLKILHRYEITFTLPPVHR
LSKDVREAPVPSLHLKLLSVVPVPEGYSVKCEYSAHKEGVLKEEILLACEGGTGTCTVRVTQARVMDRHHGTPML
LDGVKCVGAEEYDSEHSDWHGFD

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FIGURE 291

CTGAGCGGCGGGGGGCGAGTGTGCGCTCGGTCTAGGCACGGCGGGGAGTCGGTGGTCCCTGCGCGATGGCCACCT
CGGTGTTGTGCTGCCTGCGGTGCTGCAGAGACGGGGGGGACTGGCCACATCCCTCTGAAGGAGATGCCGGCCGTGC
AGCTGGACACGCAGCACATGGGAACAGATGTTGTTATTGTAAAGAATGGAAGAAGAATATGTGGAACAGGAGGTT
GTTTAGCCAGCGCACCTTTACATCAAAAACAAAAGCTATTTTGAATTCAAATCCAGTCCACAGGAATCTGGGGTA
TTGGTGTGCAACTCAGAAGGTTAACTTGAATCAGATTCTCTTGGCCGAGATATGCACAGTCTGGTGTATGAGAA
ATGATGGAGCCCTTTACCACAACAATGAAGAGAAAAATAGGCTGCCAGCAAACAGTCTTCCGCAGGAAGGAGATG
TGGTGGGTATTACTTATGACCATGTGCAATTAAATGTATACTTGAATGGAAAAACATGCATTGTCCAGCATCAG
GTATACGAGGGACAGTGTATCCAGTTGTTTATGTTGATGACAGTGCATTTTGGATTGCCAGTTCAGTGAGTTTT
ATCATACGCCTCCACCTGGTTTTGAAAAAATATTATTTGAACAGCAAATCTTCTGAATGTATTTGTTTTTAAAC
TTGTATTTCTGCACTGTTAAAAATGTTTCATCATTTAATAAACTTTACCTGGCCTATAGATGAAAATATATTCT
TAAAAATATGCTTGTTGATGCCGTCTAAGGAACCAATGTATTAGTATACCACCCTGAAGTTGTGATTTAAATA
CTTTATGTTTTGTGAAATGAAAATAAGCATTGTTGGGCAGTTTATTTAATTCTTATTTAAATAAATAGAATTATGGG
TTTAATTAACAGTATAACATGACTATATATACATATATATTTAAAGGGAATTCTTTCTTACATAATATATTTGTT
TTGATAGAGATGTAGAGTTGGGTGGGTGTTTTTGTCACTCTGAAGTTTAGACCTCATTAAATATTTGACATCTAC
AGTTGGATAATTTGCCGCTTAGTGTCTTTTTTATATACAATATAACAAAGTGAGAGAAATTTATATTACTGGC
AATTTCAATTTTGGCAGTCTATTTCTGTATCATGTACCGCTTTTCTTAAACTTAAATTGCTTATTTTGTGTGT
AATGTCATTGCTTTTGATTTGCTTTGTGAAAGGAGATAAACGTTTCAGTAATTGTCAGAGCATTGTTGCCTCA
GGCTGTGTTACCTCAATTCAGAGTAAGTAGTGGTTGATTAGTAATGTAGTATACACTGGCAGACATCTAGAATA
GTATGATGCTTTACATTTAAATGAGGTTATTCTTTTAAGGACTTTTATTGTATGTTTTCTGTAAGGAATAATAA
AATAATTGTAATTAAGGAATATACCATACTATATTAACACATTCTTCTTAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 292

ERRGAVSPRSRHGGGVGGPCAMATSVLCCLRCCRDGGTGHIPKEMPAVQLDTQHMGTDVVIVKNGRRICGTGGC
LASAPLHQNKSYFEFKIQSTGIWGIGVATQKVNLNQIPLGRDMHSLVMRNDGALYHNNEEKNRLPANSLPQEGDV
VGITYDHVELNVYLNKGKMHCPASGIRGTVPVYVDDSAILDQCFSEFYHTPPPGFEKILFEQQIF

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FIGURE 293

AAGAATGTCTCAGGAGGAAGCATGACAGAGATGTTTGTCCAGTTAAACTGGGAGATCAGAGGTATAAAAGTAAG
GATGGGCATTTTTGGACATTGAAGTGTGGGGAAGGACAACAAAAAGCATGAGGAACGTCTGGGCACGTGTAAAGT
GGATATCTCGGCACTCCCTCTGAAGCAAGCCAACTGCCTGGAGCTGCCACTGGACAGCTGTCTGGGGGCTCTCCT
TATGTTGGTCACACTTACACCCCTGTGCGGGGCTCTCCGTCTCTGATCTGTGTGTCTGCCCCCTTAGCAGACCTCAG
CGAAAGAAAGCAGATTACCCAGCGATATTGCTTACAGAACTCCCTGAAAGATGTGAAAGACGTCCGGCATTCTACA
AGTGAAGGTTTTTAAAGGCAGCAGATCTCTTAGCGGCAGATTTCTCAGGGAAGAGTGACCCATTTTGTCTGTTGGA
GTTAGGCAATGACCGACTTCAGACGCATACCGTCTACAAAAACCTCAACCCTGAATGGAACAAAGTTTTTACATT
TCCCATTAAGATATCCATGATGTTTTGGAAGTGACAGTGTGTTGATGAAGATGGAGATAAACCCCCAGATTTTCT
TGGAAGAGTTGCCATTCCCTTGCTGTCCATTAGAGATGGACAACCGAATTGTTATGTACTAAAGAATAAAGATT
AGAACAAGCTTTTAAAGGAGTTATTTACTTAGAGATGGACCTTATATATAATCCGGTGAAAGCAAGTATTAGGAC
TTTTACTCCCCGGGAAAAGCGCTTTGTTGAAGACAGCCGAAGCTGTCCAAAAGATCTTATCAAGAGATGTGGA
CCGTGTGAAAAGAATCACTATGGCAATATGGAATACAATGCAGTTCCTTAAAGCTGCTTCCAGTGGGAATCCAC
ATTAAGAAGTACAATAGCATTTCGCGGTATTTTTGATCACTGTCTGGAATTTTGAAGTATATATGATCCCCCTGGC
ATTGTTGCTGATCTTTGTCTACAATTTTCATCAGACCTGTGAAAGGCAAGGTGAGCAGCATCCAGGACAGCCAGGA
GAGCAGACATAGATGACGAGGAGGATGAAGATGACAAGGAATCTGAGAAAAAGGGTTGATTGAAAGAATCTA
TATGGTACAGGATATTGTTTCAACTGTTCAAAACGTCTTGAGAGAAAATAGCTTCTTTTGGAGAAAGGATTAAGAA
CACATTTAACTGGACGGTCCCCCTTCCCTTTCATCTCTGGCCTGTTTGATTCTGGCAGCAGCCACCATCATTTTGT
TTTCATTCCACTGCGGTACATCATTTTAACTCTGGGGCATAAAATAAATTTACTAAGAAGCTTCGAAATCCCTATTC
CATCGACAATAATGAGCTACTAGACTTCCTCTCTAGGGTACCGTCTGATGTTCAAAAGGTGCAGTATGCAGAATT
GAAACTCTGCAGCAGCCACAGCCCCCTGCGGAAGAAGCGCAGCGCTCTCT**TAG**GGCACACACCGACTTTGGACAGC
AGCACCCAATATTGTGTTTGGTTGAGTAGACCAATGTTATGGCTGTTTCACTGGTACCCAAGGTGTCTTCTGAA
ATGCATGCCCTGTGGCACCCTCTGTATACCTCTCTCCTTACAGTGCACAGACATACACACATGTGCACACACC
CTCATGCATGGGTGTCTTAGTTGCGTAGAGGGTCAGCCAGCGAAAAGCAACAACCCCAAGACTGTGAAAGACTA
ACATCCATTCTGAAATAGGAGATAACAAGGCTGCCATGGATCTGAACACCACCTTCTTGAAGACAGCCAGGAGC
CCACTTGGATTCAAGAGTGACTTTGAACTTGTTTTCACACCTCCAACAGACTCTCATTAAGATTGAGTTATTTCC
GCTCCCCAGCCCCACACTCCTTTTCAAGATTATCGTTTCATGGGCGTAAGTCTCTTCTCAGAGTTAACAAGTCTTTGG
TAGTCATCCTCTGTCCAAATATTGTATATTATTAAGGCAATTTTAAATAATTACCAGAATTAGCTCAAACCTTT
AGGGATCTTTCAGCCATGATTATTAAGGATATGTATGTGAATTTTGGGAAACCTCTCGGTGCTGGATGCCAGCC
TACAGCAGGGTCCATTGCTGGCAATGGATGGCCCAGGAAGTCCCTAGAGATCACTCACTTGAAAAATGAGGGTC
CCATGAAAGTATTTGGTTGCCTTCTGATGCCACTTCTTCTCACTTTACTTTTTGCTTATTTTCAAAATATTATAA
AATGTCAACATATAATTTAGAAAGGCAGGTGGGGGTAGGGGAGAAATGAATGAATAAATTCTCTAGGTATCTAG
AAAGATAAGAACTGAAGACCGAGAGACTAATAAGGCTGCTTACCTAATTATTATAATCATTTTCACTTGCCTGAA
TGTTTTAAGCAGGAAGTAGAAATACTTTGGCTGCCCAAATGTATCTTTTGTTTCTCTTAGAAGTAAATAAGCTA
CATACAATAAAAAATTTATTTAGAAACCCATTTCTAGAAAAATACCACCCAGAGTCCTCATTTGATAGCATCTGT
CTCCTGCAGACCTCATCATTCCACAGTATTTCCCTGCCATGTAAAAATCCTGACTTTGTGCGTATATAAAATGTA
TGCAATTAAGTCTGTTTAAATGATATTTAAGTTTTAAAGACTGTATTTTGTGACACATACTTTGTGCAGTTTTT
ATGTATGTATGTATTATAAAAAAAGTTAAGGTTAAAAAC

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FIGURE 294

MGILDIEVWGKDNKKHEERLGTCKVDISALPLKQANCLELPLDSCLGALLMLVTLTPCAGVSVSDLCVCPLADLS
ERKQITQRYCLQNSLKDVKDVGILQVKVLKAADLLAADFSGKSDPFCLELGNDRLQHTTVYKNLNPEWNKVFTF
PIKDIHDVLEVTVFEDGDGKPPDFLGKVAIPLLSIRDGQPNKYVLKNKDLEQAFKGVIIYLEMDLIYNPVKASIRT
FTPREKRFVEDSRKLSKKILSRDVDRVKRITMAIWNTMQFLKSCFQWESTLRSTIAFAVFLITVWNFELYMIPLA
LLLIFVYNFIRPVKGKVSSIQDSQESTDIDDEEDEDKSEKKGLIERIYMVQDIVSTVQNVLEEIASFGERIKN
TFNWTVPFLSSLACLILAAATIIILYFIPLRYIILIWGINKFTKKLRNPYSIDNNELLDFLSRVPSDVQKVQYAEI
KLCSSHSPLRKKRSAL

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FIGURE 295

GCTGGGAGTACAGGCAACGGGAAGGATTATGGAAAAGACTACACACTTATTTTTCACTTGCAAAGAAAACCTAGG
CTGGAACTCCAAATCAAAGAAGTGGACGAATTTGGAACTATAGTTGCCCTCATTACAAAGGCACCATTTGTCGTT
TATAAAGTACCTAAAGGAAAGATAGTCCCCAACTTGAATCAATCTCTCGTAATTAATGAAAACCATTTCTCAGTTG
CCAATTTGCAAATTACCATTGAAATTGCCAAAGCATAAGAAATTAATCAACCGTACACAGAGTACCAAAAGAGTT
TCTAAGGATCCTGTAGAAGCCCTTTGGGATAACTTGCTCCATTGGCTGGCTGAGGAGCTCTCAGAAGAAAATGCT
GAGTCTCTTTCCCTCAACTCTCCCTCTGCGCCGTAGCACCATTTCAGCTCATCAAACCTCAAGAACCCTGATGATCTC
ACAGAACAGATCCACGAGTTTCTTTGCTTCTGGAAAAAATCGCTTCCAACCTTTCACCGACAAACTTCGCCTCCTG
GCTCGACATCTCCGCAAGATTGGCAGGAGTGATCTTGCAGAAGAGCTCAAATTCAGTGGGAAAATAAAGTGTTT
ACTGAACCACAGCAGTGTTTTGATGTAAA

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FIGURE 296

AGSTGNGKDYGKDYTLIFHLQRKPRLELQIKEVDEFGNYSCPHYKGTIVVYKVPKGKIVPNLNQSLVINENHSQL
PICKLPLKLPKHKKLINRTQSTKRVS KDPVEALWDNLLHWLAEELSEENAESLSSTLPLRRSTIQLIKLKNPDDL
TEQIHEFLCFWKKSLPTFTDKLRLRLARHLRKIGRSDLAELKFKWENKVFTPEPQQCFD

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FIGURE 297

AGGTTCTCTTACATCGACCGCCTAAGAGTCGCGCTGTAAGAAGCAACAACCTCTCCTCTTCGTCTCCGCCATCAG
CTCGGCAGTCGCGAAGCAGCAACCATGCGTGAGTGCATCTCCATCCACGTTGGCCAGGCTGGTGTCCAGATTGGC
AATGCCTGCTGGGAGCTCTACTGCCTGGAACACGGCATCCAGCCCGATGGCCAGATGCCAAGTGACAAGACCATT
GGGGGAGGAGATGATTCTTCAACACCTTCTTCAGTGAGACGGGGCTGGCAAGCATGTGCCCCGGGCAGTGTTT
GTAGACTTGGAACCCACAGTCATTGATGAAGTTCGCACTGGCACCTACCGCCAGCTCTTCCACCCTGAGCAACTT
ATCACAGGCAAAGAAGATGCTGCCAATAACTATGCCCGAGGGGCACTACACCATTGGCAAGGAGATCATTGACCTC
GTGTTGGACCGAATTTCGAAGCTGGCCGACCAGTGACGGGTCTCCAGGGCTTCTTGGTTTTCCACAGCTTTGGT
GGGGGAAGTGGTTCTGGGTTACCTCGCTGCTCATGGAACGTCTCTCAGTTGATTATGGCAAGAAGTCCAAGCTG
GAGTTCTCTATTTACCCGGCGCCCCAGGTTTCCACAGCTGTAGTTGAGCCCTACAACCTCCATCCTCACCACCCAC
ACCACCCTGGAGCACTCTGATTGTGCCTTCATGGTAGACAATGAGGCCATCTATGACATCTGTGCTAGAAACCTC
GATATTGAGCGTCCAACCTATACTAACCCTGAATAGGTTAATAGGTCAAATTGTGTCTCCATCACTGCTTCCCTG
AGATTTGATGGAGCCCTGAATGTTGACCTGACAGAATTCCAGACCAACCTGGTGGCCCTATCCCGCATCCACTTC
CCTCTGGCCACATATGCCCTGTCTCTGCTGAGAAAGCCTACCATGAACAGCTTTCTGTAGCAGAGATCACC
AATGCTTGCTTTGAGCCAGCCAACCAGATGGTGAAATGTGACCCTCGCCATGGTAAATACATGGCTTGCTGCCTG
TTGTACCGTGGTGACGTGGTTCCCAAAGATGTCAATGCTGCCATTGCCACCATCAAGACCAAGCGTACCATCCAG
TTTGTGGATTGGTGCCCCACTGGCTTCAAGGTGGCATCAACTACCAGCCTCCCACTGTGGTGCCTGGTGGAGAC
CTGGCCAAGGTACAGAGAGCTGTGTGCATGCTGAGCAACACCACAGCCATTGCTGAGGCCTGGGCTCGCCTGGAC
CACAAGTTTGACCTGATGTATGCCAAACGTGCCTTTGTTCACTGGTACGTTGGGGAGGGGATGGAGGAAGGTGAG
TTTTTCAGAGGCCCGTGAGGACATGGCTGCCCTTGAGAAGGATTATGAGGAGGTTGGTGTGGATTCTGTTGAAGGA
GAGGGTGAGGAAGAAGGAGAGGAATACTAAAAGTTAAAACGTCAAAAGGTGCTGCTTTTACAGGGAAGCTTATTC
TGTTTTAAACATTGAAAAGTTGTGGTCTGATCAGTTAATTTGTATGTAGCAGTGTATGCTCTCATATACAATTAC
TGACCTATGCTCTAAAACATGAATGCTTTGTTACAGACCCAAGCTGTCCATTTCTGTGATGGGTTTTGAATAAAG
TATTCCTGTCTTAAAAAAAAAAAAAA

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FIGURE 298

MRECISIHVGQAGVQIGNACWELYCLEHGIQPDGQMPSDKTIGGGDDSFNTFFSETGAGKHVPRAVFVDLEPTVI
DEVRTGTYRQLFHPEQLITGKEDAANNYARGHYTIGKEIIDLVLDRIKRLADQCTRLQGFLVFHSFGGGTGSGFT
SLLMERLSVDYGKSKLEFSIYPAPQVSTAVVEPYNSILTTHTTLEHSDCAFMDNEAIYDICRRNLDIERPTYT
NLNRLIGQIVSSITASLRFDGALNVDLTEFQTNLVPYPRIHFPLATYAPVISA EKAYHEQLSVAEITNACFEPAN
QMVKCDP GHGKYMACCLLYRGDVVEPKDVNAAIATIKTKRTIQFVDWCPTGFKVGINYQPPTVVPGGDLAKVQRAV
CMLSNTTAIAEAWARLDHKFDLMYAKRAVHWHYVGEGMEEGEFSEAREDMAALEKDYE EVGVHSVEGE GEEGEE
Y

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FIGURE 299

CACGCTGCTACTTATTTTCTTGAATATGGATACACGGTACTGTTTATGTAATACTTATGTACTTATATAATATGT
AAAACACTGCATAACAGATAACATGAAAAAGAGCTCTGGTATAGTATGAAACATGATTCCAAAACATGGTATCAA
GTATGATGGATTTCATATTAGGTTATTGGAGAAAAGTAAAGTATTTTGAAACACACCTTTACATGTTTATCTTAGC
ATCTGGAAAGACAACCGTTATCTTCTTACAACATACTTCTTGGTACCAATTTCTGGAGATTAAAATTCTAGATTGGC
TAGGCCACGGTTCTGACCCAGTGTGGAAATTCTTATGCCTTAAGGAACTAAACTTAAAATATAAAGGATTACAG
ACTATTTATAAATTTACAAGAATATTTGCTTTGTTTGAATACCTGTTTTCATACAGGAATTTAATATAACATTAA
TATACTGGAGTCCACCAGCATTTTAGGAACTTCTTTGAGATTTTGAACTCCTTTGAAACTTCTTGAGATTTT
GAAAATCAAAGAATTATTTGTGGAAAAGGGAAGAAAATGCCTTCATTCAACACGTTTATTGGACCCTGAATGTGT
GAGACATTGTTGTAGGTAGCGTAGATACAGATATGTGCTAAATAAATACATACATAAGACCATTATCCCTGGAGA
GCTTTTGAICTGCTGTGGGAGAGAAAAGTTTGTAGTGTGATGCAGAGGTGTGACTAACTGCCATGGAGATGGGAT
GGAGTAGCTGACCTTTGAAATCAAGGATGAATTCTAGTTTTACAGGATGAAGGGCACGGGTGGCAGGAAGACATT
CCAGGCATATAGTATAGTGTATT

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FIGURE 300

MIPKHGIKYDGFILGYWRKVYFETHLYMFILASGKTTVIFLQHTSWYQFRR

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FIGURE 301

TTTTCCCGCGAACTCGGCGGCTGAGCGTGGAGGTTCTTGTCTCCCCTGGTTTGTGAAGTGCGGAAAACCAGAGG
CGCAGTCA**ATG**TCGGGA¹TCGACGATCCTGGCATTCTTCTACAGCGACAGCTTCGGGGGCGACGCCCAGGCCGACGA
GGGGCAGGCCCGCAAATCGCAGCTGCAGAGGCGCTTCAAGGAGTTCCTGCGGCAGTACCGAGTGGGCACCGACCG
CACGGGCTTCACCTTCAAATACAGGGATGAACTCAAGCGGCATTACAACCTGGGGGAGTACTGGATTGAGGTGGA
GATGGAGGATCTGGCCAGCTTTGATGAGGACCTGGCCGACTACTTGTACAAGCAGCCAGCCGAGCACCTGCAGCT
GCTGGAGGAAGCTGCCAAGGAGGTAGCTGATGAGGTGACCCGGCCCCGGCCTTCTGGGGAGGAGGTGCTCCAGGA
CATCCAGGTATGCTCAAGTCGGACGCCAGCCCTTCCAGCATTCTGATGCCCTGAAGTCGGACATGATGTACACCT
GGTGAAGATCCCTGGCATCATCATCGCGGCCCTCTGCGGTCCGTGCCAAGGCCACCCGCATCTCTATCCAGTGCCG
CAGCTGCCGCAACACCCTCACCAACATTGCCATGCGCCCTGGCCTCGAGGGCTATGCCCTGCCCAGGAAGTGCAA
CACAGATCAGGCTGGACGCCCCAAATGCCATTGGACCCGTACTTCATCAT**G**CCCGACAAATGCAAATGCGTGGA
CTTCCAGACCCTGAAGCTGCAGGAGCTGCCTGATGCAGTCCCCACGGGGAGATGCCCAGACACATGCAGCTCTA
CTGCGACAGGTACCTGTGTGACAAGGTCGTCCCTGGGAACAGGGTTACCATCATGGGCATCTACTCCATCAAGAA
GTTTGGCCTGACTACCAGCAGGGGCCGTGACAGGGTGGGCGTGGGCATCCGAAGCTCCTACATCCGTGTCTGGG
CATCCAGGTGGACACAGATGGCTCTGGCCGAGCTTTGCTGGGGCCGTGAGCCCCCAGGAGGAGGAGGAGTTCCG
TCGCCTGGCTGCCCTCCCAAATGTCTATGAGGTCACTCTCAAGAGCATCGCCCCCTCCATCTTTGGGGGCACAGA
CATGAAGAAGGCCATTGCCCTGCTCTTTGGGGGCTCCCGAAAGAGGCTCCCTGATGGACTTACTCGCCGAGG
AGACATCAACCTGCTGATGCTAGGGGACCCTGGGACAGCCAAGTCCCAGCTTCTGAAGTTTGTGGAGAAGTGTTT
TCCCATTGGGGTATACAGTCTGGGAAAGGCAGCAGCGCAGCTGGACTGACAGCCTCGGTGATGAGGGACCCTTC
GTCCCGGAATTTATCATGGAGGGCGGAGCCATGGTCCTGGCCGATGGTGGGGTCGTCTGTATTGACGAGTTTGA
CAAGATGCGAGAAGATGACCGTGTGGCAATCCACGAAGCCATGGAGCAGCAGACCATCTCTATCGCCAAGGCTGG
GATCACCACCACCCTGAACTCCCGCTGCTCCGTCTGGCTGCTGCCAACTCAGTGTTTCGGCCGCTGGGATGAGAC
GAAGGGGGAGGACAACATTGACTTCATGCCCCACCATCTTGTGCGGCTTCGACATGATCTTCATCGTCAAGGATGA
GCACAATGAGGTGAGGGATGTGATGCTGGCCAAGCATGTCTACTCTGCACGTGAGTGCACTGACACAGACACA
GGCTGTGGAGGGCGAGATTGACCTGGCCAAGCTGAAGAAGTTTATTGCCTACTGCCGAGTGAAGTGTGGCCCCCG
GCTGTGACGAGAGGCTGCAGAGAACTGAAGAACCCTACATCATCATGCGGACGGGGCCCGTCAGCACGAGAGG
GACAGTGACCGCGTCCAGCATCCCCATCACTGTGCGGCAGTTGGAGGCCATTGTGCGCATCGCGGAAGCCCTCAG
CAAGATGAAGCTGCAGCCCTTCGCCACAGAGGCAGATGTGGAGGAGGCCCTGCGGCTCTTCCAAGTGTCCACGTT
GGATGCTGCCTTGTCCGGTACCCTGTGAGGGGTGGAGGGCTTCACCAGCCAGGAGGACCAGGAGATGCTGAGCCG
CATCGAGAAGCAGCTCAAGCGCCGCTTTGCCATTGGCTCCCAGGTGTCTGAGCACAGCATCATCAAGGACTTCAC
CAAGCAGAAATACCCGGAGCACGCCATCCACAAGGTGCTGCAGCTCATGCTGCGGCGCGGCGAGATCCAGCATCG
CATGCAGCGCAAGGTTCTCTACCGCCTCAAG**TG**AGTCGCGCCGCTCACTGGACTCATGGACTCGCCACGCTCGCC
CTCCTTGGCGCTGCCTGCCATTGACAATGTTGCTGGGACCTCTGCCTCCCCACTGCAGCCCTCGAACTTCCCAGG
CACCCCTCCTTTCTGCCCCAGAGGAAGGAGCTGTAGTGTCTGCTGCTCTGGGCGCCCGCTCTAGCGGGTTCTGG
GAAGTGTGCTTTTGGCATCCGTTAATAATAAAGCCACGGTGTGTTTCAGGT

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FIGURE 302

MSGFDDPGIFYSDSFGGDAQADEGQARKSQLQRRFKEFLRQYRVGTDRTGFTFKYRDELKRHYNLGEYWIEVEME
DLASFDEDLADYLYKQPAEHLQLLEEAKEVADEVTRPRPSGEEVLQDIQVMLKSDASPSSIRSLSDMMSHLVK
IPGIIIAASAVRAKATRISIQCRCRNTLTNIAMRPGLEGYALPRKCNTDQAGRPKCPLDPYFIMPDKCKCVDFQ
TLKLQELPDVPHGEMPRHMLYCDRYLCDKVVPGNRVTIMGIYSIKKFGLTTSRGRDRVGVGIRSSYIRVLGIQ
VDTDGSGRSFAGAVSPQEEEEFRRLAALPNVYEVI SKSIAPSIFGGTDMKKAIACLLFGGSRKRLPDGLTRRGDI
NLLMLGDPGTAKSQLLKFEKCSPIGVYTSKGKSSAAGLTASVMRDPSSRNF IMEGGAMVLADGGVVCIDEFDKM
REDDRVAIHEAMEQQTISIAGITTTLNSRCSVLAAANSVFGRWDETKGEDNIDFMPTILSRFDMIFIVKDEHN
EVRDVMLAKHVITLHVSALTQTQAVEGEIDLAKLKKFIAYCRVKCGPRLSAEAAEKLKNRYIIMRTGPVSTRGTV
TASSIPITVRQLEAIVRIAEALSKMKLQPFATEADVEEALRLFQVSTLDAALSGTLSGVEGFTSQEDQEMLSRIE
KQLKRRFAIGSQVSEHSIIKDFTKQKYPEHAHVKVLQMLRRGEIQHRMQRKVLYRLK

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FIGURE 303A

CCACGCGTCCGGGGAAGATGCCCAGGGGACAGGATTGATGCATATTCTCTGATCTTCCACAGGAGTGGTCCCGTAG
GCCTCACCCCTCTCCGTCCACCATCTCTACTGCCCGCTCTGCTGGTTGGGCCTCTGGTGTATGGACTTGTACATGA
TGAAGTGTGAACCTCTAGCCACGTGTAGCGCCCTTGGGTACTTGGGAAGGAGGGACTTACCACAAGGAGCCGGATT
GCCTGGAGAGTGTGAAGGATTTGATCCGATACCTGAGGCACGAGGATGAGACCCGAGATGTGCGGCAGCAGCTGG
GAGCTGCACAGATCTTCAGAGCGACCTCCTGCCAATCCTCACGCAGCATCGCCAGGACAAGCCTCTCTTCGATG
CCGTGATCAGGCTGATGGTAAATTTGACACAGCCAGCCTTGCTCTGTTTTGGCAGCGTGCCTAAGGACTCCAGTG
TACGGCACCATTTTCTGCAGGTTCTAACGTACCTGCAAGCCTACAAAGAGGCCTTTGCCAGTGAGAAGGCATTTG
GAGTCTCAGCGAGACCTTGTATGAATTGCTACAGCTGGGCTGGGAGGATCGGCAAGAAGAAGACAACCTTGCTGA
TCGAGCGGATCCTTCTGCTGGTCAGAAATATTCTCCATGTCGCCGCCAACCTTGAGCAGGAGAAGAGTATCGATG
ATGATGCCAGCATCCACGACCGTCTCCTTTGGGCAATTCACCTCAGTGGCATGGACGACTTGCTCCTCTTCTGT
CCAGCTCATCCGCCGAGCAGCAGTGGAGCCTCCATGTGCTGGAGATCATCTCCCTCATGTTCCGAGACCAGACCC
CTGAGCAGCTAGCGGGAGTAGGGCAGGGACGCTTGGCTCAGGAGCGAAGCACGGATGTGGCAGAATTGGAGGTGC
TGCGCCAACGGGAGATGGCGGAGAAGAGAGCTCGGGCCCTCCAGCGAGGAAACAGGCACTCTCGATTTGGGGGCT
CCTACATTGTCCAGGGTTGAAATCTATTGGGGAGAAGGATGTCTGTTTTACAAAGGCCTTCACAATCTCCAGA
ACTACAGCTCAGATCTGGGAAAGCAGCCCAGGAGGGTGCCCAAGCGTCGTCAGGCTGCCAGGAGCTGTCTGTCC
ATCGCCGCTCTGTCTGAATGTGAGACTCTTCTCAGAGACTTCTGCTCTGAGTTCTTGAGAACTGCTACAACC
CGCTCATGGGCGCGGTCAAGGATCATCTGCTTCGGGAGAGAGCGCAGCAGCATGACGAGACTTACTACATGTGGG
CAATGGCTTTCTTCATGGCCTTCAACCGAGCTGCCACCTTCCGCCCCGGCCTTGTTTCTGAGACCTCAGTATCC
GTACCTTTCACTTTGTGGAGCAGAACCTCACCAACTACTACGAGATGATGCTGACAGACCGCAAGGAGGCCCGCT
CCTGGGCGCGCAGGATGCACCTGGCCCTGAAGGCCTACCAGGAGCTGCTGGCCACGGTGAACGAGATGGACATGT
GCCCAGATGAGGCTGTTAGGGAGAGCAGTCGTATCATAAAAACAACATTTTCTATATGATGGAGTACCGAGAAC
TATTCTGGCGCTCTTTGAAAAGTTTGATGAGAGATACCATCCACGCTCATTCTTCGAGACCTGGTGAAACCA
CCCACCTCTTCTCAAAATGTTGGAGCGCTTTTGCCGGAGCCGCGGGAACCTGATGGTGCAGAACAAAAGAAAA
AGAGGAAAAAGAAAAAGAAGGTTCAAGGACCAGGGTGTGCTTTCTCACAAGCCCCGGGAGCTGGAGGCCATGT
GGCCAGCCCTGGCAGAGCAGCTGCTGTCAGTGTGCCAGGACCTGAGCTCAGTGIGGACCCCGTCTGTTCCCTTTG
ATGCGGCCCTCAGAGGTGCCAGTGGAGGAGCAGCGGGTAGAAGCCATGGTGAGGATCCAAGACTGCCTTACGGCTG
GCCAGGCCCGCAAGCCCTGGCCCTCCTGCGGTCTGCCGGGAAGTGTGGCCTGAAGGAAATGCGTTTGGCTCTC
CAGTCATTTCCCCAGGGGAAGAAATGCAGTTGCTGAACAATCCTCTCCACGCCCTTCCCCGGCAGCAGGAGC
CAGAAGAAGGAGATGCAGAGGAGGAAGAGGAAGAGGAGGAGGAAGAGGAGTTACAGGTGGTCCAGGTGTCAGAGA
AGGAGTTTAACTTTCTGGAATACCTGAAACGCTTCGCATCCTCAACCATCGTGGGGCCTACGTGCTTCTCCTGC
GGAGCTACAGGCAGAACAGTGTCTCACACCAACCACTGCATCGCCAAGATGCTGCACCGGTGGCCCATGGCCTGG
GGATGGAAGCCCTGCTTTTCCAGCTGTCCCTGTTCTGCCTCTTCAATCGGCTGCTTAGTGACCCAGCTGCTGCGG
CCTACAAAGAGCTAGTGACTTTTGCCAAATACATCATTGGCAAGTTCTTTGCGTTGGCTGCCGTGAACCAGAAAG
CGTTTGTGGAGCTGTATTCTGGAAGAACACCGCAGTGTTTCGGGAAATGACCCAGGGATATGGCTCCCTCGACA
GTGGGTCTTCCAGCCACAGAGCTCCTCTGTGGAGCCCTGAGGAAGAGGCCAGCTTCAGGAACATACTCGCCC
ACAAGGATGTGGAAGGTCAAGATGTAGTGGAACCATATTGGCGCACCTGAAAGTCGTTTCTCGAACACGCAAGC
AGGTCATCCACCACCTGGTCCGATGGGCCTGGCCGACAGCGTCAAGGAGTTCCAGAAGAGGAAAGGGACCCAGA
TTGTCTTGTGGACGAGGACCAGGAGCTGGAGTTACAGCGGCTCTTTGAGGAGTTCCGGGACTCTGATGATGTTT
TTGGTCAAATCATGAAGAATATCACAGCCAAACGTTACAGGGCTCGAGTAGTGGAACAACTGTTGGCCCTGGGGT
TGGTGTCTGAGCGGAGGCAGCTATACAAGAAACGGAGAAAGAAGCTGGCGCCTTCTTGATGCAGAAATGGAGAAA
AGTCCCCGAGAGACCCCTGGCAGGAAGATCCGGAAGAGGAAGACGAACACTTGCCAGAGGACGAAAGTGAAGATG
AGGAGAGTGAGGAAGGCTTGCCATCAGGACAGGGTCAGGGCAGCTCATCTCTCTGCTGAAAACCTCGGTGAGA
GCCTTCTGTCAGGAAGGCCTCTCTGCTCCCTCCTGTGGCTCCAGAGCTCCCTGATCCGAGCAGCAAATGACCGAG
AAGAGGATGGCTGTCCAGGCAATCCCTCTGGTGCCTCTGACAGAGGAAAAATGAGGAAGCAATGGAGAACGAAC
AGTTTCAGCATCTGTACGAAGCTAGGGATCCGGCCGCCAGCTCAGGGCAGGAAACCTTCTGGAGAATTCCAG
CCAAACTGAGCTCCACCAGCTTCGGAGGGTGGCTGCTTCTTTGAGTCAGCAAGAAAACGAGGAGGAAAGGGAAG
AGGAGCCAGAGCCAGGAGTCCCCGGAGAGCAGGGTCCCAGTGAGGAGCACCGGACAGAAGCCCTGAGAGCCCTTC
TGTCAGCCCGTAAGAGGAAAGCAGGCCTGGGGCCTACAGAAGAGGAGGCCACTGGGGAGGAAGAATGGAACCTCAG

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FIGURE 303B

CGCCCAAGAAGCGGCAACTGCTGGACAGCGACGAAGAGGAAGATGATGAGGGGAGGAGGCAAGCAGTGTCTGGGAA
CGCCAAGAGTCCACAGGAAGAAACGGTTTCAGATTGAGGATGAGGATGACTGAAAGCCAGATGTGTTTGACCGAT
GTGAGTTGGAGGCACAAAAGCTACTTTTGCCTGCGTTGGAAGCAATCTTCTCTACATTGACAGCCCAGGAATTTT
AGGCAGCAGTGTGGGTGGAGTCCTTGCGGTCAGTCCTTGCCCCAGGTTTCATCAGCGTGCACAGCCGGTCTCTGG
GTCCGTCTCGTAGCAAATGAAGAGTGGCGAAAGGTTCAAGGTGGCTTGTCTCTCTAAGGACTGCGTCTTGGCT
TCTGACGGGGAGCTTTATAACCCAGCACGGTTGTTTATTCTGTCTCACAAGCACTGGATTGCTCCCATTTTCT
TTCTTTTCATCCCAGGACACATGATTGAACCCGTTTCTACAGTTGAGGGAGAGCTGGGATGCACCACTCTCAAGCT
GACAAGCATCCCTGATTTGTGTTTCATATTAAATGTGTACAATTAACAGTTGCTCATCTCAGAACGGCCAGCCAG
CCATCTGTTGTGTCTTCGGAAGAACTTTTAAGAGTAAAATTAAGACATGTCCTGAACTGAGCTTGGTAGTGTG
AGCTAATCCCATCGTGTGGGAGACAGAGGCAAGAGAATTGCCATGAGGGAGAGGAAAGAGTCATATAGCCCTACG
CGTGGGCCAATAAATGTAATTTAAAAATCAGCTTGATAATAAATATAATTTTAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

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FIGURE 304

MDLYMMNCELLATCSALGYLEGGTYHKEPDCLESVKDLIRYLRHEDETRDVRQQLGAAQILQSDLLPILTQHRQD
KPLFDAVIRLMVNLTQPALLCFGSVPKDSVRHHFLQVLTYLQAYKEAFASEKAFGVLSETLYELLQLGWEDRQE
EDNLLIERILLVLRNILHVPANLEQEKSIDDDASIHDRLLWAIHLSGMDLLFLSSSSAEQQWSLHVLEIISLM
FRDQTPEQLAGVGQGRLAQERSTDVAEEVLRLQREMAEKRRARALQGRNRHSRFGGSYIVQGLKSIGEKDVVFHKG
LHNLQNYSSDLGKQPRRVPKRRQAAQELSVHRRSVLNVRLFLRDFCSEFLENCYNPLMGAVKDHLLRERAQQHDE
TYWMWAMAFFMAFNRAATFRPGLVSETLSIRTFHFVEQNLTNYEMMLTDRKEAASWARRMHLALKAYQELLATV
NEMDMCPDEAVRESSRIKNNIFYMMEYRELFALFRKFDERYHPRSFLRDLVETTHLFLKMLERFCRSRGNLMV
QNKRRKKKKKKVQDQGVAFSQSPGELEAMWPALAEQLLQCAQDPELSVDFVVPFDDAASEVPVEEQRVEAMVRIQ
DCLTAGQAPQALALLRSAREVWPEGNAFGSPVISPGGEEMQLLKQILSTPLPRQOEPEEGDAEEEEEEEEEEELQV
VQVSEKEFNFLLEYLKRFASSSTIVRAYVLLRSYRQNSAHTNHCIKMLHRLAHGLGMEALLFQLSLFCLFNRLLS
DPAAAAYKELVTFAKYIIGKFFALAAVNQKAFVELLFWKNTAVVREMTQGYGSLDSGSSSHRAPLWSPEEEAQLQ
ELYLAHKDVEGQDVVETILAHKVVPRTRKQVIHHLVRMGLADSVKEFQKRKGTQIVLWTEDELELQRLFEFR
DSDDLGQIMKNITAKRSRARRVVDKLLALGLVSERRQLYKKRRKKLAPSCMQNGEKSPRDPWQEDPEEEDHLPE
DESEDEESEGLPSGQGGSSSLSAENLGESLRQEGLSAPLLWLQSSLIRAANDREEDGCSQAIPVPLTEENEE
AMENEQFQHLLRKLGRPPSSGQETFWRIPAKLSSQLRRVAASLSQQENEEEREPEPGVPGEQGPSEHRTE
ALRALLSARKRKAGLGPTEEETGEEWNSAPKKRQLLDSDEEEDDEGRRQAVSGTPRVHRKKRFQIEDEDD

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FIGURE 305

ATCTGAACCCAGGAAAGAAACCCATTGCGGACCCCTCTTCCCTCTCCAGACAGGTGGAGAGCGGGTGAGGGTC
TCGCTCGGCTTTCCCCCTGCACCTTTCCACCCCTCCGCGCGTCCCTGGGGGTCTCTCCGTACCGCGGGCCATGGC
CCAGAAGCCGAAGGTGGACCCCCACGTCGGGCGGCTGGGATACCTGCAGGCGCTGGTCACGGAATCCAGGAGAC
CCAAAGCCAAGACGCCAAGGAGCAAGTCTCGCCAACCTCGCCAACCTCGCTTATGACCCAGCAACTACGAGTA
TCTGCGGCAGCTGCAGGTCTGGATTATTTCTCGATTGCTGTGCGAGGAGAATGAGACCCTGGTGGAGTTTGC
TATTGGAGGCCTGTGCAACCTGTGCCAGACAGGGCCAACAAGGAGCACATCCTGCACGCAGGAGGTGTCCCACT
CATCATCAACTGCCTATCCAGCCCCAATGAGGAGACGGTGCTGTCTGCCATCACCACGCTCATGCACCTGAGCCC
GCCGGGCCGAGCTTTCTCCAGAGCTGACCGCCACGCGCGTGGTGCAGTGCATGCTTCGCTTCTCCCTCTCGGC
CAGCGCCAGGCTCCGGAACCTGGCACAGATCTTCTGGAGGACTTCTGCTCCCCCGCCAGGTGGCCGAGGCCCG
CAGCCGGCAGGCGCACTCTGCCCTGGGTATCCCACTGCCGAGGAGCGTGGCCCCACGGCAGCGCTGATCCATGGA
GACTGCGAGACCGTGGCACCCCTACTGCTGGGGACCACAGTCTGTATGTGGACGCAGGGAACGGGGAGCACATAC
TGCCCCATTGGTGCCTTTTTCAGCCATCTGAAAGGCGGGTTCTTTTCAGCAGGACAGGCATTTACACTGATGAAACG
CCACTGGGAGTGAGGAAGCCAGACTCCAGAGACACGGAGAAGATCAAACCTGGAGCTGCGTTTCATAGGCTGGCACT
CTCAATCCTACATCAGGTGCCACCACCACCAGACTCAGGCCCTGGTGTAAGAAGCGGCCAAGTGCCTGGACCCAG
AGGCTTTGCAGGACAGTGTTCTCAGGAGCTGGGCCCTGAGGCTTAGGAGAGCTGCCTTCGCTGCAGGAAATCAGGG
ATTATCCCTTAACAGAAGTGCTGGAGTAGTTTTTCAGGTATAGGAATGAGATGCCTCGTGGTGAAAGGATCTCAC
CCTGGGAAGATGTGGTGCCCCCTCCAGGGCTCTGGAGGATGGATGCCTCCCCAGGGGCTCTCCAAGCTGGGCAT
TTGGGCCTGGTGGATGCCAACCTGGATAACCTGTGGCCAGCATTGACTGTCCACCCAGCCTTGCTGTTAGGCAC
CATGACTCCAAGATGAAGATGTGGTCCCTGCCCTTGAGTGACAGCCCAGGGACTTAATGTGGCCATCGGGCATCA
AGCACAAAGGCCATGCAGGTGATGATACGTGCGGAATAGAGGCACCAGCCCTGGTAACCTGCATCTTCTCCCTTGCC
ACCCCATGGCCCCGGCTGAAAGCTTCGGCCCTCCTCTGCTGTCACTCAATGATGGGGAGCCCTACCCCAAGAGTG
TATCCACGAGGGCATCAGGGACGCAGTGAGTGTTGCTCAAGGGAGTCAGGAAGAGACGGCAACGTAAAGGATGT
GGCTCCATGTCCATGGTGCCCCCTGGTCAACATAAGGAGCGTGGGATCCGATGGAAAGGTGGAGCTCAGGGAAAA
TGGGGTCTTGCCTCTCGTGTACCCCTCAAGGCTGACCCCTTAGATGGCCCAGGAATGGCAGGTGCTACAAAA
ATGGTACCCACGTGGGCATGGAAATGGGGCAGATTAGGGGACCACTGGACTCAGAGGGGAGGGAAGGGCTCATCA
GCACCCGCTCAGGGAGCCTGTCCCTTTATGTTCCCAAATAAAGGGTCTAGAAAGACTAAAAAAAAAAAAAAAAA

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FIGURE 306

MAQKPVDPHVGR LGYLQALVTEFQETQSQDAKEQVLANLANFAYDPSNYEYLRQLQVLDLFLDSLSEENETLVE
FAIGGLCNLC PD RANKEHILHAGGVPLIINCLSSPNEETVLSAITTLMHLSPPGRSFLPELTATPVVQCMLRFSL
SASARLRNLAQIFLEDFCSPRQVAEARSRQAHSALGIPLPRSVAPRQR

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FIGURE 307

CGGCAGCCAGCCTATTCTTTGGCCGGGTGCGTGCGAGTGGTGGCTGGGCAGAGTGCACGCTGCTTGGCGCCGCA
GGCTGATCCCGCCGTCCACTCCCGGGAGCAGTGATGTTGGGCAACTCTGCGCCGGGGCCTGCGACCCGCGAGGCG
GGCTCGGCGCTGCTAGCATTGCAGCAGACGGCGCTCCAAGAGGACCAGGAGAATATCAACCCGAAAAGGCAGCG
CCCGTCCAACAACCGCGGACCCGGGCGCGCTGGCGGTACTGAAGTCCGGGAACCCGCGGGGTCTAGCGCAGCAG
CAGAGGCCGAAGACGAGACGGGTTGCACCCCTTAAGGATCTTCTGTAAATGATGAGCATGTCACCGTTCCTCCT
TGAAAAGCAAACAGTAAACAGCCTGCGTTCACCATTCATGTGGATGAAGCAGAAAAAGAAGCTCAGAAGAAGCCA
GCTGAATCTCAAAAAATAGAGCGTGAAGATGCCCTGGCTTTTAAATTCAGCCATTAGTTTACCTGGACCCAGAAAA
CCATTGGTCCCTCTTGATTATCCAATGGATGGTAGTTTTGAGTCACCACATACTATGGACATGTCAATTGTATTA
GAAGATGAAAAGCCAGTGAGTGTTAATGAAGTACCAGACTACCATGAGGATATTCACACATACCTTAGGGAAATG
GAGGTTAAATGTAAACCTAAAGTGGGTACATGAAGAAACAGCCAGACATCACTAACAGTAIGAGAGCTATCCTC
GTGGACTGGTTAGTTGAAGTAGGAGAAGAATATAAACTACAGAATGAGACCTGCAATTTGGCTGTGAACTACATT
GATAGGTTCTGTCTTCCATGTCAGTGCTGAGAGGAAAACCTCAGCTTGTGGGCAGTGTGCTATGCTGTTAGCC
TCAAAGTTTGAAGAAATATACCCCCAGAAGTAGCAGAGTTTGTGTACATTACAGATGATACCTACCCAAGAAA
CAAGTTCTGAGAATGGAGCATCTAGTTTTGAAAGTCCTTACTTTTGACTTAGCTGCTCCAACAGTAAATCAGTTT
CTTACCCAATACTTTCTGCATCAGCAGCCTGCAAACTGCAAAGTTGAAAGTTTAGCAATGTTTTTGGGAGAATTA
AGTTTGATAGATGCTGACCCATACCTCAAGTATTTGCCATCAGTTATTGCTGGAGCTGCCTTTCATTTAGCACTC
TACACAGTCACGGGACAAAGCTGGCCTGAATCATTAAACGAAAGACTGGATATACCCTGGAAAGTCTTAAGCCT
TGTCTCATGGACCTTACCAGACCTACCTCAAAGCACCACAGCATGCACAACAGTCAATAAGAGAAAAGTACAAA
AATTCAAAGTATCATGGTGTTTTCTCTCCTCAACCCACCAGAGACACTAAATCTGTAAACAATGAAAGACTGCCTTT
GTTTTCTAAGATGTAAATCACTCAAAGTATATGGTGTACAGTTTTTAACTTAGGTTTTAATTTTACAATCATTTT
TGAATACAGAAGTTGTGGCCAAGTACAAATTATGGTATCTATTACTTTTTAAATGGTTTTAATTTGTATATCTTT
TGTATATGTATCTGTCTTAGATATTTGGCTAATTTTAAGTGGTTTTTGTAAAGTATTAATGATGCCAGCTGTCAG
GATAATAAATTGATTTGGAAAACCTTAAAAAA

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FIGURE 308

MLGNSAPGPATREAGSALLALQQTALQEDQENINPEKAAPVQQPRTRAALAVLKSGNPRGLAQQORPKTRRVAPL
KDLPVNDEHVTVPFWKANSKQPAFTIHVDEAEKEAQKKPAESQKIEREDALAFNSAISLPGPRKPLVPLDYPMDG
SFESPHTMDMSIVLEDEKPVSVNEVPDYHEDIHTYLREMEVKCKPKVGYMKKQPDITNSMRAILVDWLVEVGEEY
KLQNETLHLAVNYIDRFLSSMSVLRGKLQLVGTAAMLLASKFEEIYPPEVAEFVYITDDTYTKQVLRMEHLVLK
VLTFDLAAPT VNQFLTQYFLHQQPANCKVESLAMFLGELSLIDADPYLKYLPSVIAGAAFHLALYTVTGQSWPES
LIRKTGYTTLESLKPCLMDLHQTYLKAPQHAQQSIREKYKNSKYHGVSLNPPETLNL

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FIGURE 309

GGCCGGACAGTCCGCCGAGGTGCTCGGTGGAGTCATGGCAGTGCCCTTTGTGGAAGACTGGGACTTGGTGCAAAC
CCTGGGAGAAGGTGCCTATGGAGAAGTTCAACTTGCTGTGAATAGAGTAACTGAAGAAGCAGTCGCAGTGAAGAT
TGATGATATGAAGCGTGCCGTAGACTGTCCAGAAAATATTAAGAAAGAGATCTGTATCAATAAAATGCTAAATCA
TGAAAATGTAGTAAAATTCTATGGTCACAGGAGAGAAGGCAATATCCAATATTTATTTCTGGAGTACTGTAGTGG
AGGAGAGCTTTTTGACAGAATAGAGCCAGACATAGGCATGCCTGAACCAGATGCTCAGAGATTCTTCCATCAACT
CATGGCAGGGGTGGTTTATCTGCATGGTATTGGAA TAACTCACAGGGATATTAAACCAGAAAATCTTCTGTTGGA
TGAAAGGGATAACCTCAAATCTCAGACTTTGGCTTGGCAACAGTATTTCCGTATAATAATCGTGAGCGTTTGT
GAACAAGATGTGTGCTACTTTACCATATGTTGCTCCAGAACTTCTGAAGAGAAGAGAATTTATGCAGAACCAGT
TGATGTTTGGTCCTGTGGAATAGTACTTACTGCAATGCTCGCTGGAGAATTGCCATGGGACCAACCCAGTGACAG
CTGTCTAGGAGTATTCTGACTGGAAAGAAAAAAACATACCTCAACCCCTGGAAAAAAATCGATTCTGCTCCTCT
AGCTCTGCTGCATAAAATCTTAGTTGAGAATCCATCAGCAAGAATTACCATTCCAGACATCAAAAAAGATAGATG
GTACAACAAACCCCTCAAGAAAGGGGCAAAAAGGCCCGAGTCACTTCAGGTGGTGTGTCAGAGTCTCCAGTGG
ATTTTCTAAGCACATTCAATCCAATTTGGACTTCTCTCCAGTAAACAGTGCTTCTAGTGAAGAAAATGTGAAGTA
CTCCAGTTCTCAGCCAGAACCCCGCACAGGTCTTTCTTATGGGATACCAGCCCCTCATACATTGATAAATTGGT
ACAAGGGATCAGCTTTTCCCAGCCCACATGTCCTGATCATATGCTTTTGAATAGTCAGTTACTTGGCACCCCAGG
ATCCTCACAGAACCCCTGGCAGCGGTGGTCAAAAGAATGACACGATTCTTTACCAAATTGGATGCAGACAAATC
TTATCAATGCCTGAAAGAGACTTGTGAGAAGTTGGGCTATCAATGGAAGAAAAGTTGTATGAATCAGGTTACTAT
ATCAACAACCTGATAGGAGAAACAATAAACTCATTTTCAAAGTGAATTTGTAGAAATGGATGATAAAATATTGGT
TGACTTCCGGCTTTCTAAGGGTGATGGATTGGAGTTCAAGAGACACTTCTGAAGATTAAAGGGAAGCTGATTGA
TATTGTGAGCAGCCAGAAGGTTTGGCTTCCTGCCACATTGATCGGACCATCGGCTCTGGGGAATCCTGGTGAATAT
AGTGCTGCTATGTTGACATTATTCTTCTAGAGAAGATTATCCTGTCTGCAAACCTGCAAATAGTAGTTCTTGAA
GTGTTCACTTCCCTGTTTATCCAAACATCTTCCAATTTATTTTGTGTTTCGGCATACAAATAATACCTATATCT
TAATTGTAAGCAAACTTTGGGGAAAGGATGAATAGAATTCATTTGATTATTTCTTCATGTGTGTTTAGTATCTG
AATTTGAAACTCATCTGGTGGAACCAAGTTTCAGGGGACATGAGTTTTCCAGCTTTTATACACACGTATCTCAT
TTTTATCAAAACATTTTGT

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FIGURE 310

MAVPFVEDWDLVQTLGEGAYGEVQLAVNRVTEEAVAVKIVDMKRAVDCPENIKKEICINKMLNHENVVKFYGHRR
EGNIQYLFLEYCSGGELFDRIEPDIGMPEPDAQRFHQLMAGVVYLHGIGITHRDIKPENLLDERDNLKISDFG
LATVFRYNNRERLLNKMCGTLPYVAPELLKRREFHAEPVDVWSCGIVLTAMLAGELPWDQPSDSCQEYSDWKEKK
TYLNPWKKIDSAPLALLHKILVENPSARITIPDIKKDRWYNKPLKKGAKRPRVTSGGVSESPSGFSKHIQSNLDF
SPVNSASSEENVKYSSSQPEPRTGLSLWDTSPSYIDKLVOGISFSQPTCPDHMLLNSQLLGTGSSQNPWQRLVK
RMTRFFTKLDADKSYQCLKETCEKLGQWKKSCMNQVTISTDRNNKLIFKVNLEMDDKILVDFRLSKGDGLE
FKRHFLKIKGLIDIVSSQKVWLPAT

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FIGURE 311

GCATGAGGAGAGTGTGTAGGGGCCGGGTTCCTGGATGAACCTCACCCGAGCGGTTTCTCTTTCCGGGACAACA
TGGCGCCGTCCACGCCGCTCTTGACAGTCCGAGGATCAGAAGGACTGTACATGGTGAATGGACCACCACATTTTA
CAGAAAGCACAGTGTTCCTCAAGGGAATCTGGGAAGAATTGCAAAGTCTGTATCTTTAGTAAGGATGGGACCTTGT
TTGCCCTGGGGCAATGGAGAAAAAGTAAATATTATCAGTGTCACTAACAAGGGACTACTGCCTCCTTCGATCTTC
TGAAGGCAGTTTGCCTTGAATTCTCACCCAAAAATACTGTCCTGGCAACGTGGCAGCCTTACAGTACTTCTAAAG
ATGGCACAGCTGGGATACCCAACCTACAACCTTTATGATGTGAAACTGGGACATGTTTGAAATCTTTCATCCAGA
AAAAATGCAAAATTGGTGTCCATCCTGGTCAGAAGATGAAACTCTTTGTGCCCGCAATGTTAACAATGAAGTTC
ACTTCTTTGAAAACAACAATTTTAACACAATTGCAATAAATTGCATTGCAAAAAATTAATGATTTTGTATTAT
CACCTGGACCCCAACCATAACAAGGTGGCTGTCTATGTTCCAGGAAGTAAAGGTGCACCTTCATTGTAGATTAT
ATCAGTACCCCAACTTTGCTGGACCTCATGCAGCTTTAGCTAATAAAAGTTTCTTTAAGGCAGATAAAGTTACAA
TGCTGTGGAATAAAAAAGCTACTGCTGTGTTGGTAATAGCTAGCACAGATGTTGACAAGACAGGAGCTTCCTACT
ATGGAGAACAACTCTACACTACATTGCAACAAATGGAGAAAGTGCTGTAGTGCAATTACCAAAAAATGGCCCCA
TTTATGATGTAGTTTGGAATTCTAGTTCTACTGAGTTTGTGCTGTATATGGGTTTATGCCTGCCAAAGCGACAA
TTTTCAACTTGAAATGTGATCCTGTATTTGACTTTGGAAGTGGTCCTCGTAATGCAGCCTACTATAGCCCTCATG
GACATATATTAGTATTAGCTGGATTGGAAATCTGAGGGGACAAATGGAAGTGTGGGATGTGAAAACTACAAAC
TTATTTCTAAACCGGTGGCTTCTGATTCTACATATTTGCTTGGTGCCCGGATGGTGAGCATATTTAACAGCTA
CATGTGCTCCCAGGTTACGGGTTAATAATGGATACAAAATTTGGCATTATACTGGCTCTATCTGCACAAGTATG
ATGTGCCATCAAATGCAGAATTATGGCAGGTTTCTTGGCAGCCATTTTGGATGGAATATTTCCAGCAAAAACAA
TAACCTACCAAGCAGTTCCAAGTGAAGTACCCAATGAGGAACCTAAAGTTGCAACAGCTTATAGACCCCGAGCTT
TAAGAAATAAACCAATCACAATTCCAAATTGCATGAAGAGGAACCACTCAGAATATGAAACCACAATCAGGAA
ACGATAAGCCATTATCAAAAACAGCTCTTAAAAATCAAAGGAAGCATGAAGCTAAGAAAGCTGCAAAGCAGGAAG
CAAGAAGTGACAAGAGTCCAGATTTGGCACCTACTCCTGCCCCACAGAGCACACCACGAAACACTGTCTCTCAGT
CAATTTCTGGGGACCCTGAGATAGACAAAAAATCAAGAACCCTAAAGAAGAACTGAAAGCAATCGAACAACCTGA
AAGAACAAGCAGCAACTGGAAAACAGCTAGAAAAAATCAGTTGGAGAAAATTCAGAAAGAAACAGCCCTTCTCC
AGGAGCTGGAAGATTTGGAATTGGGTATTTAAAGATTACGGAAAGCAAGTTGATGACCAGAAATCAGTGCAAAC
ACATCTTCTGTAAACCCATTGGTATACACAGAATATTCCTGTGCCACACTTAATGTCAATCTATAATTTTAAAC
CATTTATCCAAGATTCTACTAAGTGTAATAATTATTTAATAATGTCTATTAAATTGATATTTATATCTTGCATCCT
ATATCATGTCAATATGTGATATAGAAAAGAGATACGTGAATTTTTTAGCTAAGCTTGACAGATTGAAAGACAAGT
GTCATTTTTTTTTGTAGAGGTGATATATACCATGTAAATGAATAAAGACATTTTAAATTTAAAAA
AAAA

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FIGURE 312

MRRVCRGRVPWMNSHPSGFSFRDNMAPSTPLLTVRGSEGLYMVNGPPHFTTESTVFPRESGKNCKVCIFSKDGTLF
AWGNGEKVNIIISVTNKGLLSFDLLKAVCLEFSPKNTVLATWQPYSTSKDGTAGIPNLQLYDVKTGTCLKSFIQK
KMQNWCPWSSEDETLCAENVNNEVHFFENNNFNTIANKLHLQKINDFVLSPGPQPYKVAVYVPGSKGAPSFVRLY
QYPNFAGPHAALANKSFFKADKVTMLWNKKATAVLVIASTDVDKTGASYIGEQLHYIATNGESAVVQLPKNGPI
YDVVWNSSTEFCAVYGFMPAKATIFNLKCDPVDFGTGPRNAAYYSPHGHILVLAGFGNLRGQMEVWDVKNYKL
ISKPVASDSTYFAWCPDGEHILTATCAPRLRVNNGYKIWHYTGSILHKYDVPSNAELWQVSWQPFLDGIFPAKTI
TYQAVPSEVPNEEPKVATAYRPPALRNKPIITNSKLHEEEPPQNMKPQSGNDKPLSKTALKNQRKHEAKKAQEA
RSDKSPDLAPTPAPQSTPRNTVSQISGDPEIDKKIKNLKKKLKAIEQLKEQAATGKQLEKNQLEKIQKETALLQ
ELEDLELGI

FIGURE 313

[illegible]

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FIGURE 314

KKKKAYQNKILTTNGKVKKLPRISSTMYPPIRARTLLNGTRQLGKAPLSLIELCYKT

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FIGURE 315

ATGACGGTGGGCAAGAGCAGCAAGATGCTGCAGCATATTGATTACAGGATGAGGTGCATCCTGCAGGACGGCCGG
ATCTTCATTGGCACCTTCAAGGCTTTTGACAAGCACATGAATTTGATCCTCTGTGACTGTGATGAGTTCAGAAAG
ATCAAGCCAAAGAACTCCAAACAAGCAGAAAGGGAAGAGAAGCGAGTCCTCGGTCTGGTGCTGCTGCGAGGGGAG
AATCTGGTCTCAATGACAGTAGAGGGACCTCCTCCCAAAGATACTGGTATTGCTCGAGTTCCACTTGCTGGAGCT
GCCGGGGGGCCAGGGATCGGCAGGGCTGCTGGCAGAGGAATCCCAGCTGGGGTTCCCATGCCCCAGGCTCCTGCA
GGACTTGCTGGGCCAGTCCGTGGGGTTGGCGGGCCATCCCAACAGGTGATGACCCACAAGGAAGAGGTACTGTT
GCAGCCGCTGCAGCTGCTGCCACAGCCAGTATTGCCGGGGCTCCAACCCAGTACCCACCTGGCCGTGGGGGTCT
CCCCACCTATGGGGCCAGGAGCACCCCTCCAGGCATGATGGGCCACCTCCTGGTATGAGACCTCCTATGGGT
CCCCCAATGGGGATCCCCCTGGAAGAGGGACTCCAATGGGCATGCCCCCTCCGGGAATGCGGCCTCCTCCCCCT
GGGATGCGAGGCCTTCTTTTGA

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FIGURE 316

MTVGKSSKMLQHDYRMRCILQDGRIFIGTFKAFDKHMNLILCDCDEFKIKPKNSKQAEREKRVLGLVLLRGE
NLVSMTVEGPPPKDTGIARVPLAGAAGGPGIGRAAGRGIPAGVPMPQAPAGLAGPVRGVGGPSQQVMTPQGRGTV
AAAAAATASIAGAPTQYPPGRGGPPPPMGRGAPPPGMMGPPPGMRPPMGPPMGIPPGRGTPMGMPPPGMRPPPP
GMRGLL

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FIGURE 317

GGCACGAGGCCGGGCCGAGGCCATGGCGCCCTGGGCGCTCCTCAGCCCTGGGGTCCTGGTGCGGACCGGGCACAC
CGTGCTGACCTGGGGAATCACGCTGGTGCTCTTCCGACGATACCGAGCTGCGGCAATGGGAGGAGCAGGGGGA
GCTGCTCCTGCCCCTCACCTTCTGCTCCTGGTGCTGGGCTCCCTGCTGCTCTACCTCGCTGTGTCACTCATGGA
CCCTGGCTACGTGAATGTGCAGCCCCAGCCTCAGGAGGAGCTCAAAGAGGAGCAGACAGCCATGGTTCTCCAGC
CATCCCTCTTCGGCGCTGCAGATACTGCCTGGTGCTGCAGCCCCCTGAGGGCTCGGCACTGCCGTGAGTGCCGCCG
TTGCGTCCGCCGCTACGACCACCACTGCCCCCTGGATGGAGAACTGTGTGGGAGAGCGCAACCACCACTCTTTGT
GGTCTACCTGGCGCTGCAGCTGGTGGTGCTTCTGTGGGGCCTGTACCTGGCATGGTCAGGCCTCCGGTTCTTCCA
GCCCCGGGGTCTGTGGTTGCGGTCCAGCGGGCTCCTGTTCGCCACCTTCTGCTGCTGTCCCTCTTCTCGTTGGT
GGCCAGCCTGCTCCTCGTCTCGACCTCTACCTGGTGGCCAGCAACACCACCACCTGGGAATTCATCTCCTCACA
CCGCATCGCCTATCTCCGCCAGCGCCCCAGCAACCCTTCGACCGAGGCCTGACCCGCAACCTGGCCCACTTCTT
CTGTGGATGGCCCTCAGGGTCTTGGGAGACCCTCTGGGCTGAGGAGGAGGAAGAGGGCAGCAGCCCAGCTGTTTA
GGGTTGCTGGAGGCCGGGCTACCGTCTTGTGCCTGAAAACCACGGGGCCTGTCCCCAGCTGGGGTGAGCGCTCAG
AGGGCCTGGGGCCCTCACTCCTGCCACGCCTCCCAGACCCAGAACGGAGCTTCAAGTCAGACAGATCCCTGCC
TTGGTGGGCAGTTCTGCCTTCCAAGGAAGAAGGGGAAGAAAAGGACCTGTGGGTGGCTCAGGCCCAAGCAGACCC
CGGGCTCCACCCAGCCCCGCCAGGCTGCTGCCAGTGCACACTTTTACAAATTTAATATAAAGCAAGTCCAGTC
TTAAAAAGACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 318

MAPWALLSPGVLVRTGHTVLTWGITTIVLFLHDTLRQWEEQGELLPLTFLLVLGSLLLYLAVSLMDPGYVNVQ
PQPQEEELKEEQTAMVPPAIPLRRCRYCLVLQPLRARHCRECRRCVRRYDHHCPWMENCVGERNHPLFVVYLALQL
VVLLWGGLYLAWSGLRFFQPWGLWLRSSGLLFATFLLLSLFSLVASLLLVSHLYLVASNTTTWEFISSHRIAYLRQ
RPSNPFDRGLTRNLAHFFCGWPSGSWETLWAEEEEEGSSPAV

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FIGURE 319

GATCTCAGGCTCGGCTCCCCGCCCGCCGAGCCCACTGTTGACCCGGCCCGTACTGCGGCCCCGTGGCCACCATG

TCCCTGCACGGCAAACGGAAGGAGATCTACAAGTATGAAGCGCCCTGGACAGTCTACGCGATGAAGTGGAGTGTG
CGGCCCCGATAAGCGCTTTTCGCTTGGCGCTGGGCAGCTTCGTGGAGGAGTACAACAACAAGGTTTCAGCTTGTGGT
TTAGATGAGGAGAGTTTCAGAGTTTATTTGCAGAAACACCTTTGACCACCCATACCCACCACAAAGCTCATGTGG
ATCCCTGACACAAAAGGCGTCTATCCAGACCTACTGGCAACAAGCGGTGACTATCTCCGTGTGTGGAGGGTTGGT
GAAACAGAGACCAGGCTGGAGTGTGCTAAACAATAATAAGAACTCTGATTTCTGTGCTCCCTGACCTCCTTT
GACTGGAATGAGGTGGATCCTTATCTTTTAGGTACCTCAAGCATTGATACGACATGCACCATCTGGGGGCTGGAG
ACAGGGCAGGTGTTAGGGCGAGTGAATCTCGTGCTTGGCCACGTGAAGACCCAGCTGATCGCCCATGACAAAGAG
GTCTATGATATTGCATTTAGCCGGGCCGGGGTGGCAGGGACATGTTTGCCTCTGTGGGTGCTGATGGCTCGGTG
CGGATGTTTGACCTCCGCCATCTAGAACACAGCACCATCATTACGAAGACCCACAGCATCACCCACTGCTTCGC
CTCTGCTGGAACAAGCAGGACCCTAACTACCTGGCCACCATGGCCATGGATGGAATGGAGGTGGTGAATCTAGAT
GTCCGGGTTCCTTGACACCTGTGCCAGGTTAAACAACCATCGAGCATGTGTCAATGGCATTGCTTGGGCCCCA
CATTATCCTGCCACATCTGCACTGCAGCGGATGACCACCAGGCTCTCATCTGGGACATCCAGCAAATGCCCCGA
GCCATTGAGGACCCTATCCTGGCCTACACAGCTGAAGGAGAGATCAACAATGTGCAGTGGGCATCAACTCAGCCC
GACTGGATCGCCATCTGCTACAACAACTGCCTGGAGATACTCAGAGTGTAGTGTTGGTGGCGCTGTGCCACGAG
GCAGGGGCTTTTGTATTTCTGCCTCTGCCCCACCCCCAAAGTAAGAAGAAACATGTTCCAGTGGCCAGTATGT
CTTTCATTGCTTTGCACCCACTGTTACCAGAAGCTGCTCTAGGAGTTCTTGGCCAGTCACCCCATCGCCCTCTGT
GGCAGACTCAGTGCTGTGTGGCGCCCTCCTAGCCCAGGGCTGAGTTTTAAGATTTTCTCTCTCTCTCTCTCTCC
TTTGGTTCCTCAATTAA

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FIGURE 320

MSLHGKRKEIYKYEAPWTVYAMNWSVRPDKRFRALGSEFVEEYNNKVQLVGLDEESSEFICRNTFDHPYPTTKLM
WIPDTKGVYPDLLATSGDYLRVVRVGETETRLECLLNNKNNSDFCAPLTSFDWNEVDPYLLGTSSIDTTCTIWGL
ETGQVLGRVNLVSGHVKTQLIAHDKEVYDIAFSRAGGGRDMFASVGADGSVRMFDLRHLEHSTIIYEDPQHHPLL
RLCWNKQDPNYLATMAMDGMEVVILDVRVPCPTPVARLNNHRACVNGIAWAPHSSCHICTAADDHQALIWDIQMP
RAIEDPILAYTAEGEINNVQWASTQPDWIAICYNNCLEILRV

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FIGURE 321

TGGCAGTGATGTCATTCCCTTACTAGGCTTCCAAAGCCACTGCTGTGGCCACAGCTTCCATGGAGACAGGCAAGCT
GAGCCTCTATGTGGCACCAATTCCTGCAGCTGTTTGTGTTGGAGGGAAAAAATCCAAATGGACATCAACAGCTT
TCATCAACTAAATAACCACAGAAAATATTTATGAAGACTATAAAGCAATGATTACTTTTGAATTGGAAAGGAATC
ACTATTATTTGAAATGTTTCTTCAAAGTGAGCATCCGGACAGGAACCATCATGGATGCTGAGGCCATGGATGAA
GGCCTACTCGGGAAGATGATATCCTTGCACTCTCAAACCGGCACCCACAAAGGTGATATCCTAATTTACAAAGG
GAAAAAGGTACCTTAATCTGAAATCTGGCAAATGCAGCCTCAACAGAAGTGACAGAATTGAACATCGCCAATAAT
GGGACACACAGACATCACATGCCCCAGTCTGATGCACCACGGAGTCGTCTCTGATGTATTCTTGTCAAAAAATG
TTTGCTGATTCTAATCATGAAAGAACAATTAGAAAAAATCCAAATTGACAGATATTCTGCAGAATAAATGGCCT
GACCTCATCAAAAACATCAATGTCATGAAAAACACAAAACATTGCAGATAGCGTGAAATTAAGATTACAGAGAT
ATAACTTAATGCAAGATCTCTGACTGGATCCTAGACTGCAGGAAAAAGTCTGCTATAAAGAACATTTGGATCACT
TGTAGTAGCTGGGAAATAAAACAAAACATTATTTGTAAAAGGGGGAAATCTGAACATGGGTCTTGCACTATTTA
TGACAGTTTTTGGGGGACAGAGATTTCTAGATTGACAGCTGTTTTAGTACTTTCAAGGTGATGCTCTGTCTGCTG
GTTTGCATTGTTTCTGTCTGAGTTAAGAGACTGGCAGAACACAGAGTTGCAGTAGCCAAACACTGGAGAAAGCTG
GGCCCTACAGAAACCTAACGCTGAAGAAACCTCAGGAGCCAAACTGGTGGAGAAAACAAAGAGTCTCCCTCTCT
CCCTTTTCAAATAATGATCATACATCTTCAAGCTGTCTGAAATGGTTAAGGAGTTTCACTCTGTCTGCTCAGGCACAC
ACCAGAGCCAGCTAGCCACACAGACCCCATCAGAGCAAAACAGACAAGAGAATTTAATTCATATCCACATAGAA
AGGACTTCTAGGTAGGAGGTAGACCTTTAGCTCCCTTCCAATTAAAGGAGTCCCCAATTCTGGCACCTGAGAGT
CCCCTGGGTCTAACAGCTATGATATTTATGTAGTGTGTTGCTTACCTAAATGAATACAATTTCTTCCAGACACG
TGACACTGATATTAAAGTGCTAATGAGAGGGATCTATTTCTTCTGTACGCTAAAAGAGAAACAGTAGTTTCAGAT
TTCCCATCAGAAGTCCGAGGACTTTGTTCTTGATAACTACTACCAATAAAAAATTGAGTATTTGAAAAATTCCTTT
GTATTTTCCATCCATACACATTTTTTTTTTAAAGCATTTTAGGAAGTCCTCTAATTATATAGTAAAAATTGTCAGC
AATGGCCTGCTAGTTTTCTATTTGACCTAATCACAACCATCCTCGTTAGGTCCTGAGGTCTGCTCTGCTGCTTGG
CCAAAACCAAATGGTGCCAGGTCACAAAGCACTTGACATGTGAATCCTGCATCCATTCTACAATGGGTCACTAT
TGACTGAAATACTTTAATAAAAAATGATAGAGCACATAAAGCTTGCTGTTGACAGAACTTCCGTGCTCAAGCAAG
GCAGTGCTATACATGGTGAGACCTTGACAAAGTCAGTTAACTAACAGATGATCTAGAAGCAGGTGACACAATGA
AATACCTTTTGGAGCTGTTGCCTATGTCTGTGGATAGGCTCTTTGTAGCTAGGTTAGGCTTCTGTGTTAAAGTGT
GTTAGAAGAAAGCATCACATAAGGAAAATAGAACTCTATTCGTATGTTTTTTCAAACAGAAGTCAAGTCACATT
CAGGCAAACCAAATCTGTAACATTCAAGAAGATGCAGTGACTCTTCCGCATCTTAGAGCCACGGTGTCTGAGGTG
GCTGGCATGGCTCCAACACGCTGGCTTCCCTGTGAGTGGATCATTACAATATGGTGCATTTCAAATTACTGGTG
AATTCAGTGAATACTGGCTGTTTTTTTTTTTTTAGGGGTAATCTTATACATAAAATTTAGGAAAAGAAAGAGAAA
AAAGCAAAAATGACAGAAATAACTCAAAAGTTCCTAAAATTTATGTGTATCTTTTCGTACCTGTGAACCTCTGAA
TAAGTATTTATATCTGACAGGTACAAATACAATAATTATATTTTAAAGTAAACCTATTTAATAATATGAAGTAT
GGTGTTAAATACATGTATTAAAGATAAGTAACTTCAGAAGTCTTCTGACTTTTTTAATTGTAAAAATAAGTAAAA
CTGTTTTGTGCTTTTTTTTACTGTATGC

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FIGURE 322

AVMSFLTRLPKPELLWPLPWRQAS

FIGURE 323A

CGGCGCGGGTGTGTGAGAGCGGTGTGGTAGGTGTTGTAGCCGCTATGGTGAAGTTGCGCTTTGTAGCGGCCCGGGCT
AGAGAGTTGGCCTGTTCCCTGCCTTTGTGACCCGGAGGAGCTTTTGGGGGTGCGTCAAGCCCCCTGGCCTGAGGCA
GCGAACTGGTTTGTGGCCTGTTTGATTCTCTGTCAGAGGTTTGTCTGACCCAAGACAGTATCGAAAAATGCATATTAA
GTCAATTATTCTAGAGGGATTCAAGTCTATGCTCAGAGGACCGAAGTCAATGGTTTTGTACCCCTCTTCAATGC
TATCACTGGCTTAAATGGTAGTGGGAAATCCAACAATTGGACTCCATCTGCTTTTTTACTGGGCATCTCCAACCT
GTCTCAGGTTCTGGGCTTCTAATTTACAAGATTTAGTTTACAAAAATGGGCAGGCTGGTATTACCAAAGCCTCTGT
GTCAATCACTTTTGATAATTCTGACAAAAAGCAAAGTCCTTTAGGATTTGAGGTTTCATGATGAAATCACAGTAAC
AAGGCAGGTGGTTATTGGTGGTAGAAAAATAATTTAATCAATGGAGTCAATGCCAACAACACCAGAGTACAGGA
TCTCTTCTGTTCTGTTGGCCTTAATGTTAACAACCCTCACTTTCTCATCATGCAGGGCCGAATTACAAAAAGTATT
GAATATGAAACCACCAGAGATTTTATCCATGATAGAAGAAGCAGCTGGAACCAGGATGTATGAATACAAAAAAT
AGCTGCACAGAAAATATAGAAAAAAGGAGGCTAAGCTGAAAGAAATTAAGACGATACTTGAAGAAGAGATTAC
TCCAACCATTCAAAAAATTAAAGAGGAAAGATCGTCTACTTTGGAGTACCAAAAAAGTAATGAGAGAAATAGAACA
TTTGAGTCGTTTATATATTGCTTATCAGTTTTTGTCTGGCTGAAGATACCAAAGTACGCTCAGCTGAGGAATTTAA
AGAAATGCAAGATAAAGTTATAAAGCTTCAGGAAGAATTGTCTGAGAATGATAAAAAAATAAAAGCACTTAATCA
TGAAATAGAAGAATTGAAAAAAGAAAAGATAAGGAACTGGAGTTATACTTCGATCTTTAGAAGATGCTCTTGC
AGAGGCTCAGCGAGTTAATACTAAATCTCAAAGCGCATTGTATCTCAAGAAGAAAAATCTGGCATGTGAGGAAAG
CAAACGCAAAGAGCTGGAaaaaaatatggtttgaggactcaaaaacttttagcagcaaaaggaaaaagagggttaaaaa
GATAACAGATGGACTGCATGCCCTTCAAGAAGCAAGTAATAAAGATGCTGAAGCTCTGGCAGCTGCACAGCAGCA
CTTCAATGCTGTTTCCGCTGGCCTGTCCAGTAATGAAGATGGAGCAGAAGCAACTCTTGCTGGTCAAATGATGGC
CTGTAAAAATGATAAAGTAAAGCTCAGACAGAAGCCAAACAGGCTCAGATGAAGTTGAAGCATGCTCAACAGGA
ATTAAGAATAAACAGCTGAAGTTAAGAAGATGGATAGTGGCTACAGGAAGGATCAAGAAGCTCTAGAAGCTGT
AAAAAGACTTAAAGAAAAACTTGAAGCTGAAATGAAAAAGCTAAATTATGAAGAAATAAAGAGGAAAGCCTTTT
GGAAAAGCGCAGGCAGCTGTCTCGTGATATTGGTAGATTGAAAGAAACATATGAAGCTCTATTAGCCAGATTTCC
CAATCTTCGATTTGCATACAAGGATCCAGAGAAGAACTGGAATAGAAATTGTGTGAAAGGACTTGTGGCTTCTCT
GATTAGTGTGAAAGACACTTCTGCAACCACAGCTTTAGAATTAGTGGCTGGAGAACGACTCTACAATGTTGTAGT
AGACACAGAAGTTACTGGTAAAAAGCTACTAGAAAGGGGGAACTGAAACGTCGATACACTATAATTCCACTCAA
TAAATTTTCCAGCCAGATGTATTGCACCAGAAACTCTGAGAGTTGCTCAGAATCTTGTGGCCCTGACAACGTTCA
TGTGGCTCTTTCTTGGTTGAATATAAACCCAGAACCTCAGAAAGCAATGGAGTTTGTCTTTGGAACAACATTTGT
TTGTGACAATATGGATAATGCCAAAAAGTGGCCTTTGATAAGAGGATAATGACTAGAACTGTAACCTCTCGGAGG
TGATGTGTTTGATCCTCATGGGACATTGAGTGGAGGTGCTCGATCCCAGGCAGCTTCCATTTTAACCAAGTTTCA
AGAACTCAAAGATGTTTCCAGGATGAACTGAGAATCAAAGAGAATGAGCTGCGGGCTCTAGAAGAGGAATTAGCAGG
TCTTAAAAACACTGCTGAAAAGTATCGCCAACATAAACAGCAGTGGGAGATGAAAACCTGAAGAGGCAGATTTATT
ACAAACCAAGCTCCAGCAAAGCTCATATCAAGCAACAAGAAGAAATTAGATGCCCTTAAAAAACCAATTGAGGA
AAGTGAGGAGACTTTGAAAAACACTAAAGAAATCCAAAGAAAAGCAGAAGAAAAATATGAAGTATTGAAAAATAA
AATGAAAAATGCAGAAGCTGAAAGAGAGCGAGAATGAAAGATGCTCAGAAAAAACTGGATTGTGCCAAAAACAA
GGCAGATGCATCTAGCAAGAAGATGAAAGAAAAACAAACAGGAAGTTGAAGCTATCACTCTGGAACCTGGAAGAGCT
CAAGAGAGAGCATAACATCTTACAAACAACAGCTTGAAGCTGTAATGAAGCTATCAAATCCTATGAAAGTCAGAT
TGAAGTAATGGCAGCTGAGGTGGCTAAAAATAAGGAGTCAGTAAATAAGCTCAAGAAGAGGTGACCAAGCAAAA
AGAGGTGATAACAGCCCCAAGACACTGTAATTAAGCTAAATATGCAGAAGTGGCAAAACACAAGGAGCAAAACAAT
GATTCTCAGCCTTAAAAATTAAGGAATTAGACCACCACATCAGCAAACATAAACGGGAGGCTGAAGATGGTGTCTGC
AAAGGTATCCAAAATGTTGAAAGATTATGACTGGATTAATGCAGAGAGACACCTCTTTGGCCAACCAATAGTGC
CTATGATTTCAAAACTAACAACCCTAAAGAAGCTGGTCAGAGACTTCAGAAGTTGCAAGAAATGAAGGAGAACT
AGGAAGAAATGTCAATATGAGAGCTATGAATGTATGACAGAAGCTGAAGAGCGATGCAATGACTTGATGAAGAA
GAAGAGAATTGTAGAAAATGACAAATCCAAAATCTTACAACATATAGAAGACCTTGACCAGAAGAAAAACCAAGC
CCTAAATATTGCATGGCAAAAGGTGAACAAGGACTTTGGGTCTATTTTTTCTACTCTTTTGCCTGGTGCTAATGC
TATGCTTGCACCACCAGAGGGTCAAACCTGTTTTGGATGGTCTGGAGTTCAAGGTTGCCTTAGGAAATACCTGGAA
AGAAAACCTAACTGAACTTAGTGGTGGTCAGAGGTCTTAGTGGCCTTGTCTAATAACTGTCCATGCTTCTCTT
CAAACCTGCTCCAATTTATATCCTTGATGAGGTAGATGCAGCCTTGGATCTTTCTCATACCCAAAACATTGGACA

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FIGURE 323B

GATGCTGCGTACTCATTTCACACATTCTCAGTTCATTGTGGTGTCACTAAAAGAAGGTATGTTCAACAATGCAAA
CGTTCTTTTCAAAACCAAGTTTGTGGATGGTGTCTTCTACAGTAGCCAGATTTACTCAATGTCAAAATGGAAAGAT
TTCAAAGGAAGCAAAATCCAAGGCAAAACCACCCAAAGGAGCACATGTGGAAGTTTAAACTACAAAGTTATTTCT
TCATCTTGACCTGTTTTTTTAAATGTAACTTTTAAGGACTTGAGATAACTAATTTGTTTATATACAAAAATTAA
TGTTACTGTGTTACTTAACCCATGTTTTCTCTTTATATAATCACTTATCGCTTACAAATGAGCATATATTCCTCA
TCTCTTAAGTAGTCTAATTATGGTCCAATTATTGTGGTGTGATTTTATGCATATCCATCAAAATGTTTTTTTC
TTATGCGGGTCTTTTATATATTAGGGATCCTGAGATACCCGATTCTATATGTAAAAGCTAATATACAAAAAAGCA
GATTAAATTACATGATAAATGTAGCTGAAAAAAAAAAAAA

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FIGURE 324

MHIKSIILEGFKSYAQRTEVNGFDPLFNAITGLNGSGKSNILDSICFLLGISNLSQVRASNLDLVYKNGQAGIT
KASVSITFDNSDKKQSPGLGFEVHDEITVTRQVVIGGRNKYLINGVNANNTRVQDLFCVGLNVNPNHFLIMQGRI
TKVLNMKPPEILSMIEEAAGTRMYEYKKIAAQKTIEKKEAKLKEIKTILEEEITPTIQKLKEERSSSYLEYQKVMR
EIEHLSRLYIAYQFLLAEDTKVRSAEELKEMQDKVIKLQEELSENDKKIKALNHEIEELEKRKDKETGVILRSLE
DALAEAQRVNTKSQSAPDLKKKNLACEESKRKELEKNMVEDSKTLAAKEKEVKKITDGLHALQEASNKDAEALAA
AQQHFNASAGLSSNEDGAEATLAGQMMACKNDISKAQTEAKQAQMKLKHAAQELKNKQAEVKKMDSGYRKDQEA
LEAVKRLKEKLEAEMKKLNYEENKEESLLEKRRQLSRDIGRLKETYEALLARFPNLRFAKDPKKNWNRNCVKGL
VASLISVKDTSATTALELVAGERLYNVVVDTEVTGKKLLERGERLKRRTIIPLNKISARCIAPETLRVAQNLVGP
DNVHVALSLVEYKPELQKAMEFVFGTTFVCDNMDNAKKVAFDKRIMTRITVTLGGDVFDPHGTLSSGGARSQAASIL
TKFQELKDVQDELRIKENELRALEEEELAGLKNTAEKYRQLKQQWEMKTEEADLLQTKLQQSSYHKQQEELDALKK
TIEESEETLKNTKEIQKAEKYEVLNKMKNAAEAERERELKDAQKKLDCAKTKADASSKKMKEKQQEVEAITLE
LEELKREHTSYKQQLAEAVNEAISKYESQIEVMAAEVAKNKESVNKAQEEVTKQKEVITAQDTVIKLNMQKWQNTN
SKTMILSLKIKELDHHISKHKREAEDGAAKVSMLKDYDWINAERHLFGQPNSAYDFKTNNPKEAGQRLQKLQEM
KEKLGRNVNMRAMNVLTEAEERCNDLMKKKRIVENDKSKILTTIEDLDQKKNQALNIAWQKVNKDFGSIFSTLLP
GANAMLAPPEGQTVLDGLEFKVALGNTWKENLTLSGGQSRSLVALSLILSMLLFKPAPIYILDEVDAALDLSHTQ
NIGQMLRTHFTHSQFIVVSLKEGMFNANVLFKTKFVDGVSTVARFTQCQNGKISKEAKSKAKPPKGAHVEV

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FIGURE 325

AGCAATGGCGGTTCCCGGCGTGGGGCTCTTGACCCGTTTGAACCTGTGTGCCCGGAGAAGAACTCGAGTCCAGCG
GCCTATCGTCAGGCTTTTGAGTTGCCCAGGAAGTGTGGCCAAAGACCTTAGGAGAGACGAGCAGCCTTCAGGGAG
CGTGAGACAGGCTTTGAAGACAAGATTCCCAAAAGGAGATTCTCTGAGATGCAAAATGAAAGACGAGAACAGGC
ACAGCGGACTGTTTTAATACATTGCCCAGAGAAAAATCAGTGAAAACAAGTTTCTTAAATATTTATCCCAATTTGG
ACCTATTAATAATCATTTCCTCTATGAAAGCTTTGGTCTCTATGCTGTCGTAGAATTTTGCCAAAAGGAAAGCAT
AGGTTCACTGCAGAATGGGACTCATACTCCAAGCACGGCCATGGAGACTGCAATTCATTGAGATCACGTTTCTT
CAATCTGAAGTTGAAAAACCAGACTTCTGAACGGTCACGCGTACGGTCAAGTAATCAGTTGCCACGTTCAAACAA
GCAGCTTTTTGAATTACTTTGTTATGCAGAAAGTATAGACGATCAGCTGAACACTCTCTTGAAGGAGTTCCAGCT
AACAGAGGAGAACACTAAGCTCCGATATCTCACCTGTTCTCTTATTGAAGACATGGCCGCGCGTATTTTCCAGA
CTGCATAGTCAGACCCTTTGGCTCCTCAGTCAACACTTTTGGGAAGTTAGGATGTGATTTGGACATGTTTTTGG
TCTAGATGAAACCAGAAACCTCAGCGCTCACAAGATCTCAGGAAATTTTCTGATGGAATTTCAAGTGAAAAATGT
TCCTTCAGAAAGAATTGCAACTCAGAAGATCCTGTCTGTGTTAGGAGAGTGCCTTGACCACCTTTGGCCCTGGCTG
TGTGGGTGTGCAAAAAATATTAAATGCCCGGTGTCCGCTCGTGAGGTTCTCACACCAGGCCTCCGGATTTTCAGTG
TGATTTGACTACGAACAATAGGATTGCCTTGACAAGTTCCGAACCTCCTTTATATATATGGTGCCCTAGACTCAAG
AGTGAGAGCCTTGGTGTTTCAAGTGTACGGTGTGGGCTCGAGCACATTCATAACAAGTAGTATTCTCTGGTGCATG
GATTACAAATTTCTCCCTTACAATGATGGTCATCTTTTTTCTCCAGAGAAGATCACCCCTATTCTTCCAACACT
AGATTCCTTAAAAACCCTAGCAGATGCAGAAGATAAATGTGTAATAGAAGGCAACAACCTGCACATTTGTTTCGTGA
CTTGAGTAGAATTAAACCTTCACAGAACACAGAAACATTAGAATTACTACTGAAGGAATTTTTTGAGTATTTTGG
CAATTTTGCTTTTCGATAAAAAATTCATAAATATTCGACAGGGAAGGGAGCAAAACAAACCTGATTCTTCTCCTCT
GTACATTGAGAATCCATTTGAACTTCTCTCAACATAAGCAAAAATGTAAGTCAAAGCCAGCTGCAAAAATTTGT
AGATTTGGCCCGAGAAAGTGCCTGGATTTTACAACAGGAAGATACAGATCGACCTTCCATATCAAGTAATCGGCC
CTGGGGGCTGGTATCCCTATTGCTACCATCTGCTCCAAACAGAAAGTCCTTTACCAAGAAGAAAAGCAATAAGTT
TGCAATTGAAACAGTCAAAAACCTTGCTAGAATCTTTAAAAGGTAACAGAACAGAAAATTTACAAAAACAGTGG
GAAGAGAACAATTAGTACTCAGACATTGATGGCTGCTACATTGTGTAAAGAACTGGGCTTAGCCTATCAATGGTC
TGTGGACTTACTTGGAACAACTGATTTGAACTTTACAGATCTCAGCTTTTCTGATGTCACCTTTTCATGATC
TTCTCATTGGCCCCCTTAACCTGGTCTGAAGTTCTGGGATGTTTTAGTTTGATCAGTCTGATACTCAGTGGCAC
TTTATTAAACATCAGCTGTGGAGTGTGGCGGTGCACACCTGTAGTCCCAGCTGCTCAGGAGGCTGAGGCAGGAG
GATCTCTTGAGCCCAGGATTTTGAATCCATCGTGGACAACATAGCAAGATTCCATCTCT

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FIGURE 326

MAVPGVGLLTRNLCCARRRTRVQRPIVRLLSCPGTVAKDLRRDEQPSGSVETGFEDKIPKRRFSEMQRERREQAQ
RTVLIHCPEKISENKFLKYLSQFGPINNHFFYESFGLYAVVEFCQKESIGSLQNGTHTPSTAMETAIPFRSRFFN
LKLKNQTSERSRVRSSNQLPRSNKQLFELLCYAESIDDQLNTLLKEFQLTEENTKLRYLTCSLIEDMAAAYFPDC
IVRPFSSVNTFGKLGCDLDMFLDLDETRNLSAHKISGNFLMEFQVKNVPSEIATQKILSVLGECLDHFPGCV
GVQKILNARCPVRFHQASGFQCDLTNNRIALTSELLIYGALDSVRVALVFSVRCWARAHSLSIPGAWI
TNFSLTMMVIFFLQRRSPILPTLDSLKTLADAEDKCVIEGNNCTFVRDLSRIKPSQNTETLELLLKEFFEYFGN
FAFDKNSINIRQGREQNKPDSSPLYIQNPFETSLNISKVNSQSQLOKFVDLARESAWILQQEDTDRPSSSNRPW
GLVSLLLPSAPNRKSFTKKKSNKFAIETVKNLLESILKGNRTENFTKTSKRTISTQT

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FIGURE 327

TTCTGCTTATCATGGTTACCAACAAAATGACTGCTGCCTTTAGAAAACCTAGTGGGAAACAGGTGGCGACAGACA
AAGTTGCAGAAAAGCTGAGCTCTACTCTCTCATGGGTGAAGAACACAGTATCGCATACAGTCAGTCAGATGGCCA
GTCAGGTGGCAAGTCCATCTACTTTCATTACATACCACATCCTCATCTACCACACTATCAACACCAGCCCTTTTAC
CATCTTCCCATCACAGTTGAGTCCAGACGTCTTAGAACTCCTGGCTAAACTGGAAGAACAGAATATATTGTTAG
AAACGGATAGTAAGTCTTTAAGATCTGTAAATGGGTCAAGAAGAAACAGTGGCTCTTCTCTTGTGTGCGAGTTCAT
CAGCCTCTAGCAACCTCAGTCACCTTGAAGAAGATTCTTGGATTCTTGGGGAAGAATTGTTAATGAATGGGAAG
ATGTACGCAAAAAGAAGGAAAAGCAAGTTAAGGAACCTTGTTTCATAAAGGGATACCCCATCACTTTAGAGCAATAG
TTTGGCAACTTTTATGCAGTGCACAAAGTATGCCAATTAAGGATCAGTATTCAGAACTCCTGAAAATGACCTCGC
CTTGTGAAAAATTGATCCGAAGGGACATTGCTAGAACTTACCCTGAACACAACCTTTTTTAAGGAAAAAGATAGCC
TTGGACAGGAGGTTTTATTAAATGTAATGAAGGCTTACTCTTTAGTAGATCGTGAGGTTGGTTACTGTCAAGGAA
GTGCTTTTTATAGTTGGATTGTTGCTTATGCAGATGCCAGAAGAAGAAGCTTTCTGTGTATTTGTTAAATTAATGC
AAGATTATAGACTTCGTGAACCTTTTTAAACCAAGTATGGCAGAATTGGGCCTTTGTATGTACCAGTTTGAATGTA
TGATACAGGAGCATCTTCCAGAGCTCTTTGTACATTTTCAATCTCAGAGTTTTTCATACCTCAATGTATGCATCAT
CCTGGTTTTCTGACTATCTTTCTTACAACCTTTTCCACTACCAGTTGCAACAAGGATATTTGATATCTTTATGTCTG
AGGGTTTAGAAATAGTGTTCGTGTAGGATTAGCACTTCTTCAGATGAATCAGGCAGAAGTATGCAACTTGACA
TGGAAGGGATGTTACAGCACTTTCAAAAGGTCATTCCACATCAGTTTGATGGTGTCCAGACAAGCTAATCCAAG
CAGCTTACCAAGTCCAATACAATTCAAAAAAATGAAAAAGCTTGAAAAGGAATACACTACAATAAAAAACGAAAG
AAATGGAAGAGCAAGTTGAAATTAAAGGTTACGCACAGAAAATAGACTTTTAAACAGCGCATCGAGACATTAG
AAAAACATAAATGCAGTTCCAACATAACGAAGATTTTGTGCTACAGCTAGAGAAGGAATTGGTCCAAGCCCGAC
TGAGTGAAGCTGAGTCTCAGTGTGCATTAAAAGAGATGCAGGATAAAGTCTTGGATATAGAGAAGAGGAATAACT
CCCTTCCTGATGAGAATAATATTGCAAGGCTTCAGGAAGAACTCATTGCTGTGAAACTTAGAGAAGCAGAAGCCA
TTATGGGTTTGAAGAAGCTTAGACAGCAAGTCAAGGATTTAGAGGAACACTGGCAGCGCCACTTAGCTCGTACTA
CTGGGAGATGGAAGACCCACCCAAGAAAAATGCTATGAATGAGTTACAGGATGAACCTGATGACCATTTCGACTTA
GAGAAGCTGAAACACAAGCAGAAATAAGAGAAATAAAACAAAGGATGATGGAAATGGAACACAGTTGGTTGAAT
CCGCAGATGTGGAGCCTGCATATATGAAGGGCTGACCCTATCTCTGCTCCTTCCAGAGTATCTGGCATGTGA
TGAGCTCGCCACAAACATTTAGTGATTTCGAGTAAGGCTCTGGTTGATTACAGTTTCTACTTTCTGACACTCTG
TTGCTGGTTTGAATAAAAAATTTCTTCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 328

MVTNKMTAAFRNPSGKQVATDKVAEKLSSSTLSWVKNTVSHTVSQMASQVSPSTSLHTTSSSTTLSTPALSPSSP
SQLSPDVLELLAKLEEQNILLETDKSLRSVNGSRNSGSSSLVSSSSASSNLSHLEEDSWILWGRIVNEWEDVRK
KKEKQVKELVHKGIPHHFRAIVWQLLCSAQSMPIKDQYSELLKMTSPCEKLIRRD IARTYPEHNFFKEKDSLGOE
VLFNVMKAYSLVDREVGVCQGSFIVGLLLMQMPEEEAFVFKVLMQDYRLRELFKPSMAELGLCMYQFECMIQE
HLPELFVHFQSQSFHTSMYASSWFLTIFLTTFPLPVATRIFDIFMSEGLEIVFRVGLALLQMNQAEMLQDMEGM
LQHFQKVIPHQFDGVPDKLIQAAYQVQYNSKKMKKLEKEYTTIKTKEMEEQVEIKRLRTENRLLKQRIETLEKHK
CSSNYNEFDVLQLEKELVQARLSEAESQCALKEMQDKVLDIEKRNNSLPDENN IARLQEELI AVKLREAEAIMGL
KELRQQVKDLEEHWQRHLARTTGRWKDPPKKNAMNELQDELMTIRLREAEQAEIREIKQRMMEETQLVESADV
EPAYMKG

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FIGURE 329

TGGTGAAAACATGATCTTGCTATGTTGCTCAGGCTGGTTGTCTGGCATTTCCTTTGTCCTTTATTCTTTATACTA
GCTAAACCCTGGAGTATCCTTGAAGCCTTTACTGGCATAACAGAGTACCTGAATCTTACTTTGGAGCCTAGCATGG
GTCATAAATATATCTGATTTCATTAACCTGTGAGACAGCTGAGAGAACACAGACTCCTTACCTGTATCTCCAGGCA
TATCTGGTTTTTCTCTGCCTAATAGATTTTCCTGCTTTCTAGTTAGTAATATTGAGAAAGAAGAAAGGCTTATTT
ATCATTGCTTTTTTCCACTGTGAATCATCTGTTCTTCCATGAACATTCTGGGGAGCACCTCCTGATTAACT
CCTGTCTCCCTGACCACTATCCTGCTGTCATTGGACTTCTTGAAGCACATGGGCTACTGCCCCAGGACACTGGGA
TTTGAGAGGAGTTTAGTGGAATTGTCAGGTCTTCAAAGCATTTATTATTCCTTTTATACGGAGATTTTCACTAT
TGAGACTTAAATGAAGTGAAGAAATGAGATTGAACATTTAATATTTTGGATGTAACTTTGAAGAAAGTATGCTT
TGGTGCTTAAATTTGTATATGATTTTAGGTAAGAACTTTGATAATATTGGCATAANNNNNNNNNNNNNNNNNNN
NN
NN
NN
GCTACTTAGATTTCAGCTTTCTGAGATGTTATTGTTAAACATTAAGGCTAATTTATTATAATGAAAATGTAACTT
TGAGGTATGTTAATATATAAACATCTTTTTCTTTGGCCTAAAAGGTCTTTAGTATTTCAGCACACTGGGTAAAGT
TCAGTTTAGACACAATCAAATTGGCATCTTTTAAACATAAGTGAAATATAGAGAGCTTGAACCTGAGTTACTTAA
AGAAGATACAGTATAATTAATTATACAGAACAAAACAAAGATGTGTTTAGAGTGAATCTGGCCTGACTCTTGTC
ATCAGCCCCCTAGTAGCCTATCTTCAGCCTTTGGGAAGTCTTAACTTCCCAGGTAAACTAGAATATTCTGGAAC
GAGCTGTCCAAATTTTCATCTTAAAGTGGATCATTGACTCTGAAACACGATTCTCATGGCAGAAAAAGCCCTGGT
GTTTCCTTGGAGCTGGGGATAAAGGCCAGTGAGCCAGCCTGTGATGAGAGCTGCCCCCTGGCACTATCTGAGTGGA
AAGCTCATTGGGACAGCCATGCAGCTATCAGAGCCGACTGAAGCCCTGTCCCTTACCCCTCAGGCACCTGATGCT
TAACTTGCCTCCTGGGAAATAATGATCTAGCATTTACTTGAACAATGATTAATCATGTTCTTTAATAATTGCTG
ACATTTGTATTTTAAAGCTGTATACCAATGTTTCGTAATTTGACATTGATTTTCTAACCATTAGAGATATTTAATTAA
AACTTGGAAATGAAAGAAACAAATGA

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FIGURE 330

GENMILLCCSGWLSGIFFVLYSLY

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FIGURE 331

GGGAGCAGAGTCGACTGGGAGCGACCGAGCGGGCCGCCGCCGCCGCCATGAACCCCGAATATGACTACCTGTTTA
AGCTGCTTTTGATTGGCGACTCAGGCGTGGGCAAGTCATGCCTGCTCCTGCGGTTTGCTGATGACACGTACACAG
AGAGCTACATCAGCACCATCGGGGTGGACTTCAAGATCCGAACCATCGAGCTGGATGGCAAACTATCAAAC TTC
AGATCTGGGACACAGCGGGCCAGGAACGGTTCGGGACCATCACTTCCAGCTACTACCGGGGGGCTCATGGCATCA
TCGTGGTGTATGACGTCACTGACCAGGAATCCTACGCCAACGTGAAGCAGTGGCTGCAGGAGATTGACCGCTATG
CCAGCGAGAACGTCAATAAGCTCCTGTTGGGCAACAAGAGCGACCTCACCACCAAGAAGGTGGTGGACAACACCA
CAGCCAAGGAGTTTGCAGACTCTCTGGGCATCCCCCTTCTTGGAGACGAGCGCCAAGAATGCCACCAATGTCGAGC
AGGCGTTCATGACCATGGCTGCTGAAATCAAAAAGCGGATGGGGCCTGGAGCAGCCTCTGGGGGCGAGCGGCCCA
ATCTCAAGATCGACAGCACCCCTGTAAAGCCGGCTGGCGGTGGCTGTTGCTTAGGAGGGGCACATGGAGTGGGACA
GGAGGGGGCACCTTCTCCAGATGATGTCCCTGGAGGGGGGAGGAGGTACCTCCCTCTCCCTCTCCTGGGGCATT
GAGTCTGTGGCTTTGGGGTGTCTGGGCTCCCCATCTCCTTCTGGCCCATCTGCCTGCTGCCCTGAGCCCCGGTT
CTGTGAGGGTCCCTAAGGGAGGACACTCAGGGCCTGTGGCCAGGCAGGGCGGAGGCCTGCTGTGCAGTTGCCTCT
AGGTGACTTTTCAAGATGCCCCCTACACACCTTTCTTTGGAACGAGGGCTCTTCTGTGGTGTCCCTCCCACCC
CCATGTATGCTGCAC TGGGTTCTCTCCTTCTTCTTCTGCTGTCTGCCCCAAGAACTGAGGGTCTCCCCGGCCTC
TACTGCCCTGGCTGCAGTCAGTGCCCAGGGCGAGGAATGTGGCCAGGGGATCCAGGACCTGGGATCCAGGGCCCT
GGGCTGGACCTCAGGACAGGCATGGAGGCCACAGGGGGCCAGCAGCCCACCCTTTCCTCTCCCCACTGCCTCCTC
TCCCTTCTCTACACTCCCAGCTCGAGCCGTCCAGCTGCGGTGGGATCTGAGTATATCTAGGGCGGGTGGGCGGGTA
GCAGTGCTGGGCCTGTGTCTTGAGCCTGGAGGGAGACTGCTCCTGCCGCCCTCTGCCCTGCCGGAGACAGACCCA
TGCGCTGCCTGCCACCGTGCCCTTTGTCCCATGTGAGGCGGAGGCGGAAGGCCACCCTGCCAGAGGCTGGG
CACCAGCCTTAACCCTCACTCTGCTAGCACCTCCTCCCTTCCCCAAGGTAGCACATCTGGCTCACTCCCCACTC
CGTCTCTGGAGCCCACCAGGGAAGGCCCTCATCCCCTGCCGCTACTTCTCTGGGGAATGTGGGTTCATCCAGGA
TTGGGGGCCTCTCTGCTCACCCACTCTGCACCCAGGATCCTAGTCCCCTGCCCTCTGGCACAGCTGCTTCCTGCA
AGAAAGCAAGTCTTTGGTCTCCCTGAGAAGCCATGTCCCTCGTGCTGTCTCTTGCCCTGTCCACCTGTGCCCTGC
CCTCCAGCTTGTATTTAAGTCCCTGGGCTGCCCCCTGGGGTGCCCCCGCTCCAGGTTCCTCTGGTGTGAT
GTCAGGCATTTTGCAAGGAAAAGCCACTTGGGGAAAGATGGAAAAGGACAAAAAAATTAATAAATTTCCATTGG
CCCTCGGGTGAGCTGAGGGTTTTTGCAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGG
AAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGG

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FIGURE 332

MNPEYDYLKLLLLIGDSGVGKSCLLLRFADDTYTE SYISTIGVDFKIRTIELDGKTIKLQIWDTAGQERFRTITS
SYIRGAHGIIIVVDVTDQESYANVKQWLQEIDRYASENVNKLKLVGNKSDLTTKKVVDNTTAKEFADSLGIPFLET
SAKNATNVEQAFMTMAAEIKKRMGPGAASGGERPNLKIDSTPVKPAAGGCC

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FIGURE 333

GCGCGACACTGACCTTCAGCGCCTCGGCTCGGCCATGGCGCCCTCCAGGAAGTTCTTCGTTGGGGGAACTGGAA
GATGAACGGGCGGAAGCAGAGTCTGGGGGAGCTCATCGGCACCTCTGAACGCGGCCAAGGTGCCGGCCGACACCGA
GGTGGTTTGTGCTCCCCCTACTGCCTATATCGACTTCGCCCCGGCAGAAGCTAGATCCCAAGATTGCTGTGGCTGC
GCAGAACTGCTACAAAGTGACTAATGGGGCTTTTACTGGGGAGATCAGCCCTGGCATGATCAAAGACTGCGGAGC
CACGTGGGTGGTCTCTGGGACACTCAGAGAGAAGGCATGTCTTTGGGGAGTCAGATGAGCTGATTGGGCAGAAAGT
GGCCCATGCTCTGGCAGAGGGACTCGGAGTAATCGCCTGCATTGGGGAGAAGCTAGATGAAAGGGAAGCTGGCAT
CACTGAGAAGGTTGTTTTTCGAGCAGACAAAGGTCATCGCAGATAACGTGAAGGACTGGAGCAAGGTCGTCTCTCGC
CTATGAGCCTGTGTGGGCCATTGGTACTGGCAAGACTGCAACACCCCAACAGGCCCAGGAAGTACACGAGAAGCT
CCGAGGATGGCTGAAGTCCAACGTCTCTGATGCGGTGGCTCAGAGCACCCGTATCATTATGGAGGCTCTGTGAC
TGGGGCAACCTGCAAGGAGCTGGCCAGCCAGCCTGATGTGGATGGCTTCCTTGTGGGTGGTGCTTCCCTCAAGCC
CGAATTCGTGGACATCATCAATGCCAAACAATGAGCCCCATCCATCTTCCCTACCCCTTCCCTGCCAAGCCAGGGAC
TAAGCAGCCCAGAAGCCCAGTAAGTGGCCTTTCCCTGCATATGCTTCTGATGGTGTCTCTGCTCCTTCCCTGTGG
CCTCATCCAAACTGTATCTTCCCTTTACTGTTTATATCTTACCCCTGTAATGGTTGGGACCAGGCCAATCCCTTCT
CCACTTACTATAATGGTTGGAATAAACGTCACCAAGGTGGCTTCTCCTTGGCTGAGAGATGGAAGGCGTGGTGG
GATTGCTCCTGGGTTCCTTAGGCCCTAGTGAGGGCAGAAGAGAAACCATCCTCTCCCTTCTTACACCGTGAGGC
CAAGATCCCCCTCAGAAGGCAGGAGTGCTGCCCTCTCCCATGGTGCCCGTGCCCTCTGTGCTGTGTATGTGAACCAC
CCATGTGAGGGAATAAACCTAGCACTAGG

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FIGURE 334

MAPSRKFFVGGNWKMNGRKQSLGELIGTLNAAKVPADTEVVCAPPTAYIDFARQLDPKIAVAAQNCYKVTNGAF
TGEISPGMIKDCGATWVVLGHSERRHVFGESEDELIGQKVAHALAEGLGVIACIGEKLDEREAGITEKVVFEQTKV
IADNVKDWSKVVLAYEPVWAIGTGKTATPQQAQEVHEKLRGWLKSNVSDAVAQSTRIIYGGSVTGATCKELASQP
DVDGFLVGASLKPEFVDIINAKQ

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FIGURE 335

GTGCGGGAATCACACACATACCTCAGAAATGCCGGGTCTAAGTTGTAGATTTTATCAACACAAATTCCTGAGGTG
GAAGATGTAGTGATGGTGAATGTCAGATCCATTGCTGAAATGGGGGCTTATGTCAGCTTGCTGGAATACAACAAC
ATTGAAGGCATGATTCTTCTTAGTGAATTATCCAGAAGGCGTATCCGTTCTATCAACAAACTCATCCGAATTGGC
AGGAATGAGTGTGTGGTTGTCATTAGGGTGGACAAAGAAAAAGGATATATTGATTTGTCAAAAAGAAGAGTTTCT
CCAGAGGAAGCAATCAAATGTGAAGACAAATTCACAAAATCCAAAAGTGTATAGCATTCTTCGTCATGTTGCT
GAGGTGTTAGAATACACCAAGGATGAGCAGCTGGAAAGCCTATTCCAGAGGACTGCCTGGGTCTTTGATGACAAG
TACAAGAGACCTGGATATGGTGCCTATGATGCATTTAAGCATGCAGTCTCAGACCCATCTATTTTGGATAGTTTA
GATTTGAATGAAGATGAACGGGAAGTACTCATTAAATAATTAATAGGCGCTTGACCCACAGGCTGTCAAAATT
CGAGCAGATATTGAAGTGGCTTGTTATGGTTATGAAGGCATTGATGCTGTAAAAGAAGCCCTAAGAGCAGGTTTG
AATTGTTCTACAGAAAACATGCCCATTAAAGATTAATCTAATAGCTCCTCCTCGGTATGTAATGACTACGACAACC
CTGGAGAGAACAGAAGGCCCTTCTGTCTCAGTCAAGCTATGGCTGTTATCAAAGAGAAGATTGAGGAAAAGAGG
GGTGTGTTCAATGTTCAAATGGAGCCCAAAGTGGTCACAGATACAGATGAGACTGAACTTGCGAGGCAGATGGAG
AGGCTTGAAAGAGAAAAATGCCGAAGTGGATGGAGATGATGATGCAGAAGAAATGGAAGCCAAAGCTGAAGATTAA

CTTTGTGGGAAACAGAGTCCAATTTAAGGAACACAGAGCAGCGCTTCCTGGCTGTAAATCCTAGACTTGAAAGTT
TTCCAGTATTGAAAACCTCAAAGCTGAATATTTTTTATTTCTAAGTATTTAAATGTTCTAACAGATCAGAACATG
AAATGCCCTCCTAAATGTCAGCTGTTGTCACACAGTAGCTCCAACACTTTGAGCATTTTTAAGGGAGTGGCCTCA
TTTCACTAGAGACAAATCTTTAAGAATAGTTCTAAAATTGGGCTTGTGATTTCCATTTCTGATGTCTCCAGATTG
GCACCCCTTTCTAGTTCAATGCCTCACGAGATTTGCCAGGGGCATCCAAGGCAAACAATCCCAATCTTTCTATAT
AAAATGTATTCAAGCAAACATCAAATAAATTTCTGGGATATTT

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FIGURE 336

MPGLSCRFYQHKFPEVEDVVMVNVRSIAEMGAYVSLEYNNIEGMILLSELSRRRIRSINKLIRIGRNECVVVIR
VDKEKGYIDLKRRVSPEEAIKCEDKFTKSKTVYSILRHVAEVLEYTKDEQLESLEFQRTAWVFDDKYKRPYGYAY
DAFKHAVSDPSILDSLDLNEDEREVLINNINRRLLTPQAVKIRADIEVACYGYEGIDAVKEALRAGLNCSTENMPI
KINLIAPPRYVMTTTLERTEGLSVLSQAMAVIKEKIEEKRGVFNVQMEPKVVTDTDETALARQMERLERENAEV
DGDDDAEEMEAKAED

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FIGURE 337

GGGGGCCAGTTACCATATTGTCCGGAGTGGGTCTTGACATTTCAGGAAAGATACATCCTCAGACCTTTCAAAT
TGTCATGCCTCTCTAACCTAAAACAGCCCTCATTAAATGCACCTTAATCCGAGCACTGTATGGCTTGGAAAGAAT
TATGAGTGAGGAGAGGAGCCCTTTCTTATTGGCCAAAGCCGTGGATCCCAGACACCCCAATATGATGACAGATGT
GGTTAAACTTCTCTCTGCGGTATGCATTGTAGGGGAAGAAAGCATCCTTGAAGAAGTTTTAGAAGCTTTAACTTC
AGCTGGTGAAGAAAAAAATTGACAGATTTTTTTGTATTGTGGAAGGCCTCCGGCACAATTCAGTTCAACTGCA
AGTAGCTTGTATGCAGCTCATCAATGCCCTGGTTACATCTCCTGATGATTTGGATTTAGGCTTCACATCAGAAA
TGAATTTATGCGTTGTGGATTGAAAGAGATATTGCCAAATTTAAAATGCATTAAGAATGATGGCCTGGATATCCA
ACTTAAAGTCTTTGATGAGCATAAAGAAGAAGATTTGTTTGAGTTATCCCATCGCCTTGAAGATATTAGAGCTGA
ACTTGATGAAGCATATGATGTTTACAACATGGTGTGGAGCACAGTTAAAGAACTAGAGCAGAGGGATATTTTAT
TTCTATTCTTCAGCATCTTTTGCTGATTGCAATGATTATTTTATAAGGCAACAATACTTCAAATTAATTGATGA
GTGTGTATCCCAGATTGTATTGCATAGAGATGGAATGGATCCAGACTTCACATATCGAAAAAGACTAGATTTAGA
TTTAACCCAGTTTGTAGACATTTGCATAGATCAAGCAAACTAGAAGAGTTTGAAGAGAAAAGCATCAGAACTTTA
CAAGAAATTTGAAAAAGAGTTTACCGACCACCAAGAACTCAGGCTGAATTGCAGAAAAAAGAGGCAAAGATTAA
TGAGCTTCAAGCAGAGCTACAAGCTTTAAGTCTCAGTTTGGTGCCTTGCCAGCTGATTGTAATATTCCTTTGCC
TCCCTCTAAAGAAGGTGGAAGTGGCCACTCAGCACTTCCTCCTCCGCTCCACTGCCTTCTGGTGGAGGGGTGCC
GCCTCCACCTCCTCCCCACCACCTCCTCCACTTCAGGAATGCGGATGCCATTGAGTGGTCTGTGCCTCCACC
ACCTCCCCTGGGATTCTTGGAGGACAAAATTCCTCCTCTACCAATCCTGCCATTGGGTTGAAACCAAAGAA
AGAATTTAAACCTGAAATCAGCATGAGAAGATTGAATTGGTTAAAGATCAGACCTCATGAAATGACTGAAACTG
TTTCTGGATAAAAGTAAATGAAAATAAGTATGAAAACGTGGATTGCTTTGTAACTTGAGAATACATTTTGTG
CCAACAAAAAGAGAGAAGAGAAGAGGAAGATATTGAAGAGAAGAAATCGATTAAGAAAAAAATTAAAGAACTTAA
GTTTTTAGATTCTAAAATTGCCCAGAACCTTTCAATCTTCCTGAGCTCTTTTCGGGTGCCATATGAGGAAATCAG
AATGATGATATTGGAAGTAGATGAAACACGGTTGGCAGAGTCTATGATTCAGAACTTAATAAAGCATCTTCCTGA
TCAAGAGCAATTAATTCATTGTCTCAGTTCAAGAGTGAATATAGCAACTTATGTGAACCTGAGCAGTTTGTGGT
TGTGATGAGCAATGTGAAGAGACTACGGCCACGGCTCAGTGCTATTCTCTTTAAGCTTCAGTTTGAAGAGCAGGT
GAACAACATCAAACCTGACATCATGGCTGTCAGTACTGCCTGCGAAGAGATAAAGAAGAGCAAAAGCTTTAGCAA
GTTGCTGGAACCTTGATTGCTAATGGGAACTACATGAATGCTGGCTCCCGGAATGCTCAAACCTTCGGATTTAA
CCTTAGCTCTCTCTGTAACTAAAGGACACAAAATCAGCAGATCAGAAAACAACGCTACTTCATTTCTGGTAGA
AATATGTGAAGAGAAGTACCCTGATATACTGAATTTTGTGGATGATTTGGAACCTTTAGACAAAGCTAGTAAAGG
TTTGTGCCTTTTTAAGAAACATTTTCATGGCTCTGATCTTCAGTGCTAAAAGACTGAAAATTATACCTTTTATTTG
TATGTACTTTCCACTTTCTCACAGTGTTCATACCCAATATCTCATT**TAAAAA**TAAAGAGAGTTGTAGGATAT
TAAAAAAAAAAAAAAAAAAAAAG

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FIGURE 338

MSEERSLSLLAKAVDPRHPNMTDVVKLLSAVCIVGEESILEEVLEALTSAGEEKKIDRFFCIVEGLRHNSVQLQ
VACMQLINALVTSPDDLDLRLHIRNEFMRCGLKEILPNLKCIKNDGLDIQLKVFDEHKEEDLFELSHRLEDIRAE
LDEAYDVYNMVWSTVKETRAEGYFISILQHLLLRNDYFIRQQYFKLIDECVSQIVLHRDGMDFDFTYRKRLDLD
LTQFVDICIDQAKLEEFEEKASELYKKFEKEFTDHQETQAELOKKEAKINELQAELOAFKSQFGALPADCNIPLP
PSKEGGTGHSALEPPPPPLPSGGGVPPPPPPPPPLPGMRMPFSGVPPPPPLGFLGGQNSPPLPILPFGPKPKK
EFKPEISMRRLNWLKIRPHEMTENCFWIKVNENKYENVDLLCKLENTFCCQKERREEEDIEEKKSIIKKIKELK
FLDSKIAQNLSIFLSSFRVPYEEIRMMILEVDETRLAESMIONLIKHLDPQEQNLNLSQFKSEYSNLCEPEQFVV
VMSNVKRLRPRLSAILFKLQFEEQVNNIKPDIMAVSTACEEIKKSKSFSKLELVLLMGNYMAGSRNAQTGFN
LSSLCKLKDTKSADQKTLLHFLVEICEEKYPDILNFVDDLEPLDKASKGLCLFKKHFMALIFSARLKIIPFIC
MYFPLSHSVFIPNISE

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FIGURE 339

AAGAGCAAGGGATCACTGTGCTGGGTTTAAATGCGGTATTTGACATCTTGGTGATAGGCAAATTCAATGTTCTGG
AAATTGTCCAGAAGGTACTACATAAGGACAAGTCATTAGAGAATCTCGGCATCCTCAGGAACGGGGGCCTCCTCT
TCAGAATGACCCCTGCTCACCTCTGGAGGGGCTGGGATGCTCTACGTGCGCTGGAGGATCATGGGCACGGGCCCCG
CGGCCTTACCAGAGGTGGACAACCCGGCCTCCTTTGCTGACAGCATGCTGGTGAGGGCCGTAAACTACAATTACT
ACTATTCATTGAATGCCCTGGCTGCTGCTGTGTCCCTGGTGGCTGTGTTTTGATTGGTCAATGGGCTGCATCCCC
TCATTAAGTCCATCAGCGACTGGAGGGTAATTGCACCTGCAGCACTCTGGTTCCTGCCTAATTGGCCTGATATGCC
AAGCCCTGTGCTCTGAAGACGGCCACAAGAGAAGGATCCTTACTCTGGGCCTGGGATTTCTCGTTATCCCATTTC
TCCCCGCGAGTAACCTGTTCTTCCGAGTGGGCTTCGTGGTCGCGGAGCGTGTCTCTACCTCCCCAGCGTTGGGT
ACTGTGTGCTGCTGACTTTTGGATTTCGGAGCCCTGAGCAAACATACCAAGAAAAAGAAACCCATTGCCGCTGTG
TGCTGGGAATCTTATTCATCAACACGCTGAGATGTGTGCTGCGCAGCGCGAGTGGCGGAGTGAGGAACAGCTTT
TCAGAAGTGCTCTGTCTGTGTGTCCCTCAATGCTAAGGTTCACTACAACATTGGCAAAAACCTGGCTGATAAAG
GCAACCAGACAGCTGCCATCAGAACTACCGGGAAGCTGTAAGATTAAATCCCAAGTATGTTTCATGCCATGAATA
ATCTTGGAATATCTTAAAGAAAGGAATGAGCTACAGGAAGCTGAGGAGCTGCTGTCTTTGGCTGTTCAAATAC
AGCCAGACTTTGCCGCTGCGTGGATGAATCTAGGCATAGTGCAGAATAGCCTGAAACGGTTTGAAGCAGCAGAGC
AAAGTTACCGGACAGCAATTAACACAGAAGGAAATACCCAGACTGTTACTACAACCTCGGGCGTCTGTATGCAG
ATCTCAATCGCCACGTGGATGCCTTGAATGCGTGGAGAAATGCCACCGTGCTGAAACCAGAGCACAGCCTGGCCT
GGAACAACATGATTATACTCTCGACAATACAGGTAATTTAGCCCCAGCTGAAGCAGTTGGAAGAGAGGCACTGG
AATTAATACCTAATGATCACTCTCTCATGTTCTCGTTGGCAAACGTGCTGGGGAAATCCCAGGAATACAAGGAAT
CTGAAGCTTTTATTCCTCAAGGCAATTAAGCAAATCCAAATGCTGCAAGTTACCATGGTAATTTGGCTGTGCTTT
ATCATCGTTGGGGACATCTAGACTTGGCCAAGAAACACTATGAAATCTCCTTGCAGCTTGACCCACGGCATCAG
GAACTAAGGAGAATTACGGTCTGCTGAGAAGAAAGCTAGAACTAATGCAAAAGAAAGCTGTCTGATCCTGTTTCC
TTCATGTTTTGAGTTTGAAGTGTGTGTCATGAGGCATATCATTAAATAGTATGTGGTTACATTTAACCATTTAAAA
GTCTTAGACATGTTATTTTACTGATTTTTTTCTATGAAAACAAAGACATGCAAAAAGATTATAGCACCAGCAATA
TACTCTGAATGCGTGATATGATTTTTTCATTGAAATTGTATTTTTTCAGACAACTCAAATGTAATTTCTAAAATTC
CAAAAATGTCTTTTTTAATTAAACAGAAAAAGAGAAAAAATTATCTTGAGCAACTTTTAGTAGAATTGAGCTTAC
ATTTGGGATCTGAGCCTTGTCGTGTATGGACTAGCACTATTAACTTCAATTATGACCAAGAAAGGATACACTGG
CCCCTACAATTTGTATAAATATTGAACATGTCTATATATTAGCATTTTTTATTTAATGACAAAGCAAATTAAGTTT
TTTTATCTCTTTTTTTTAAACAACATACTGTGAACCTTTGTAAGGAAATATTTATTTGTATTTTTATGTTTTGAA
TAGGGCAAATAATCGAATGAGGAATGGAAGTTTTAACATAGTATATCTATATGCTTTTCCCCATAGGAAGAAATT
GACTCTTGCAAGTTTTTGGATGCTCTGACTTGTGCAATTTCAATACACAGGAGATTATGTAATGTAATATTTTTCA
TAAGCGGTTACTATCAATTGAAAGTTCAAGCCATGCTTTAGGCAAGAGCAGGCAGCCTCACATCTTTATTTTTGT
TACATCCAAGGTGAAGAGGGCAACACATCTGTGTAAGCTGCTTTTTAGTGTGTTTATCTGAAGGCCGTTTTCCAT
TTTGCTTAATGTAACACAGACATTATCCAGAAAAATGCAAAATTTCTATCAAATGGAGCCACATTCGGGGAATT
CGTGGTATTTTTAAGAATTGAGTTGTTCTGCTGTTTTTTATTTGATCCAAACAATGTTTTGTTTTGTTCTCTC
TGTATGCTGTTGACCTAATGATTTATGCAATCTCTGTAATTTCTTATGCAGTAAATTAATAACAACTAG

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FIGURE 340

MLRNGGLLFRMTLLTSGGAGMLYVRWRIMGTGPPAFTEVDNPASFADSM LVRAVNYNYYYYSLNAWLLLCPPWWLCF
DWSMGCIPLIKSISDWRVIALAALWFCLIGLICQALCSEDGHKRRILTLGLGFLVIPFLPASNLFFRVGFVVAER
VLYLPSVG YCVLLTFGFGALSKHTKKKKPIAAVVLGILFINTLRCVLRSGEWRSEEQLFRSALSVCPLNAKVHYN
IGKNLADKGNQTAAIRNYREAVRLNPKYVHAMNNLGNILKERNELQEAEE LLSLAVQIQPDFAAAWMNLGIVQNS
LKRFEAAEQSYRTAIKHRRKYPDCYYNLGRLYADLNRHVDALNAWRNATVLKPEHSLAWNMIILLDNTGNLAQA
EAVGREALELIPNDHSLMFS LANVLGKSQEYKESEALFLKAIKANPNAA SYHGNLAVLYHRWGHLDLAKKHYEIS
LQLDPTASGTKENYGLLRKLELMQKKAV

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FIGURE 341

ATGAGTTGGAGCTTTCTGACTCGCCTGCTAGAGGAGATTACAACCATTCCACATTTGTGGGGAAGATCTGGCTC
ACTGTTCTGATTGTCTTCCGGATCGTCCTTACAGCTGTAGGAGGAGAATCCATCTATTACGATGAGCAAAGCAAA
TTTGTGTGCAACACAGAACAGCCGGGCTGTGAGAATGTCTGTTATGATGCGTTTGCACCTCTCTCCCATGTACGC
TTCTGGGTGTTCCAGATCATCCTGGTGGCAACTCCCTCTGTGATGTACCTGGGCTATGCTATCCACAAGATTGCC
AAAATGGAGCACGGTGAAGCAGACAAGAAGGCAGCTCGGAGCAAGCCCTATGCAATGCGCTGGAAACAACACCGG
GCTCTGGAAGAAACGGAGGAGGACAACGAAGAGGATCCTATGATGTATCCAGAGATGGAGTTAGAAAGTGATAAG
GAAAATAAAGAGCAGAGCCAACCCAAACCTAAGCATGATGGCCGACGACGGATTCGGGAAGATGGGCTCATGAAA
ATCTATGTGCTGCAGTTGCTGGCAAGGACCGTGTGTGAGGTGGGTTTTCTGATAGGGCAGTATTTCTGTATGGC
TTCCAAGTCCACCCGTTTTATGTGTGCAGCAGACTTCCTTGTCCTCATAAGATAGACTGCTTTATTTCTAGACCC
ACTGAAAAGACCATCTTCTTCTGATAATGTATGGTGTACAGGCCTTTGCCTCTTGCTTAACATTTGGGAGATG
CTTCATTTAGGGTTTGGGACCATTGAGACTCACTAAACAGTAAAAGGAGGGAACCTGAGGATCCGGGTGCTTAT
AATTATCCTTTCACTTGGAATACACCATCTGCTCCCCCTGGCTATAACATTGCTGTCAAACCAGATCAAATCCAG
TACACCGAACTGTCCAATGCTAAGATCGCCTACAAGCAAAAACAAGGCCAACACAGCCCAGGAACAGCAGTATGGC
AGCCATGAGGAGAACCTCCCAGCTGACCTGGAGGCTCTGCAGCGGGAGATCAGGATGGCTCAGGAACGCTTGGAT
CTGGCAGTTCAGGCCTACAGTCACCAAAACAACCTCATGGTCCCCGGGAGAAGAAGGCCAAAGTGGGGTCCAAA
GCTGGGTCCAACAAAAGCACTGCCAGTAGCAAATCAGGGGATGGGAAGAACTCTGTCTGGATTTAA

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FIGURE 342

MSWSFLTRLLEEIHNNSTFVGKIWLTVLIVFRIVLTAVGGESIYYDEQSKFVCNTEQPGCENVCYDAFAPLSHVR
FWVFQIILVATPSVMYLGAIHAKMEHGEADKKAARSKPYAMRWKQHRALEETEEDNEEDPMMYPEMELES DK
ENKEQS QPKPKHDGRRRIREDGLMKIYVLQLLARTVFEVGFLIGQYFLYGFQVHPFYVCSRLPCPHKIDCFISRP
TEKTIFLLIMYGV TGLCLLLNIWEMLHLGFGTIRD SLNSKRRELEDPGAYNYPFTWNTPSAPPGYNI AVKPDQIQ
YTELSNAKIAYKQNKANTAQEQQYGSHEENLPADLEALQREIRMAQERLDLAVQAYSHQNNPHGPREKKAKVGSK
AGSNKSTASSKSGDGKNSVWI

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FIGURE 343

CTCGAGATTTACCGGGGGCCTGGCTGCACGTTCCCTGTGCGCGTTCTGCGGCACGGGCGGTGGGACGTTGGTGG
GGTTGCGCTGCGGGGAGGAAGAGGCGACTTTCCACCTTCTAAGCCCGCCTCGGGTCGCGATGTCGTCCGGGGCCG
GGTCTCGGCGGCCGCGGGAGCCCGGAGCACGAGCTGCAGCGGCGGGGAGCAGAAACGGCGGCGGCACGACG
CGCAGCAGCTGCAGCAGCTCAAGCACCTGGAGTCCTTTTATGAGAAACCTCCTCCTGGGTTTATAAAGGAGGACG
AGACGAAGCCAGAAGACTGTATACCAGATGTGCCCGGCAATGAACATGCCAGGGAGTTTCTGGCTCACGCTCCGA
CTAAAGGACTGTGGATGCCCTTGGGAGAGAGGTCAAAGTTATGCAATGTTGGCGTTGCAAACGGTATGGCCATC
GAACAGGCGACAAAGAATGCCCTTTCTTTATCAAAGGCAACCAGAAGTTAGAACAGTTCCGAGTCGCACATGAAG
ATCCTATGTACGACATCATTCGCGAGAATAAAAGACATGAAAAGGATGTAAGGATCCAGCAGTTAAAGCAGTTAC
TGGAGGACTCCACCTCAGATGACGACGGGAGCAGCTCCAGCTCCTCGGGGGACAGAGAGAAGCGCAAGAAAAGGA
AGAAAAAGAAAAGCACAAGAAACGCAAGAAGGAGAAGAAAAAGAAAGAAACGGAAGCACAAGGCTTCCAAGT
CCAGTGAGAGCTCTGACTCAGAGTGAACAGCACCACCCACAGGCCAAAGGACAGAGCCGCCGCGAGAGTGAGAGA
CTGGACATCTAGCACAGCCCTGGGCCCTCACC GCCTCCTGGTGCCAAGTGACCACTGCAGAGCAGGTGGGCTCCT
GCGACACCTGTGTCTCTACCTTATGGTCACCGTGTCTGTGACTGCTTCAGTAGGCCGCTGCAGTGGGAGGTGAT
GAGAAGACACTGAAGGGGCAGACACTCTAGGGCAC TGCCACGGCGCGTTTGCCCTCCATGGTGTGGTAACTCAT
TTTCCATGAACCTAAGGCTTCACCTTCTTTGTGGTTTGGGATAAGGTAAATCTCGAG

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FIGURE 344

MSSGAGSRRPREPPEHELQRRREQKRRRHDAQQLQQLKHLESFYKPPPGFIKEDETKPEDCIPDVPGNEHAREF
LAHAPTKGLWMPLGREVKVMQCWRCKRYGHRTGDKECPFFIKGNQKLEQFRVAHEDPMYDIIRENKRHEKDVRIO
QLKQLLEDSTSDDDGSSSSSSGDREKRKKRKKKEKHKKRKEKKKKKKRKHKASKSSESSDSE

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FIGURE 345A

ATGGCCTCAGGAGCCGGAGGAGTCGGAGGGGGCGGTGGCGGCAAGATCCGGACGCGGCGTTGCCACCAGGGGCCA
ATTAAGCCTTACCAGCAGGGGCGACAACAGCATCAGGGCATTCTTAGCAGGGTTACAGAATCTGTTAAGAATATT
GTGCCAGGGTGGTTACAAAGATACTTCAACAAGATGAAGATGTATGCAGCTGTTCAACAGACACAAGCGAGGTT
CCACGCTGGCCAGAAAATAAAGAGGACCATCTGGTATATGCCGATGAGGAGAGCTCTAATATTACTGATGGGAGA
ATCACACCTGAGCCAGCAGTCAGTAATACAGAAGAACCTTCAACAACCTAGTACTGCTTCAAATTATCCAGATGTG
TTAACAAGGCCTTCTCTTCATCGGAGCCATCTGAATTTTTCCATGTTGGAATCCCCTGCATTACACTGTCAGCCA
TCTACATCCTCGGCATTCCCAATTGGCAGTTCGGGATTTTCCCTTGTAAGGAAATTAAAGATTCTACCTCTCAG
CATGATGATGATAACATCTCAACTACCAGTGGTTTTCTTCAAGAGCTTCTGATAAAGATATAACTGTTTCAAAG
AACACTTCATTGCCACCTCTGTGGTCCCCAGAAGCTGAACGTTCTCACTCACTCTCACAGCACACTGCCACCAGC
TCAAAAAAACAGCATTCAACTTGTCTGCCTTTGGAACACTTTCCCTTCACTTGGGAATTCTTCAATCCTTAAA
ACCAGTCAGCTTGGAGATTCTCCTTTTTATCCTGGAACAAACATACGGTGGGGCAGCAGCTGCTGTAAGACAG
TCTAAACTACGAAATACACCTTATCAGGCACCAGTTAGAAGACAAATGAAAGCTAAGCAACTCAGTGCACAATCT
TACGGTGTGACCAGTTCAACAGCTCGGCGAATATTGCAGTCTTTAGAGAAGATGTCAAGCCCTTTAGCGGATGCA
AAAAGAATTCCATCCATTGTTTCTCTCTCTGAATTTCTCTCTTGATAGGAGTGGGATAGATATCACAGATTTT
CAGGCCAAAAGAGAAAAGGTGGATTCTCAATATCCTCCTGTTTCAAGAGACTTATGACCCCAAAGCCAGTTTCCATA
GCAACAAATCGAAGTGTATTTTAAACCATCTCTGACTCCTTCTGGTGAATTCAGGAAGACTAATCAAAGAATA
GATAACAAGTGCAGTACTGGATATGAAAAAATATGACACCCGGACAAAATAGAGAACAACGAGAAAGTGGCTTT
TCATATCCAAATTTAGTTTGCCTGCAGCCAATGGTTTATCTTCTGGAGTAGGTGGTGGAGGTGGCAAGATGAGA
CGAGAAAGACACGCCTTGTGCTTCTAAACCTCTGGAGGAGGAGGAAATGGAAGTTCAGTATTACCGAAAAATC
TCTCTACCGATCACCAGTTCTCACTGCCTACCTTTAATTTTAGTTCCCTGAGATCACAACCTTCTCTCCATCA
CCCATCAATTCGTCTCAAGCATTAAACAAAGGTACAAATGACCTCTCCGAGCAGCACTGGCAGTCCCATGTTT
AAATTTTTCATCTCCAATCGTAAAAATCTACTGAGGCAAATGTACTACCTCCATCATCTATTGGATTTACATTTAGT
GTGCCTGTTGCAAAACAGCAGAACTTTCTGGTTCTAGTAGTACTTTAGAACCAATTATAAGTAGTTCAGTCTCAT
CATGTCACCTACAGTGAACAGTACAAATTGTAAGAAGACACCACCTGAAGATTGTGAGGGTCTTTTTAGACCTGCA
GAAATCCTGAAAGAAGGAAGTGTCTAGATATTCTGAAAAGCCCTGGTTTCGCATCGCCGAAGATAGATTCTGTT
GCTGCTCAGCCCACCGCAACAAGCCAGTAGTTTATACAAGACCAGCAATAAGTAGCTTTTCTTCTAGTGGAATT
GGGTTTGGGGAGAGTTTAAAAGCTGGGTCTCATGTCAGTGTGATACATGTCTACTCCAGAACAAGTTACAGAC
AACAAATGCATAGCCTGTCAAGCAGCAAAATTGTCACCCAGAGATACTGTAAACAGACTGGAATTGAAACACCA
AATAAAAGTGGCAAAACAACTCTTCTGCATCAGGGACAGGCTTTGGAGACAAATTTAAACCAGTGATAGGCACT
TGGGATTGTGATACCTGTTTAGTGCAAAATAAACCTGAAGCAATAAAATGTGTAGCCTGTGAAACACCGAAACCT
GGAACCTGTGTGAAGCGAGCCCTTACATTGACAGTGGTTTCGGAAAGTGTGAGACTATGACTGCTTCATCTTCC
AGCTGCACTGTAACCACTGGTACCTTAGGATTTGGAGATAAATTCAAAGGCCCATTTGGATCTTGGGAGTGTTC
GTATGCTGTGTTTCTAATAATGCAGAAGACAATAAGTGTGTGTCTGTATGTCTGAGAAACAGGAAGTTCAGTA
CCTGCTTCAAGTAGCAGCACTGTACCTGTCTCTCTGCCTTCTGGAGGCTCTCTAGGATTGGAAAAGTTCAAGAAA
CCCAGGGAAGCTGGGACTGTGAATTGTGCCTAGTGCAGAATAAGGCAGACTCTACCAATGTTTGGCATGTGAA
AGTGCAAGCCAGGCACAAAATCTGGGTTTAAAGGCTTTGACACATCTTCTCATCTTGAACCTCAGCAGCCTCC
TCATCCTTCAAATTTGGTGTCTCATCATCCTCTTCTGGGCCCTTCTCAGACTTTAACAAGCACTGGAAATTTTAAA
TTTGGAGATCAGGGAGGATTCAAATAGGTGTGTCTCATCTGATTCTGGGTCTATAAACCCCATGAGTGAAGGCTTT
AAATTTTCTAAACCAATAGGAGATTTTAAATTTGGAGTTTCTCTGAATCTAAGCCCGAAGAAGTTAAAAAGAT
AGTAAGAATGATAATTTTAAAGTTGGACTTTCTTCTGGTTTAAAGCAACCCAGTTCTTTAACTCCATTTCAATTT
GGGGTATCTAATCTTGGACAGGAAGAAAAGAAAGGAAGTCCCAATCTTCTCTGCAGGTTTTAGCTTTGGT
ACAGGTGTTATTAACCTCCACCCCTGCTCCTGCTAACACCATAGTGACCTCTGAGAACAAGAGCAGCTTCAACCTT
GGAACCATAGAAACCAAGAGTGTCTCAGTGGCTCCTTTTACATGTAAGACATCAGAAGCTAAAAAGAAAGAAATG
CCTGCCACCAAGGAGGATTCTCTTTTGGCAACGTGGAGCCTGCCTCTCTGCCATCTGCCTCAGTGTGTTTGTG
GGAAGGACAGAAGAGAAACAGCAAGAGCCTGTCTACTTCCCTAGTTTTTGGGAAGAAAGCTGACAATGAA
GAGCCAAAGTGTCAACCAGTGTCTTCTTTGGGAAATTCAGAGCAAACCAAGATGAGAATTCTTCAAAGTCCACA
TTTAGTTTTAGTATGACAAAACCATCTGAGAAGGAATCTGAACAGCCAGCAAAAGCCACTTTTGCCTTTGGAGCT
CAAACCTAGTACTACAGCTGATCAAGGTGCAGCAAGCCAGTTTTTGTAGTTCTTGAACAACAGTTCCTCTAGTTCA

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FIGURE 345B

AGTACACCAGCCACTTCTGCTGGTGGTGGCATATTGGTAGTTCACCTCTTCCCTCCAATCCACCTGTGGCTACC
TTTGTGTTTGGACAGTCCAGCAATCCTGTGAGCAGCTCTGCCTTTGGTAACACTGCTGAATCCAGCACCTCTCAG
TCTTTGCTATTTTCTCAAGATAGCAAACCTAGCAACCACATCCAGCACAGGTACAGCTGTCACCCCATTTGTCTTT
GGTCCAGGAGCCAGCAGTAATAATACTACCACCTCTGGTTTTCGGCTTTGGAGCCACAACCACATCTAGCTCTGCA
GGATCCTCCTTTGTATTTGGAACCTGGACCCTCAGCACCATCTGCCAGTCCAGCATTTGGTGCTAACCAGACCCCA
ACATTTGGACAAAGTCAAGGTGCCAGCCAGCCCAATCCCCAGGCTTTGGATCTATATCATCTTCCACAGCATTA
TTTCCCACTGGTTCTCAGCCTGCACCACCTACTTTTGGGACAGTGTCAAGCAGTAGCCAGCCCCCTGTGTTGGA
CAGCAACCTAGTCAGTCTGCATTTGGCTCTGGAACAACCTCCTAATTCTAGTTCGGCTTTCCAGTTTGGCAGCAGC
ACTACAAATTTCAACTTCACAAACAACAGTCCATCAGGAGTGTTCACATTTGGTGCAAATTTAGCACACCTGCA
GCCTCAGCCCAGCCTTCAGGCTCGGGGGGCTTTCCATTTAACCAGTCTCCAGCAGCATTTACAGTGGGGTCAAAT
GGGAAAAATGTGTTCTCTTCTTCTGGAACCTCATTCTCTGGTCGCAAGATAAAGACTGCTGTTAGACGCAGGAAA
TAAAGGTCACATTGGTGTGTACTCAATTTTAACAACAGCTGGTGCCCTGCTTTCAGATACTGGATTGTACTTTG
TGCTGGGGTTATCTGAAGTCAGATCTGCCTAAGGACTTCTTTAATTTTGGAAATTTTCCCTCCTTTCTCTTCGTTA
CAGAAGCCCCACCCTGCCTCACCCACCCTTTTTTAAATAAATAAATAGCTAGACTGGTGACTGATTCTTCAGCAA
AAATATTTTATGATCCAGCAGATTATTCAGTATTGACATAGTCTGGCTGTACCCAGGAATGGAGCCTGCACGG
TGAATGGCTTTGTATAGAACCTCTTTGTCTACACCATTATGTGCGCTGATAACGTTTCATGGAACGCGTTGAAATT
GTAATTATATCTGAGGAATTCTGTATAGATTAGAAATCTGTATAGATTAGAGAGTGTGAAACGGATGATTTCTA
TGCTGAGTTTGTGCTGGTGTATGTGTGAAGTGAGTGAGTTGGGTGTATTGTGCGCTAAACTTTTCTGATAGAGGA
AGCCTGATTAAAGAATGGTCCGTGCTAAGGACTTGTAGATCTAGTTCACCTCTCCATTTAATAATTATATGCTAT
TTCTATATTTTCAATCTCCTATCACCTGTCTTGCCTTTTTCATTATTTTATTATGAACTTGTGTAAATACAATT
TTGTTTCTGTACTTTTTGGCATAACATAAATCTGTGAACTTGAAATTTGAATTTTGTGTTAGAGATTTTTTGT
GTTTGTGTTAGTCTTGTCTCAGATTTTATTATGTAAATCCCATTTTCAAAGTTGCCTAAATCCATTTGGAAATCT
TTAAAAAAAATTTGGGATTCTTAAAGTTGAATTTATTGGCTTTTCTGATCCAGTTTTGTTGGACCAAAAACC
AGTATTGTACAAAGTATTAAGCATATATTTTATATTTACTAAAATGGTCTGTGGTGACTTTTGGATAATAAGGA
AAAGTTTAATATTAAGCCATGTTTATTACAGTATAATTAACATGTTAACCATGGGATAAATGCCATCAATAAA
AAATTATGACAT

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FIGURE 346

MASGAGGVGGGGGKIRTRRCHQGP IKPYQQGRQQHQGILSRVTESVKNIVPGWLQRYFNKNEDVCSCSTDTSEV
PRWPENKEDHLVYADEESSNITDGRIITPEPAVSNTTEEPSTTSTASNYPDVLTREPSLHRSHLNFMSLESPALHCQP
STSSAFFIGSSGFSVLVKEIKDSTSQHDDDNISTTSGFSSRASDKDITVSKNTSLPPLWSPEAERSHSLSQHTATS
SKKPAFNLSAFGTLSPSLGNSSILKTSQLGDSFPYPGKTTYGGAAA VRQSKLRNTPYQAPVRRQMKAKQLSAQS
YGVTSSTARILQSLEKMSSPLADAKRIPSIVSSPLNSPLDRSGIDITDFQAKREKVD SQYPPVQRLMTPKPVSI
ATNRSVYFKPSLTPSGEFRKTNRIDNKCSTGYEKNMTPGQNREQRESGFSYPNFSLPAANGLSSGVGGGGGKMR
RERHAFVASKPLEEEEMEVPVLPKISLPITSSSLPTFNFSspeittsspspinssqaltnkvqmtspssstgspmf
KFSSPIVKSTEANVLPSSIGFTFSVPVAKTAELSGSSSTLEPIISSAHHVTTVNSTNCKKTPPEDCEGPF RPA
EILKEGSLVDILKSPGFASPKIDSVAAQPTATSPVVYTRPAISSFSSSGIGFGESLKAGSSWQCDTCLLQNKVTD
NKCIAQAAKLSPRDTAKQTGIETPNKSGKTTLSASGTGFGDKFKPVIGTWDCDTCLVQNKPEAIKCVACETPKP
GTCVKRALTLTVSESAETMTASSSSCTVTTGTLGFGDKFKRPIGSWECSVCCVSNNAE DNKCVSCMSEKPGSSV
PASSSSTVPVSLPSGGSLGLEKFKKPEGSWDCELCLVQNKADSTKCLACESAKPGTKSGFKGFD TSSSSSNSAAS
SSFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSGSINPMSEGFKFSKPIGDFKFGVSSSESKPEEVKKD
SKNDNFKFGLSSGLSNPVSLTPFQFGVSNLQEEKKEELPKSSSAGFSFGTGVINSTPAPANTIVTSENKSSFNL
GTIETKSASVAPFTCKTSEAKKEEMPATKGGFSFGNVEPASLPASVFLGRTEEKQQEPVISTSLVFGKKADNE
EPKCQPVFSFGNSEQTKDENSSKSTFSFSMTKPSEKESEQPAKATFAFGAQTSTADQGAAPVFSFLNNSSSSS
STPATSAGGGIFGSSTSSSNPPVATFVFGQSSNPVSSSAFGNTAESSTSQSLLSQDSKLATTSSTGTAVTFVVF
GPGASSNNTTTSFGFGGATTSSSAGSSFVFGTGP SAPSASPAGANQTPTFGQSQGASQPNPPGFGSISSTAL
FPTGSQPAPPTFGTVSSSSQPPVFGQQPSQSAFGSGTTPNSSSAFQFGSSTTNFNFTNNSPSGVFTFGANSSTPA
ASAQPSGSGGFPFNQSPAFTVGSNGKNVFSSSGTSFSGRKKIKTAVRRRK

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FIGURE 347

CCTTCACACAGCTCTTTTACCATGCCTGGATCACTTCCTTTGAATGCAGAAGCTTGCTGGCCAAAAGATGTTGGG
ATTGTTGCCCTTGAGATCTATTTTCCTTCTCAATATGTTGATCAAGCAGAGTTGGAAAAATATGATGGTGTAGAT
GCTGGGAAGTATACCATTGGCTTGGGCCAGGCCAAGATGGGCTTCTGCACAGATAGAGAAGATATTAACCTCTCTT
TGCATGACTGTGGTTTCAAGATCTTATGGAGAGAAATAACCTTTCTATGATTGCATTGGGCGGCTGGAAGTTGGA
ACAGAGACAATCATCGACAAATCAAAGTCTGTGAAGACTAATTTGATGCAGCTGTTTGAAGAGTCTGGGAATACA
GATATAGAAGGAATCGACACAATAATGCAIGCTATGGAGGCACAGCTGCTGTCTTCAATGCTGTAACTGGATT
GAGTCCAGCTCTTGGGATGGACGGTATGCCCTGGTAGTTGCAGGAGATATTGCTGTATATGCCACAGGAAATGCT
AGACCTACAGGTGGAGTTGGAGCAGTAGCTCTGCTAATTGGGCCAAATGCTCCTTTAATTTTTGAACGAGGGCTT
CGTGGGACACATATGCAACATGCCTATGATTTTTACAAGCCTGATATGCTATCTGAATATCCTATAGTAGATGGG
AAACTCTCCATACAGTGCTACCTCAGTGCATTAGACCGCTGCTATTCTGTCTACTGCAAAAAGATCCATGCCCAG
TGGCAGAAAGAGGGAAATGATAAAGATTTTACCTTGAATGATTTTGGCTTCATGATCTTTCACTCACCATATTGT
AAACTGGTTCAGAAATCTCTAGCTCGGATGTTGCTGAATGACTTCCTTAATGACCAGAATAGAGATAAAAAATAGT
ATCTATAGTGGCCTGGAAGCCTTTGGGGATGTTAAATTAGAAGACACCTACTTTGATAGAGATGTGGAGAAGGCA
TTTATGAAGGCTAGCTCTGAACCTTTCAGTCAGAAAACAAAGGCATCTTTACTTGTATCAAATCAAATGGAAAT
ATGTACACATCTTCAGTATATGGTTCCCTTGCATCTGTTCTAGCACAGTACTCACCTCAGCAATTAGCAGGGAAG
AGAATTGGAGTGTCTTTTCTTATGGTTCTGGTTTGGCTGCCACTCTGTACTCTCTTAAAGTCACACAAGATGCTACA
CCGGGGTCTGCTCTTGATAAAATAACAGCAAGTTTATGTGATCTTAAATCAAGGCTTGATTCAAGAACTGGTGTG
GCACCAGATGCTTTCGCTGAAAACATGAAGCTCAGAGAGGACACCCATCATTGGTCAACTATATCCCCAGGGT
TCAATAGATTCACTCTTTGAAGGAACGTGGTACTTAGTTAGGGTGGATGAAAAGCACAGAAGAACTTACGCTCGG
CGTCCCACTCCAAATGATGACACTTTGGATGAAGGAGTAGGACTTGTGCATTCAAACATAGCAACTGAGCATATT
CCAAGCCCTGCCAAGAAAGTACCAAGACTCCCTGCCACAGCAGCAGAACCTGAAGCAGCTGTATTAGTAATGGG
GAACATTAAGATACTCTGTGAGGTGCAAGACTTCAGGGTGGGGTGGGCATGGGGTGGGGGTATGGGAACAGTTGG

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FIGURE 348

MPGSLPLNAEACWPKDVGIVALEIYFPSQYVDQAELEKYDGVDAGKYTIGLGQAKMGFCTDREDINSLCMTVVQN
LMERNNLSYDCIGRLEVGTETIIDKSKSVKTNLMQLFEESGNTDIEGIDTTNACYGGTAAVFNAVNWIESSWDG
RYALVVAGDIAVYATGNARPTGGVGAVALLIGPNAPLIFERGLRGTHMQHAYDFYKPDMLSEYPIVDGKLSIQCY
LSALDRCYSVYCKKIHAQWQKEGNDKDFTLNDFGFMIFHSPYCKLVQKSLARMLLNDFLNDQNRDKNSIYSGLEA
FGDVKLEDITYFDRDVEKAFMKASSELFQKTKASLLVSNQNGNMYTSSVYGLASVLAQYSPQQLAGKRIGVFSY
GSGLAATLYSLKVTQDATPGSALDKITASLCDLKSRLDSRTGVAPDVFAENMKLREDTHHLVNYIPQGSIDSLFE
GTWYLVVRVDEKHRRTYARRPTPNDDTLDEGVGLVHSNIATEHIPSPAKKVPRLPATAAEPEAAVISNGEH

FIGURE 349

[illegible]

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FIGURE 350

MAAEKQVPGGGGGGGSGGGGGRGAGGEENKENERPSAGSKANKEFGDSLSLEILQIIKESQQQHGLRHGDFORY
RGYCSRRQRRLRKTILNFKMGNRHKFTGKKVTEELLTDNRYLLLVLMDAERAWSYAMQLKQEANTEPRKRFHLLSR
LRKAVKHAEELERLCKSNRVDKTKLEAQAYTAYLSGMLRFEHQEWKAAIEAFNKCKTIYEKLASAFTEEQAVLY
NQRVEEISPNIRYCAYNIGDQSAINELMQMRLRSGGTEGLLAEKLEALITQTRAKQAATMSEVEWRGRTVPVKID
KVRIFLLGLADNEAAIVQAESEETKERLFESMLSECRDAIQVVREELKPDQKQRDYILEGEPGKVSNLQYLHSYL
TYIKLSTAIKRNNENMAKGLQRALLQQQPEDDSKRSRPQDLIRLYDIIILQNLVELLQLPGLEEDKAFQKEIGLKT
LVFKAYRCFFIAQSYVLVKKWSEALVLYDRVLKYANEVNSDAGAFKNSLKDLPDVQELITQVRSEKCSLQAAAIL
ESNDAHQTETSSSQVDKNKPLVERFETFCLDPSLVTKQANLVHFPPGFQPIPCPKPLFFDLALNHVAFPPLEDKLE
QKTKSGLTGYIKGIFGFRS

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FIGURE 351

CCTAGTACACCGCAATCATGTCTATTATGTCCTATAACGGAGGGGCCGTCATGGCCATGAAGGGGAAGAACTGTG
TGGCCATCGCTGCAGACAGGCGCTTCGGGATCCAGGCCCAGTTGGTGACCACGGACTTCCAGAAGATCTTTCCCA
TGGGTGACCGGCTGTACATCGGTCTGGCCGGGCTCGCCACTGACGTCCAGACAGTTGCCCAGCGCCTCAAGTTCC
GGCTGAACCTGTATGAGTTGAAGGAAGGTCGGCAGATCAAACCTTATACCCTCATGAGCATGGTGGCCAACCTCT
TGTATGAGAAACGGTTTGGCCCTTACTACACTGAGCCAGTCATTGCCGGGTGGACCCGAAGACCTTTAAGCCCT
TCATTTGCTCTCTAGACCTCATCGGCTGCCCCATGGTGACTGATGACTTTGTGGTCAGTGGCACCTGCGCCGAAC
AAATGTACGGAATGTGTGAGTCCCTCTGGGAGCCCAACATGGATCCGGATCACCTGTTTGAACCATCTCCAAG
CCATGCTGAATGCTGTGGACCGGGATGCAGTGTGAGGCATGGGAGTCATTGTCCACATCATCGAGAAGGACAAAA
TCACCACCAGGACACTGAAGGCCCGAATGGACTAACCCTGTTCCCAGAGCCCACCTTTTTTTCTTTTTTTGAAAT
AAAATAGCCTGTCTTTC

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FIGURE 352

MSIMSYNGGAVMAMKGKNCVAIAADRRFGIQAQLVTTDFQKIFPMGDRLYIGLAGLATDVQTVAQRLKFRNLNLYE
LKEGRQIKPYTLMSMVANLLYEKRFPGPYYTEPVIAGLDPKTFKPFICSIDLIGCPMVTDDFVVS GTCAEQMYGMC
ESLWEPNMDPDHLFETISQAMLNAVDRDAVSGMGVIVHII EKDKITTRTLKARMD

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FIGURE 353

GAAAGTCAGTGAGCAAATCGCGGACCACCGGGGCTGCCAGCTCGCCTGACTCCCGGCCTCTTGCGCTCCTAGGGG
CGGAGAAGGGTGCGGGCTCTTCGCCCTTTGTGTCTCCTTCTTTCACTAACTTCTGGACTTTCCAGCTCTTCCGA
AGTTCGTTCTTGCGCAAAGCCCAAAGGCTGGAAAAACCGTCCACGATGACCAGCATGACTCAGTCTCTGCGGGAGG
TGATAAAGGCCATGACCAAGGCTCGCAATTTTGAGAGAGTTTGGGAAAGATTACTCTGTCTCTGCTGCTCCTG
GGAAAGTGATTGTGAAATGAAAGTAGAAGAAGAGCATACCAATGCAATAGGCACTCTCCACGGCGGTTTGACAG
CCACGTTAGTAGATAACATATCAACAATGGCTCTGCTATGCACGGAAAGGGGAGCACCCGGAGTCAGTGTGATA
TGAACATAACGTACATGTCACCTGCAAAATTAGGAGAAGATATAGTGATTACAGCACATGTTCTGAAGCAAGGAA
AAACACTTGCATTTACCTCTGTGGATCTGACCAACAAGGCCACAGGAAAATTAATAGCACAAGGAAGACACAAA
AACACCTGGGAAACTGAGAGAGAACAGCAGAATGACCTAAAGAAACCCAACAATGAATATCAAGTATAGATTTGACT
CAAACAATTGTAATTTTGAATAAACTAGCAAAACCAGAAAAAAAAAAAAAAAAAAAAA

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FIGURE 354

MTSMTQSLREVIKAMTKARNFERVLGKITLVSAAPGKVICEMKVEEHTNAIGTLHGGLTATLVDNISTMALLCT
ERGAPGVSDMNITYMSPAKLGEDIVITAHVLKQGKTLAFTSVDLTNKATGKLIAQGRHTKHLGN

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FIGURE 355A

TTCCGGCGGGGGAGGCGCCGGGAAGTCGATGGCGCGCGCGGCTCCTGCAGGAGGCCACTGTCTGCAGCTCCCGTG
AAGATGTTCCACTCCAGACCCACCCCTGGGCGGAACCTCCTCGGCCAGGTCTTCCCCGGGGCCCTGGCCCTTCCCTT
GGAGCCATGCTGGGCCCCTAGCCCGGGTCCCTCGCCGGGCTCCGCCACAGCATGATGGGGCCCAGCCCAGGGCCG
CCCTCAGCAGGACACCCCATCCCCACCCAGGGGCC TGGAGGGTACCCTCAGGACAACATGCACCAGATGCACAAG
CCCATGGAGTCCATGCATGAGAAGGGCATGTGCGACGACCCGCGCTACAACCAGATGAAAGGAATGGGGATGCGG
TCAGGGGGCCATGCTGGGATGGGGCCCCCGCCAGCCCCATGGACCAGCACTCCCAAGGTTTCCCCCTCGCCCCCTG
GGTGGCTCTGAGCATGCCTCTAGTCCAGTTCCAGCCAGTGGCCCGTCTTCGGGGCCCCAGATGTCTTCCGGGCCA
GGAGGTGCCCCGCTGGATGGTGTGACCCCCAGGCCTTGGGGCAGCAGAACCAGGGGCCCAACCCATTTAACCAG
AACCAGCTGCACCAGCTCAGAGCTCAGATCATGGCCTACAAGATGCTGGCCAGGGGGCAGCCCCCTCCCCGACCAC
CTGCAGATGGCGGTGCAGGGCAAGCGGCCGATGCCCGGGATGCAGCAGCAGATGCCAACGCTACCTCCACCCTCG
GTGTCCGCAACAGGACCCGGCCCTGGCCCTGGCCCTCGGCCCGGGTCCCGGCCCGGCACCTCCAAATTAC
AGCAGGCCTCATGGTATGGGAGGGCCCAACATGCCCTCCCCCAGGACCTCGGGCGTGGCCCCCGGGATGCCAGGC
CAGCCTCCTGGAGGGCCTCCCAAGCCCTGGCCTGAAGGACCCATGGCGAATGCTGCTGCCCCCAGGACACCCCT
CAGAAGCTGATTCCCCCGCAGCCAACGGGCCGCCCTTCCCCCGCGCCCCCTGCCGTCCCACCCGCGCCTCGCCC
GTGATGCCACCGCAGACCCAGTCCCCCGGGCAGCCGGCCAGCCCGCGCCCATGGTGCCACTGCACCAGAAGCAG
AGCCGCATCACCCCCATCCAGAAGCCGCGGGGCTCGACCCTGTGGAGATCCTGCAGGAGCGCGAGTACAGGCTG
CAGGCTCGCATCGCACACCCGAATTCAGGAACCTGAAAACCTTCCCGGGTCCCTGGCCGGGGATTTGCGAACCAAA
GCGACCATTGAGCTCAAGGCCCTCAGGCTGCTGAACTTCCAGAGGCAGCTGCGCCAGGAGGTGGTGGTGTGCATG
CGGAGGGACACAGCGCTGGAGACAGCCCTCAATGCTAAGGCCTACAAGCGCAGCAAGCGCCGAGTCCCTGCGCGAG
GCCCCGATCACTGAGAAGCTGGAGAAGCAGCAGAAGATCGAGCAGGAGCGCAAGCGCCGGCAGAAGCACCAGGAA
TACCTCAATAGCATTCTCCAGCATGCCAAGGATTTCAAGGAATATCACAGATCCGTACAGGCAAAATCCAGAAG
CTGACCAAGGCAGTGGCCACGTACCATGCCAACACGGAGCGGGAGCAGAAGAAAGAGAACGAGCGGATCGAGAAG
GAGCGCATGCGGAGGCTCATGGCTGAAGATGAGGAGGGGTACCGCAAGCTCATCGACCAGAAGAAGGACAAGCGC
CTGGCCTACCTCTTGACAGCAGACAGACGAGTACGTGGCTAACCTCACGGAGCTGGTGCCGACGACAAGGCTGCC
CAGGTCGCCAAGGAGAAAAAAGAAAAAGAAAAAAGAAAGGCAGAAAATGCAGAAGGACAGACGCCTGCCATT
GGGCCGGATGGCGAGCCTCTAGACGAGACCAGCCAGATGAGCGACCTCCCGGTGAAGGTGATCCACGTGGAGAGT
GGGAAGATCCTCACAGGCACAGATGCCCCCAAAGCCGGGCAGCTGGAGGCCTGGCTCGAGATGAACCCGGGGTAT
GAAGTAGTCCGAGGTCTGATAGTGAAGAAAGTGGCTCAGAAGAAGAGGAAGAGGAGGAGGAAGAGCAGCCG
CAGGCAGCACAGCCTCCCACCCTGCCCCGTGGAGGAGAAGAAGAAGATTCCAGATCCAGACAGCGATGACGTCTCT
GAGGTGGACGCGCGGCACATCATTGAGAATGCCAAGCAAGATGTGATGATGAATATGGCGTGTCCAGGCCCTT
GCACGTGGCCTGCAGTCTACTATGCCGTGGCCCATGCTGTCACTGAGAGAGTGGACAAGCAGTCAGCGCTTATG
GTCAATGGTGTCTCAAACAGTACCAGATCAAAGGTTTGGAGTGGCTGGTGTCCCTGTACAACAACAACCTGAAC
GGCATCTGGCCGACGAGATGGGCCTGGGGAAGACCATCCAGACCATCGCGCTCATCACGTACCTCATGGAGCAC
AAACGCATCAATGGGCCCTTCTCATCATCGTGCTCTCTCAACGCTGTCCAACCTGGGCGTACGAGTTTGACAAG
TGGGCCCCCTCCGTGGTGAAGGTGTCTTACAAGGGATCCCCAGCAGCAAGACGGGCCCTTTGTCCCCCAGCTCCGG
AGTGGGAAGTTCAACGTCTTGCTGACGACGTACGAGTACATCATCAAAGACAAGCACATCCTCGCCAAGATCCGT
TGGAAGTACATGATTGTGGACGAAGGTCACCGCATGAAGAACCACCACTGCAAGCTGACGCAGGTGCTCAACACG
CACTATGTGGCACCCCGCCGCTGCTGCTGACGGGCACACCGCTGCAGAACAAAGCTTCCCGAGCTCTGGGCGCTG
CTCAACTTCTGCTGCCCACCATTCTCAAGAGCTGCAGCACCTTCGAGCAGTGGTTTAAACGCACCCTTTGCCATG
ACCGGGGAAAAGGTGGACCTGAATGAGGAGGAAACATTCTCATCATCCGGCGTCTCCACAAAGTGCTGCGGCCC
TTCTTGCTCCGACGACTCAAGAAGGAAGTCGAGGCCAGTTGCCCCGAAAAGGTGGAGTACGTATCAAGTGCGAC
ATGTCTGCGCTGCAGCGAGTGTCTTACCGCCACATGCAGGCCAAGGGCGTGTGCTGACTGATGGCTCCGAGAAG
GACAAGAAGGGCAAAGCGGCACCAAGACCCTGATGAACACCATCATGCAGCTGCGGAAGATCTGCAACCACCCC
TACATGTTCCAGCACATCGAGGAGTCTTTTTCCGAGCACTTGGGGTTCACTGGCGGCATTGTCCAAGGGCTGGAC
CTGTACCGAGCCTCGGTAATTTGAGCTTCTTGATAGAATTCTTCCAAACTCCGAGCAACCAACCACAAAGTG
CTGCTGTTCTGCCAAATGACCTCCCTCATGACCATCATGGAAGATTACTTTGCGTATCGCGGCTTTAAATACCTC
AGGCTTGATGGAACCAGGAAGGCGGAGGACCGGGCATGCTGCTGAAAACCTTCAACGAGCCCGGCTCTGAGTAC
TTCATCTTCTGCTCAGCACCCGGGCTGGGGGGCTCGGCCTGAACCTCCAGTCGGCAGACACTGTGATCATTTTT

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FIGURE 355B

GACAGCGACTGGAATCCTCACCAGGACCTGCAAGCGCAGGACCGAGCCCACCGCATCGGGCAGCAGAACGAGGTG
CGTGTGCTCCGCCTCTGCACCGTCAACAGCGTGGAGGAGAAGATCCTAGCTGCAGCCAAGTACAAGCTCAACGTG
GACCAGAAGGTGATCCAGGCCGGCATGTTTCGACCAGAAGTCTCCAGCCATGAGCGGGCGCGCCTTCCTGCAGGCC
ATCCTGGAGCACGAGGAGCAGGATGAGAGCAGACACTGCAGCACGGGCAGCGGCAGTGCCAGCTTCGCCCACACT
GCCCCCTCCGCCAGCGGGCGTCAACCCCGACTTGGAGGAGCCACCTCTAAAGGAGGAAGACGAGGTGCCCGACGAC
GAGACCGTCAACCAGATGATCGCCCGGCACGAGGAGGAGTTTGATCTGTTTCATGCGCATGGACCTGGACCGCAGG
CGCGAGGAGGCCCGCAACCCCAAGCGGAAGCCGCGCCTCATGGAGGAGGACGAGCTCCCCCTCGTGGATCATCAAG
GACGACGCGGAGGTGGAGCGGCTGACCTGTGAGGAGGAGGAGGAGAAGATGTTTCGGCCGTGGCTCCCGCCACCGC
AAGGAGGTGGACTACAGCGACTCACTGACGGAGAAGCAGTGGCTCAAGGCCATCGAGGAGGGCACGCTGGAGGAG
ATCGAAGAGGAGGTCCGGCAGAAGAAATCATCACGGAAGCGCAAGCGAGACAGCGACGCCGGCTCCTCCACCCCG
ACCACCAGCACCCGAGCCGCGACAAGGACGACGAGAGCAAGAAGCAGAAGAAGCGCGGGCGGCCGCTGCCGAG
AAACTCTCCCCCTAACCCACCCCAACCTCACCAAGAAGATGAAGAAGATTGTGGATGCCGTGATCAAGTACAAGGAC
AGCAGCAGTGGACGTCAGCTCAGCGAGGTCTTCATCCAGCTGCCCTCGCGAAAGGAGCTGCCCGAGTACTACGAG
CTCATCCGCAAGCCCGTGGACTTCAAGAAGATAAAGGAGCGCATTTCGCAACCACAAGTACCGCAGCCTCAACGAC
CTAGAGAAGGACGTCATGCTCCTGTGCCAGAACGCACAGACCTTCAACCTGGAGGGCTCCCTGATCTATGAAGAC
TCCATCGTCTTGCACTCGGTCTTACCAGCGTGCGGCAGAAAATCGAGAAGGAGGATGACAGTGAAGGCGAGGAG
AGTGAGGAGGAGGAAGAGGGCGAGGAGGAAGGCTCCGAATCCGAATCTCGGTCCGTCAAAGTGAAGATCAAGCTT
GGCCGGAAGGAGAAGGCACAGGACCGGCTGAAGGGCGGCCGGCGGCCGAGCCGAGGGTCCCAGCCAAAGCCG
GTCGTGAGTGACGATGACAGTGAGGAGGAACAAGAGGAGGACCGCTCAGGAAGTGGCAGCGAAGAAGACTGAGCC
CCGACATTCCAGTCTCGACCCCGAGCCCCCTCGTTCCAGAGCTGAGATGGCATAGGCCTTAGCAGTAACGGGTAGC
AGCAGATGTAGTTTCAGACTTGGAGTAAACTGTATAAAACAAAAGAATCTTCCATATTTATACAGCAGAGAAGCT
GTAGGACTGTTTGTGACTGGCCCTGTCTGGCATCAGTAGCATCTGTAACAGCATTAACTGTCTTAAAGAGA

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FIGURE 356

MSTDPPLGGTPRPGSPGPGSPGAMLGPSPGSPGSAHSMGPGSPGPPSAGHP IPTQGPGGYPDNMHQMHPK
MESMHEKMSDDPRYNQMGMRSGGHAGMGPPPSPMDQHSQGYPSPLGGSEHASSPVSPASGPSSGPQMSSGPG
GAPLDGADPQALGQQNRGPTPFNQNLHLQRAQIMAYKMLARGQPLPDHLQMAVQGKRPMGPMQQQMFILPPPSV
SATGPGPGPGPGPGPGPAPPNYSRPHGMGGPNMPPPGPSGVPPGMPGQPPGGPPKPWPEGPMANAAAPTSTPQ
KLIPPQPTGRPSAPPAPVPPAASPVMPPQTQSPGQPAQPAPMVPLHQKQSRITPIQKPRGLDPVEILQEREYRLQ
ARIAHRIQELENLPGSLAGDLRTKATIELKALRLLNFQRLRQEVVCMRRDTALETALNAKAYKRSKRQSLREA
RITEKLEKQKQIEQERKRRQKHQEYLNLSILQHAKDFKEYHRSVTGKIQLTKAVATYHANTEREQKKENERIEKE
RMRRLMAEDEEGYRKLIDQKKDKRLAYLLQQTDEYVANLTELVPQHKAQVAKEKKKKKKKKKAENAEGQTPAIG
PDGEPLDETSQMSDLPVKVIHVESGKILTGTDAPKAGQLEAWLEMNPGYEVAPRSDSEESGSEEEEEEEEEEQPQ
AAQPPTLPVEEKKKIPDPDSDDVSEVDARHIIENAKQDVEDDEYGVSQALARGLQSYAVAHAVTERVDKQSALMV
NGVLKQYQIKGLEWLVS LYNNNLNGIILADEMGLGKTIQTIALITYLMEHKRINGPFLIIVPLSTLSNWAYEFDKW
APSVVKVSYKGS PAARRAFVPQLRSGKFNVLLTTYEYIIKDKHILAKIRWKYMIVDEGHRMKNHHCKLTQVLNTH
YVAPRRLLLTGTPLQNKLPPELWALLNFLPTIFKS CSTFEQWFNAPFAMTGEKVDLNEEETILIIIRRLHKVLRPF
LLRRLKKEVEAQLPEKVEYVIKCDMSALQVLYRHMQAQGVLLTDGSEKDKKGKGGTKTLMNTIMQLRKICNHPY
MFQHIEESFSEHLGFTGGIVQGLDLYRASGKFELLDRIPLKLRATNHKVLLFCQMTSLMTIMEDYFAYRGFKYLR
LDGTTKAEDRGMLLKTTFNEPGSEYFIFLLSTRAGGLGLNLQSADTVIIFDSDWNPHQDLQAQDRAHRIGQQNEVR
VLRLCTVNSVEEKILAAAKYKLNVDQKVIQAGMFDQKSSSHERRAFLQAILEHEEQDESRHCSTGSGSASFHTA
PPPAGVNPDLPEPPLKEEDEVPDDETQNMIAHHEEFDLFMRMDLDRRREEARNPKRKPRLMEEDLP SWI IKD
DAEVERLTCEEEEEKMFGRGSRHRKEVDYSDSLTEKQWLKAIIEEGTLEEIEEEVRQKKSSRKRKRDSDAGSSTPT
TSTRSRDKDESKKQKKRGRPPAEKLSPPNPNLTKKMKI DAVIKYKDSSSGRQLSEVFIQLPSRKELPEYYEL
IRKPVDFKKIKERIRNHKYRSLNDLEKDVMLLCQNAQT FNLEGS LIYEDSIVLQSVFTSVRQKIEKEDDSEGEES
EEEEEGEEGSESESRSVKVIKLRKEKAQDR LKGRRRPSRGSRAKPVVSDDDSEEEQEEDRSGSGSEED

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FIGURE 357

AGCAACGGGGTGCGGCAGGGTGGGGAACGCGGGAGCGGGGCCAGCTCCCAGGAAAGCTGGTCTGCGAGCGGGCCC
TGCCCCGGCTCCCAGGTCCCTGCGCGACCCCGCCCTTCCCAGACCCCAGCCGGGCTGCCGCCCGCGTCCCGGAAG
CTCCAGCCTGAACC**ATG**TTTTTCACTTGTGGCCCAAATGAGGCCATGGTGGTCTCCGGGTTCTGCCGAAGCCCC
CAGTCATGGTGGCTGGAGGGCGTGTCTTTGTCTGCCCTGCATCCAACAGATCCAGAGGATCTCTCTCAACACAC
TGACCCTCAATGTCAAGAGTGAAAAGGTTTACACTCGCCATGGGGTCCCCATCTCAGTCACTGGCATTGCCCAGG
TAAAAATCCAGGGGCAGAACAAGGAGATGTTGGCGGCCGCTGTCAGATGTTCTGGGGAAGACGGAGGCTGAGA
TTGCCCACATTGCCCTGGAGACGTTAGAGGGCCACCAGAGGGCCATCATGGCCACATGACTGTGGAGGAGATCT
ATAAGGACAGGCAGAAATTCTCAGAACAGGTTTTCAAAGTGGCCTCCTCAGACCTGGTCAACATGGGCATCAGTG
TGGTTAGCTACACTCTGAAGGACATTACGATGACCAGGACTATTTGCACTCTTTGGGGAAGGCTCGAACAGCTC
AAGTCCAAAAAGATGCACGGATTGGAGAAGCAGAGGCCAAGAGAGATGCTGGGATCCGGGAAGCTAAAGCCAAGC
AGGAAAAGGTGTCTGCTCAGTACCTGAGTGAGATCGAGATGGCCAAGGCACAGAGAGATTACGAACTGAAGAAGG
CCGCCTATGACATCGAGGTCAACACCCGCCGAGCACAGGCTGACCTGGCCTATCAGCTTCAGGTGGCCAAGACTA
AGCAGCAGATTGAGGAGCAGCGGTGCAGGTGCAGGTGGTGGAGCGGGCCCAGCAGGTGGCAGTGCAGGAGCAGG
AGATCGCCCCGGCGGGAGAAGGAGCTGGAGGGCCGGGTGCGGAAGCCAGCGGAAGCGGAGCGCTACAAGCTGGAGC
GCCTAGCCGAGGCAGAGAAGTCCCACTAATTATGCAGGCGGAGGCAGAAGCCGCGTCTGTGCGGATGCGTGGGG
AAGCTGAGGCCTTTGCCATAGGGGCCCCGAGCCCGAGCCGAGGCTGAGCAGATGGCCAAGAAGGCAGAAGCCTTCC
AGCTGTACCAAGAGGCTGCTCAGCTGGACATGCTGCTAGAGAAGCTGCCCCAGGTGGCAGAGGAGATCAGTGGTC
CCTTGACTTCAGCCAATAAGATCACACTGGTGTCCAGCGGCAGTGGGACCATGGGGGCAGCCAAAGTGAAGTGGGG
AAGTACTGGACATTCTAACTCGCCTGCCAGAGAGTGTGGAAAGACTCACAGGCGTGAGCATCTCCCAGGTGAATC
ACAAGCCTTTGAGAACAGCC**TG**AGCCTTCAGCCCTCACAGATGCCAGCCTCATAGCTGAAGTTGCCTGAATGAT
CCTCCTGTTGCATGTAACCCACTGGCCTCCCTGAGCATGTCCATTGACAGTGAGGTCCCACCCCTCATCTCTCTCT
TGCCAAATAGTTTGTGCTTGTCTTGAAGGGGGTTGCTCCCCCTTGCCAACCTCACACTGCTATGATTGCCAACTC
CAGCGGTCCCATGTGAGCCTTCTGATGATCCCACTCCACCCACCTCAACTTATTTAACTTCCTAATTAAATCAG
ACTGTTTGAGCCTGTTGTCTAGAATATTTTCTGACCAAGACTGAGGGATGGGCTGGAGGTTTTCAACTTTGCTA
CCCAAATAAATTGCTGTAAGTAAGTACTAAAAAAAAAA

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FIGURE 358

MFFTCGPNEAMVVS GF CRSPV MVAGGRVFV L P C I Q Q I Q R I S L N T L T L N V K S E K V Y T R H G V P I S V T G I A Q V K I Q G
Q N K E M L A A A C Q M F L G K T E A E I A H I A L E T L E G H Q R A I M A H M T V E E I Y K D R Q K F S E Q V F K V A S S D L V N M G I S V V S Y T
L K D I H D D Q D Y L H S L G K A R T A Q V Q K D A R I G E A E A K R D A G I R E A K A K Q E K V S A Q Y L S E I E M A K A Q R D Y E L K K A A Y D I
E V N T R R A Q A D L A Y Q L Q V A K T K Q Q I E E Q R V Q V Q V V E R A Q Q V A V Q E Q E I A R R E K E L E A R V R K P A E A E R Y K L E R L A E A
E K S Q L I M Q A E A E A S V R M R G E A E A F A I G A R A R A E A E Q M A K K A E A F Q L Y Q E A A Q L D M L L E K L P Q V A E E I S G P L T S A
N K I T L V S S G S G T M G A A K V T G E V L D I L T R L P E S V E R L T G V S I S Q V N H K P L R T A

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FIGURE 359

GACAGCCTCCGCCACATCCTCCACCTCTCTTGGTCCAGCGAGCGTTGCCGGGCCAGGGTCAAGCGGAGGGCTCCG
ACGGCGCGGACGGGAGCGAAGCGCCGAGCCATGGCGCACCAAACGGGCATCCACGCCACGGAAGAGCTGAAGGAAT
TCTTTGCCAAGGCACGGGCTGGCTCTGTGCGGCTCATCAAGTTGTGATTGAGGACGAGCAGCTCGTGCTGGGTG
CCTCGCAGGAGCCAGTAGGCCGCTGGGATCAGGACTATGACAGGGCCGTGCTGCCACTGCTGGACGCCCAGCAGC
CCTGCTACCTGCTCTACCGCCTCGACTCACAGAATGCTCAGGGCTTCGAATGGCTCTTCCTCGCCTGGTCGCCTG
ATAACTCCCCCGTGC GGCTGAAGATGCTGTACGCGGCCACGCGGGCCACAGTGAAAAAGGAGTTTGGAGGTGGCC
ACATCAAGGATGAGCTCTTCGGGACTGTGAAGGATGACCTCTCTTTTGTGGGTACCAGAAACACCTGTCGTCTT
GTGCGGCACCTGCCCCGCTGACCTCGGCTGAGAGAGAGCTCCAGCAGATCCGCATTAACGAGGTGAAGACAGAGA
TCAGTGTGGAAGCAAGCACCAGACCCTGCAGGGCCTCGCCTTCCCCCTGCAGCCTGAGGCCCAGCGGGCACTCC
AGCAGCTCAAGCAGAAAATGGTCAACTACATCCAGATGAAGCTGGACCTAGAGCGGGAAACCATTGAGCTGGTGC
ACACAGAGCCCACGGATGTGGCCCAGCTGCCCTCCCGGTGCCCGAGATGCTGCCCGCTACCACTTCTTCCTCT
ACAAGCACACCCATGAGGGCGACCCCTTGAGTCTGTAGTGTTCATCTACTCCATGCCGGGGTACAAGTGCAGCA
TCAAGGAGCGAATGCTCTACTCCAGCTGCAAGAGCCGCTCCTCGACTCCGTGGAGCAGGACTTCCATCTGGAGA
TCGCCAAGAAAATTGAGATTGGCGATGGGGCAGAGCTGACGGCAGAGTTCCCTCTACGACGAGGTGCACCCCAAGC
AACACGCCTTCAAGCAGGCCTTCGCCAAGCCCAAGGGCCAGGGGGCAAGCGGGGCCATAAGCGCCTCATCCGCG
GCCCCGGTGAAAAATGGGGATGACAGCTAGGAGGCTGGAGCAGGGCCGGCCACGTGTGGACTGTGGGGCTGCCAC
CTTCCGCTCCCTGCCACCATCCTCCTTCTGGGCTCCAGGAAAGTGTTCCTGGGAGGTGAGGAGGCTGGCAGCT
GAACGCACTTGCAGCGTCCGAGGGCCACCGGGCTGGCATTCTTGTGACCCTTCCCTGTTGCTGTCCCTGCATCTCG
TCTGTGTGCCCAGGGTGTCCGGGGACCCCTGCCTGGCTGGCTTAAGGGGGCTGGGTCAGGGGCCTGGCATGAACCT
GGCCTCCCGGGGAGCTGAGACTAGGGTCCCAGCACAGCCAGAAACCTTTGGCCACAAGAAGTGGGGTCAGTCAG
GGCTGGGGCAGGGGTCACTGCAGTTTGGGATGGTTGAATGCTGTATTTCTAAAGAATAAAATATTTTTAAATC

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FIGURE 360

MAHQTGIIHATEELKEFFAKARAGSVRLIKVVIEDEQLVLGASQEPVGRWDQDYDRAVLPLLLDAQQPCYLLYRLDS
QNAQGFEWLFLAWSPDNSPVRLKMLYAATRATVKKEFGGGHIKDELFGTVKDDLSFAGYQKHLSSCAAPAPL TSA
ERELQQIRINEVKTEISVESKHQTLQGLAFPLQPEAQRALQQLKQKMNVIQMKLDLERETIELVHTEPTDVAQL
PSRVPRDAARYHFFLYKHTHEGDPLESVVFIYSMPGYKCSIKERMLYSSCKSRLLDSVEQDFHLEIAKKIEIGDG
AELTAEFLYDEVHPKQHAFKQAFAPKGPGGKRGHKRLIRGPGENGDDS

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FIGURE 361

GGAATTTGGAAGCCCTCAAATCCCATTCTTAATCTGATGAGTCTATGGACCAATTTGTGGAGGACAGTATATTAA
ATAGATCTGATTTTTGCCATCAATGTAAGGAGGATAAAAACTTGCATACCAATTGTACACCCTTGCAAAATCTTT
CTCTGATGTTGGAGAAAATGGGCCAGTGAGATCATGGATATAGAAGTACAGTCAATGTTTCAGCTGTACCCTCCCA
CAATCCCACCTTCCTTCCTCAACACAATTCAAACAAATAGACTCAGACTGTTTCAGGCTCCAAGGACAGGAAGTGCA
GTGTAGGCAAAATTGCAAAAATTGAGGGCACAGGGGTGGAGATGGGGGGGTGAATAACAAGCTGTGCTAAATAA
TTACGTGTAAATATATTTTTTCATTTTTAAAAATTGATTTCTTTTGCACATTCCATGACAATATATGTCACATTT
TTAAAATAAATGCAAAGAAGCATACATCCAAGCCACTGAGCTCATTTGTCTTCTGTTTTGATAAAGTGGTAAAGA
AGGAAC TAACATGGGAATGCATTGCTACAATTTAAATAAGCATACCAAGATAAATTCATTTATGGTGCTTTGAGT
ATATGAGACCCTCTTCTACCAGACAGATGATCAGTGTTAGATTTATAGAGAAGGGATTATCAAATTCCTATGGCC
AAGAAGGTCAGAGA

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FIGURE 362

MRPSSTRQMISVRFIEKGLSNHGOEQ

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FIGURE 363

GGGGGAATACTTCCAAGTTGTAGTGTTGTTGTTTTCAGCCTGCTGCTGCTGCTGCTGTTGCGGCTAGGGGAACCG
TCGTGGGGAAGGATGGTGTGCGAAAAATGTGAAAAGAACTTGGTACTGTTATCACTCCAGATACATGGAAAGAT
GGTGCTAGGAATACCACAGAAAGTGGTGGAAGAAAGCTGAATGAAAATAAAGCTTTGACTTCAAAAAAAGCAAGA
TTTGATCCATATGGAAAGAATAAGTTCTCCACTTGTAGAATTTGTAAAAGTTCTGTGCACCAACCAGGTTCTCAT
TACTGCCAGGGCTGTGCCTACAAAAAAGGCATCTGTGCGATGTGTGGAAAAAAGGTTTTGGATACCAAAAACTAC
AAGCAAACATCTGTCTAGATGTATTGATGGAATTTCTGGCTTTCTAAATGATTTTACTTTCTGCCTTGAATTTTC
AAGGCATAGATGTCAACTTACAGAATAACATGTTTAAAGATAATTAAGTTTAAACCAGAGATTGATGTTACTCAT
TTGCTCTCATGTTCTAACAGCACAGTGTACTAGTCTTTGTGGTAAATGGTTATTTTCCTTATAAGAATTTAAGA
ACTAAGTGGCAAATTCATGAAAATATTTCTCAGTTCTGTATGCACTTTTATTTAACATTATTCATATAATTCTC
CCCCCACCACCTTTATTTATAGATACTGCCCAAGTGAGAAGGAGATAATAGATACTTTGCTCTGAATTTGGCATCC
AGAGTAACATTTCTCCCCTCACTCCCTTGCTGGTGTGCATAGTTATTAGAATCAGCAGCCTCTTAACATAATTGCGG
TTTCATGGATATATAAATGTTTCAAGCCATTATTGCTGAATGGTTCTTTAGTTATTAACCTAGACCCAATTCAAA
GACCAGTTGGATTTATGATATTTTTTATTTGTTCTTGCAGCCAAAGTGCCAGTTTCTTTAATATGTGACCAAGAA
CACAAGGAGCATCCATATGGCCAAATAAATACATGAATTTTAGAAAAACATATTACTTTGAATTCAAATTGTCA
TGAAAACCAGAACAGTGTGTTGTCCTTGTGTCATGTAATGAAAATAAATCCATGCTATGAGAAAAGCTCTTTGAAG
CTAAAAAAAAAAAAAAAAAAAAAAAAAAG

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FIGURE 364

MVCEKCEKKLGTVITPDTWKDGARNTTESGGRKLNENKALTSKKARFDPYGKNKFSTCRICKSSVHQPGSHYCQG
CAYKKGICAMCGKKVLDTKNYKQTSV

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FIGURE 365

AGAATCCCGGACAGCCCTGCTCCCTGCAGCCAGGTGTAGTTTCGGGAGCCACTGGGGCCAAAGTGAGAGTCCAGC
GGTCTTCCAGCGCTTGGGGCCACGGCGGGCGGCCCTGGGAGCAGAGGTGGAGCGACCCCATACGCTAAAGATGAAA
GGCTGGGGTTGGCTGGCCCTGCTTCTGGGGGCCCTGCTGGGAACCGCCTGGGCTCGGAGGAGCCAGGATCTCCAC
TGTGGAGCATGCAGGGCTCTGGTGGATGAACTAGAATGGGAAATTGCCCAGGTGGACCCCAAGAAGACCATTTCAG
ATGGGATCTTTCCGGATCAATCCAGATGGCAGCCAGTCAGTGGTGGAGGTGCCTTATGCCCGCTCAGAGGCCCCAC
CTCACAGAGCTGCTGGAGGAGATATGTGACCGGATGAAGGAGTATGGGGAACAGATTGATCCTTCCACCCATCGC
AAGAACTACGTACGTGTAGTGGGCCGGAATGGAGAATCCAGTGAATGGACCTACAAGGCATCCGAATCGACTCA
GATATTAGCGGCACCCTCAAGTTTGCGTGTGAGAGCATTGTGGAGGAATACGAGGATGAACTCATTGAATTCTTT
TCCCGAGAGGCTGACAATGTTAAAGACAACTTTGCAGTAAGCGAACAGATCTTTGTGACCATGCCCTGCACATA
TCGCATGATGAGCTATGAACCACTGGAGCAGCCACACTGGCTTGATGGATCACCCCCAGGAGGGGAAAATGGTG
GCAATGCCTTTTATATATTATGTTTTTACTGAAATTAAGTGAATAATGAAACCAAAAGTAC

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FIGURE 366

MKGWGWIALLLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTIQMGSFRINPDGSQSVVEVPYARSE
AHLTELLEEEICDRMKEYGEQIDPSTHRKNYVRVVGNGESSELDLQGIRIDSDISGTLKFACESIVEEYEDELIE
FFSREADNVKDKLCSKRTDLCDBALHISHDEL

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FIGURE 367

TCCGGTCTTGTCCACGCTAGGGGGTGCACGTACTCCCAACTGTGGTCGCGCTCTCACCCCTTCTGCTGCTCTCGT
GGCCCCCTCGCGATGGCGGGCATCCTGTTTGAGGATATTTTCGATGTGAAGGATATTGACCCGGAGGGCAAGAAG
TTTGACCGAGTGTCTCGACTGCATTGTGAGAGTGAATCTTTCAAGATGGATCTAATCTTAGATGTAAACATTCAA
ATTTACCCTGTAGACTTGGGTGACAAGTTCCGGTTGGTCATAGCTAGTACCTTGTATGAAGATGGTACCCTGGAT
GATGGTGAATACAACCCCACTGATGATAGGCCTTCCAGGGCTGACCAGTTTGAGTATGTAATGTATGGAAAAGTG
TACAGGATTGAGGGAGATGAACTTCTACTGAAGCAGCAACACGCCTCTCTGCGTACGTGTCCTATGGGGGCCTG
CTCATGAGGCTGCAGGGGGATGCCAACAACCTGCATGGATTGAGGTGGACTCCAGAGTTTATCTCCTGATGAAG
AAGCTAGCCTTCTGAACCTCGCCTGAAGCCAGCCTCTCTGCCAAGTCACTCAGGTGATGGGCATTGTTCAAGCCT
GAGTGGCAGCCGCTCTTGCTCACCTGTTGAGGAAGGGCTGGCTCACTGTCCACCGTGGCGGCATCTTTAACTGGC
CTCCACTCAATGGGAACTGACTCGCCTGTGAAAGACACAGTGGGAGAGCTGAAAATGAATCAGAAGCTTTATGT
ATATGATTTTTTAAATTAACTTTACTTTTTTCAGACTGCCCTCCCCTTTTTGTAAAAAGTCCATTTACTGT

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FIGURE 368

MAGILFEDIFDVKDIDPEGKKFDRVSRHCESESFKMDLILDVNIQIYPVDLGDKFRLVIASSTLYEDGTLDDGEY
NPTDDRPSRADQFEYVMYGKVYRIEGDETSTEAATRLSAYVSYGGLLMRLQGDANNLHGFEVDSRVYLLMKKLAF

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FIGURE 369

GAGGCAGTTCTGTTGCCACTCTCTCTCCTGTCAATGATGGATCTCAGAAATACCCCAGCCAAATCTCTGGACAAG
TTCATTGAAGACTATCTCTTGCCAGACACGTGTTTCCGCATGCAAAATCGACCATGCCATTGACATCATCTGTGGG
TTCCTGAAGGAAAGGTGCTTCCGAGGTAGCTCCTACCCCTGTGTGTGTGTTCCAAGGTGGTAAAGGGTGGCTCCTCA
GGCAAGGGCACCACCCTCAGAGGCCGATCTGACGCTGACCTGGTTGTCTTCCTCAGTCCTCTCACCACCTTTTCAG
GATCAGTTAAATCGCCGGGGAGAGTTTCATCCAGGAAATTAGGAGACAGCTGGAAGCCTGTCAAAGAGAGAGAGCA
CTTTCCGTGAAGTTTGAGGTCCAGGCTCCACGCTGGGGCAACCCCCGTGCGCTCAGCTTCGTACTGAGTTCGCTC
CAGCTCGGGGAGGGGTGGAGTTCGATGTGCTGCC TGCCTTTGATGCCCTGGGTGAGTTGACTGGCAGCTATAAA
CCTAACCCCCAAATCTATGTCAAGCTCATCGAGGAGTGCACCGACCTGCAGAAAGAGGGCGAGTTCTCCACCTGC
TTCACAGAACTACAGAGAGACTTCCTGAAGCAGCGCCCCACCAAGCTCAAGAGCCTCATCCGCCTAGTCAAGCAC
TGGTACCAAAATTGTAAGAAGAAGCTTGGAAGCTGCCACCTCAGTATGCCCTGGAGCTCCTGACGGTCTATGCT
TGGGAGCGAGGGAGCATGAAAACACATTTCAACACAGCCCAAGGATTTCGGACGGTCTTGGAATTAGTCATAAAC
TACCAGCAACTCTGCATCTACTGGACAAAGTATTATGACTTTAAAAACCCCATTTATTGAAAAGTACCTGAGAAGG
CAGCTCACGAAACCCAGGCCTGTGATCCTGGACCCGGCGACCTACAGGAAACTTGGGTGGTGGAGACCCAAAG
GGTTGGAGGCAGCTGGCACAAGAGGCTGAGGCCTGGCTGAATTACCCATGCTTTAAGAATTGGGATGGGTCCCCA
GTGAGCTCCTGGATTCTGCTGGCTGAAAGCAACAGTACAGACGATGAGACCGACGATCCCAGGACGTATCAGAAA
TATGGTTACATTGGAACACATGAGTACCCTCATTTCTCTCATAGCCCAGCACGCTCCAGGCAGCATCCACCCCA
CAGGCAGAAGAGGACTGGACCTGCACCATCCTCTGAATGCCAGTGCATCTTGGGGGAAAGGGCTCCAGTGTATC
TGGACCAGTTCCTTCATTTTCAGGTGGGACTCTTGATCCAGAGAAGACAAAGCTCCTCAGTGAGCTGGTGTATAA
TCCAAGACAGAACCCAAGTCTCCTGACTCCTGGCCTTCTATGCCCTCTATCCTATCATAGATAACATTCTCCACA
GCCTCACTTCATTCCACCTATTCTCTGAAAATATTCCCTGAGAGAGAACAGAGAGATTTAGATAAGAGAATGAAA
TTCCAGCCTTGACTTTCTTCTGTGCACCTGATGGGAGGGTAATGTCTAATGTATTATCAATAACAATAAAAAATAA
AGCAAAATACCAAAAA

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FIGURE 370

MMDLRNTPAKSLDKFIEDYLLPDTCFRMQIDHAIDIICGFLKERCFRGSSYPVCVSKVVKGSSGKGTTLRGRSD
ADLVVFLSPLTTFQDQLNRRGEFIQEIRRQLEACQERERALS VKFEVQAPRWGNPRALS FVLSSLQLGEGVEFDVL
PAFDALGQLTGSYKPNPQIYVKLIEECTDLQKEGEFSTCFTELQRDFLKQRPTKLKSLIRLVKHWYQNCKKKLGK
LPPQYALELLTVYAWERGSMKTHFNTAQGFRTVLELVINYQQLCIYWTKYDFKNPIIEKYLRRLTKPRPVILD
PADPTGNLGGGDPKGWRQLAQEAELNYPCKNWDGSPVSSWILLAESNSTDDETDPRTYQKYGYIGTHEYPH
FSHRPSTLQAASTPQAEEDWTCTIL

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FIGURE 371

ATGGGGGACGCTCCCAGCCCTGAAGAGAACTGCACCTTATCACCCGGAACCTGCAGGAGGTTCTGGGGGAAGAG
AAGCTGAAGGAGATACTGAAGGAGCGGGAACTTAAATTTACTGGGGAACGGCAACCACGGGCAAACCACATGTG
GCTTACTTTGTGCCCATGTCAAAGATTGCAGACTTCTTAAAGGCAGGGTGTGAGGTAACAATTCTGTTTGC GGAC
CTCCACGCATACCTGGATAACATGAAAGCCCCATGGGAACCTCTAGAACTCCGAGTCAGTTACTATGAGAATGTG
ATCAAAGCAATGCTGGAGAGCATTGGTGTGCCCTTGGAGAAGCTCAAGTTCATCAAAGGCACTGATTACCAGCTC
AGCAAAGAGTACACACTAGATGTGTACAGACTCTCTCCGTGGTCACACAGCACGATTCCAAGAAGGCTGGAGCT
GAGGTGGTAAAGCAGGTGGAGCACCCCTTTGCTGAGTGGCCTCTTATACCCCGGACTGCAGGCTTTGGATGAAGAG
TATTTAAAAGTAGATGCCCAATTTGGAGGCATTGATCAGAGAAAGATTTTACCTTTGCAGAGAAGTACCTCCCT
GCACTTGGCTATTCAAAACGGGTCCATCTGATGAATCCTATGGTTCCAGGATTAACAGGCAGCAAAATGAGCTCT
TCAGAAGAGGAGTCCAAGATTGATCTCCTTGATCGGAAGGAGGATGTGAAGAAAAAAGTGAAGAAGGCCTTCTGT
GAGCCAGGAAATGTGGAGAACAATGGGGTTCTGTCTTCATCAAGCATGTCCTTTTTTCCCCTTAAGTCCGAGTTT
GTGATCCTACGAGATGAGAAATGGGGTGGAAACAAACCTACACAGCTTACGTGGACCTGGAAAAGGACTTTGCT
GCTGAGGTTGTACATCCTGGAGACCTGAAGAATTCTGTTGAAGTCGCACTGAACAAGTTGCTGGATCCAATCCGG
GAAAAGTTTAATACCCCTGCCCTGAAAAAAGTGGCCAGCGCTGCCCTACCCAGATCCCTCAAAGCAGAAGCCAATG
GCCAAAGGCCCTGCCAAGAATTCAGAACAGAGGAGGTCATCCCATCCCGGCTGGATATCCGTGTGGGGAAAATC
ATCACTGTGGAGAAGCACCCAGATGCAGACAGCCTGTATGTAGAGAAGATTGACGTGGGGGAAGCTGAACCACGG
ACTGTGGTGAGCGGCCTGGTACAGTTCGTGCCCAAGGAGGAAGTGCAGGACAGGCTGGTAGTGGTGCTGTGCAAC
CTGAAACCCCAAGATGAGAGGAGTCGAGTCCCAAGGCATGCTTCTGTGTGCTTCTATAGAAGGGATAAACCGC
CAGGTTGAACCTCTGGACCCTCCGGCAGGCTCTGCTCCTGGTGAGCACGTGTTTGTGAAGGGCTATGAAAAGGGC
CAACCAGATGAGGAGCTCAAGCCCAAGAAGAAAGTCTTCGAGAAGTTGCAGGCTGACTTCAAAATTTCTGAGGAG
TGCATCGCACAGTGGAAAGCAAACCAACTTCATGACCAAGCTGGGCTCCATTTCTGTAAATCGCTGAAAGGGGGG
AACATTAGCTTAGCCAGCCCAGCATCTTCCCCCTTCTTCCACCACTGAGTCATCTGCTGTCTCTTCAGTCTGCTC
CATCCATCACCCATTTACCCATCTCTCAGGACA

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FIGURE 372

MGDAPSPEEKHLITRNLQEVLGEEKLKEILKERELKIYWGTTGKPHVAYFVPMSKIADFLKAGCEVTILFAD
LHAYLDNMKAPWELLELRVSYENVIKAMLESIGVPLEKLKFIKGTDYQLSKEYTLDVYRLSSVVTQHDSKKAGA
EVLKQVEHPLLSGLLYPGLQALDEEYLKVDAQFGGIDQRKIFTFAEKYLPALGYSKRVHLMNPMVPGLTGSKMSS
SEESKIDLLDRKEDVKKKLKKAFCPEGNVENNGVLSFIKHVLFPLKSEFVILRDEKWGGNKTYTAYVDLEKDFA
AEVVHPGDLKNSVEVALNKLLDPIREKFNTPALKKLASAAYPDPSKQKPMAGPAKNSEPEEVIPSRLDIRVGKI
ITVEKHPDADSLYVEKIDVGEAEERTVVSGLVQFVPKEELQDRLVVVLCNLKPQKMRGVESQGMLLCASIEGINR
QVEPLDPPAGSAPGEHVFVKGYEKGQPDDEELKPKKKVFEKLQADFKISEECIAQWKQTNFMTKLGSISCKSLKGG
NIS

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FIGURE 373

GAGAGGCGCCAGGCCGGCGGGCGGGCCAGCAGCTTCTTCTTCTCCTCGCACAGCCAGGCCGGCCCCCTGCTCGAGT
CCC GCGTCGCCATGGCCGCGGTTCCCGAGTTGCTGCAGCAGCAGGAGGAGGACCGCAGCAAGCTGAGATCTGTAT
CTGTGGACCTGAATGTTGATCCCTCGCTTCAGATTGACATACCTGATGCGCTCAGTGAGAGAGACAAAGTCAAAT
TTACAGTGCACACAAAGACCACACTGCCACGTTTCAGAGCCCAGAGTTTTCTGTTACAAGGCAACATGAAGACT
TTGTGTGGCTACATGACACTCTTATTGAAACAACAGACTATGCTGGGCTTATTATTCCACCTGCTCCTACGAAGC
CCGACTTTGATGGTCTCGAGAGAAGATGCAGAACTGGGAGAAGGTGAAGGGTCTATGACCAAAGAAGAATTTG
CCAAGATGAAACAAGAACTGGAAGCTGAGTATCTCGCTGTGTTTAAAGAAGACTGTGTCTCCCATGAAGTCTTTC
TTCAGCGGCTTTCTTCTCACCTGTTCTCAGTAAAGATCGCAACTTTCATGTTTCTGGAATATGATCAGGATC
TAAGTGTTAGGCGGAAAAATACTAAAGAGATGTTTGGTGGCTTCTCAAAGTGTGGTGAAAAGTGTGTGATGAAG
TCCTTTTTACTGGAGTTAAGGAGGTAGATGACTTCTTTGAGCAAGAGAAGAACTTCCTTATTAACATATTACAATA
GGATCAAAGATTCTTGTGTGAAAGCTGACAAAATGACCAGATCTCATAAAAAATGTTGCCGATGACTATATCCACA
CCGCAGCCTGCTTACATAGCCTGGCTTTAGAAGAGCCCACAGTCATCAAAAAGTACCTATTGAAGGTTGCTGAGC
TATTTGAAAAACTAAGGAAAGTAGAGGGTCGAGTTTCATCAGATGAAGATTTGAAGCTAACAGAGCTCCTCCGAT
ACTACATGCTCAACATTGAAGCTGCTAAGGATCTCTTATACAGACGCACCAAAGCCCTCATTGACTATGAGAAT
CAAACAAAGCTCTGGATAAGGCCCGGTTAAGAGAGCAAAGACGTCAGTTGGCTGAGGCGACACCAGCAGGAGTGCT
GCCAGAAATTTGAACAACCTTTCCGAATCTGCAAAAGAAGAACTGATAAAATTTCAAACGGAAGAGAGTGGCAGCAT
TTAGAAAGAACTAATTGAAATGTCTGAAGTGGAAATAAAACATGCCAGGAACAATGTCTCCCTTTTGCAGAGCT
GTATTGACTTGTTCAGAATAACTTGATATGCCTTCACTCAGAAGAAAAGAAATGAATGTGAAAGAAAGCCAAGCA
TCATTGCACTTAAATCATTACCACGGAAGATATATTAGCTTCAACTTTAGTTTAAAATTATGTGAATAAATATT
TTGATTTCTACAAATCTTAACATTTAACCATGTTGGTTTAAAAATATTATTGCTTGCTACTTGGACATAAATAAT
TTTTCTTGTGCATTTAATACCTCTGGGCAGAATCAAATACTGGGTCTCCCGTAGTTCGTCTTTAGTTACTAA
GAAAGGTGTAGGACACATTAGCCTTCTGGAACAAGTAGAAGCCATCACCTGGCCCATGTCCCTACAAACCCAT
GATTGTCAGGGAGGTGCCAGTTACAGCAGGTGATTGAGCTACTTGAGGTCGGTAACAGACCTTCCATTCTCACT
GAAGGTGGGGTTTGTGTTTTTGTGTTTTGCCCCTGTTACTCCACTGGTAGTCATCTGGTGTGTTGTACTATAACAACAG
CAAGAAAACTCATTATCTTTATATACTCTTTGCACCTCCTTTTTTTAGTCGAGATATAAATATTTGAGGGGAG
AGAAATATCTACAGGTATATATGGAACAAATAATGTGGTCTGCTTTATAAGATGGCCAGATCTACATTAGGAA
AGTATAAGCCCCCTCCCTAATGGCCGCTGGGGGGTGAGGGCGGTGTGTTGTATGTCTTTGGGTGTTTGTGTTTTTT
ATAAAGCATATAATAAAAAATAATCGTGCTACT

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FIGURE 374

MAAVPELLQQQEEDRSKLRSVVDLNVDPQLQIDIPDALSERDKVKFTVHTKTTLPTFQSPEFSVTRQHEDFVWL
HDTLIETTDYAGLIIPPAPTKPDFDGPREKMQKLGEGECSMTKEEFAMKQELEAEYLAVFKKTVSSHEVFLQRL
SSHPVLSKDRNFHFVLEYDQDLSVRRKNTKEMFGGFFKS VVKSADDEVLTGVKEVD DFFEQEKNF LINYYNRIKD
SCVKADKMTRSHKNVADDYIHTAACLHSLALEEPTVIKKYLLKVAELFEKLRKVEGRVSSDEDLKLTELLRYMYL
NIEAAKDLLYRRTKALIDYENS NKALDKARLKS KDVKLAEAHQQECCQKFEQLSESAKEELINFKRKRVA AFRKN
LIEMSELEIKHARNNVSLLOSCIDLFKNN

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FIGURE 375

CCGGACTGCGGAAGG**ATGG**AGCTGGCCGCCGGAAGCTTCTCGGAGGAGCAGTTCTGGGAGGCCTGCGCCGAGCTC
CAGCAGCCCGCTCTGGCCGGGGCCGACTGGCAGCTCCTAGTGGAGACCTCGGGCATCAGCATCTACCGGCTGCTG
GACAAGAAGACTGGACTTTCATGAGTATAAAGTCTTTGGTGTCTTGGAGGACTGCTCACCAACTCTACTGGCAGAC
ATCTATATGGACTCAGATTACAGAAAACAATGGGACCAGTATGTTAAAGAACTCTATGAACAAGAATGCAACGGA
GAGACTGTGGTCTACTGGGAAGTGAAGTACCCTTTTCCCATGTCCAACAGAGACTATGTCTACCTTCGGCAGCGG
CGAGACCTGGACATGGAAGGGAGGAAGATCCATGTGATCCTGGCCCGGAGCACCTCCATGCCTCAGCTTGGCGAG
AGGTCTGGGGTGATCCGGGTGAAGCAATACAAGCAGAGCCTGGCGATTGAGAGTGACGGCAAGAAGGGGAGCAAA
GTTTTTCATGTATTACTTCGATAACCCGGGTGGCCAAATTCCGTCTGGCTCATTAACTGGGCCGCCAAGAATGGA
GTTCTTAACCTTCTTGAAAGACATGGCAAGAGCCTGTGAGAACTACCTCAAGAAAACCT**TAAG**AAAGAGAAGTGGGA
ACATTGCATCCATGGGTTGATGTCTCTGGAAGTGCAACCACCCAATGTCTCTGGAAGTGCCACCTGGAAGTGCCA
CCTGGAAGTGTCTCTGGAAGAGCACCCACCACTGTTTACGCCTTCCCTGCTGTTTCTGTCTTCAGAGGCCTACAC
ACTACCACATCCTTTCTAAGCATGTTTGCCTGACATCCAGCTCACTCGTCTGCTTCCTTTCTCGCTCCCCCATC
CTGGGCTGGGCTGCCTTCTTCTACAGTTCAATATGGGGCAGACTAGGGAAACCTTTGCTTGCTTACTATTAGGAG
GGGAAGTCTTCAGTAGGGAACACGATCATTCCATTGTGCAATTTTACGGGGATGGGTGGGCGGAGGGACACAACA
AAATTTAAGAATGACTATTTGGGCGGGCTGGCTCTTTTGCAGCTTGTGATTCTTCCAGCTTGGGAGGGGCTGCT
GGAAGTGGCATTTCGTTTCAGAGCTGACTTTCAGTGCACCCAACTGGATGACGTGCCAATGTCCATTTGCCTTAT
GCTTTGTGGAGCTGATTAGGCTGGGATTTGAGGTGATAATCCAGTAAGTCTTTCCTCGTTCCTACTTGTGGAGGA
TCAGTAGCTGTTATGATGCCAGACCATTGGAGAAGTATCAGAGGCCTGACCGGACACATAATACGACAACCACA
TTTTTCCTCATCATCCATGAGGAAATGGATGATTTCTCTTTTCCATATGTCACTGGGGGAAAGGCTGCCTGTACC
TCTCAAGCTTTGCATTTTACTGGAACTGAGGCGTCAAGATGGCTGTGGCAGCTAGCAAAAGCAAAGATGCTTTG
TGCATAGCCTTGTGAAAAAGTATCTTTCTATGCAATAAGATGAATTTTCTCCCAGAATATTTAGAAATGTAGAA
GGGATAACAGTTCACAGCCAGGTAAATTTAACTGGTGGCTTAATGACTCTGCACCTTTTTCTCAGGAATTCTGC
CTAAGTTGTCTGCCTTTTCTACCACCAAAAAGACTTTTAGTTTTCTATGCTTTCTCCTGAATTTTGGTAGGGTAA
GTATTTCTATGTCAAAGGCACAGCCTTGATGATCTCAGGGAAAAATTTTAATCACTGTGTATAATGATACTGAAC
CTTGATTAATAACAGAAATTCAGGATGTAAAGCCAAGAATGGGATTTATTAATGTGGGATACCTCAGACTGTTT
GTTTTCTTTCTGGGAAGAAAAGTGTGTTCTATAATGAATAAATATAGAGTGGTTTTT

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FIGURE 376

MELAAGSFSEEQWEACAELOQPALAGADWQLLVETSGISITYRLDKKTGLHEYKVFGVLEDCSPTLLADIYMS
DYRKQWDQYVKELYEQECNGETVVYWEVKYPPFMSNRDYVYLRQRDLMEGRKIHVILARSTSMPLGERSGVI
RVKQYKQSLAIESDGKKGSKVFMYYFDNPGGQIPSWLINWAAKNGVPNFLKDMARACQNYLKKT

FIGURE 377

[illegible]

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FIGURE 378

MAAGGSDPRAGDVEEDASQLIFPKEFETAETLLNSEVHMLLEHRKQONESAEDEQELSEVFMKTLNYTARFSRFK
NRETIASVRSLLLQKKLHKFELACLANLCPETAESKALIPSLEGRFEDEELQQILDDIQTKR SFQY

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FIGURE 379

GTCTGAGCAGCCAACACACCAGCCCAGACAGCTGCAAGTCACCATGGACGCTGAAGGCCTGGCGCTGCTGCTGC
CGCCCGTCACCCTGGCAGCCCTGGTGGACAGCTGGCTCCGAGAGGACTGCCCAGGGCTCAACTACGCAGCCTTGG
TCAGCGGGGCAGGCCCTCGCAGGCGGCGCTGTGGGCCAAATCCCCTGGGGTACTGGCAGGGCAGCCTTTCTTCG
ATGCCATATTTACCCAACCTCAACTGCCAAGTCTCCTGGTTCCCTCCCCGAGGGATCGAAGCTGGTGCCGGTGGCCA
GAGTGGCCGAGGTCCGGGGCCCTGCCCAGCTGCTGCTGCTGGGGGAACGGGTGGCCCTCAACACGCTGGCCCGCT
GCAGTGGCATTGCCAGTGTGCGCCGCTGCAGTGGAGGCCGCCAGGGGGGCGGCTGGACTGGGCACGTGGCAG
GCACGAGGAAGACCACGCCAGGCTTCCGGCTGGTGGAGAAGTATGGGCTCCTGGTGGGCGGGGCGCCTCGCACC
GCTACGACCTGGGAGGGCTGGTGATGTTGAAGGATAACCATGTGGTGGCCCCCGGTGGCGTGGAGAAGGCGGTGC
GGGCGGCCAGACAGGCGGCTGACTTCGCTCTGAAGGTGGAAGTGGAAATGCAGCAGCCTGCAGGAGGTCTGCCAGG
CAGCTGAGGCTGGCGCCGACCTTGTCCTGCTGGACAACCTTCAAGCCAGAGGAGCTGCACCCACGGCCACCGCGC
TGAAGGCCAGTTCCCGAGTGTGGCTGTGGAAGCCAGTGGGGGCATCACCTGGACAACCTCCCCAGTTCTGCG
GGCCGCACATAGACGTCATCTCCATGGGGATGCTGACCCAGGCGGTCCCAGCCCTTGATTTCTCCCTCAAGCTGT
TTGCCAAAGAGGTGGCTCCAGTGCCCAAAATCCACTAGTCTAAACCGGAAGAGGATGACACCGGCCATGGGTTA
ACGTGGCTCCTCAGGACCCTCTGGGTACACATCTTTAGGGTCAGTGAACAATGGGGCACATTGGCACTAGCTT
GAGCCCAACTCTGGCTCTGCCACCTGCTGCTCCTGTGACCTGTCAGGGCTGACTTCACCTCTGCTCATCTCAGTT
TCCTAATCTGTAAAATGGGTCTAATAAAGGATCAACCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 380

MDAEG LALLLPVTLAALVDSWLREDCPGLNYAALVSGAGPSQAALWAKSPGVLAGQPFFDAIFTQLNCQVSWFL
PEGSKLVPVARVAEVRGPAHCLLLGERVALNTLARCSGIASAAAAAVEAARGAGWTGHVAGTRKTTPGFRLVEKY
GLLVGGAASHRYDLGGLVMLKDNHVVPGGVEKAVRAARQAADFALKVEVECSSLQEVVQAAEAGADLVLLDNFK
PEELHPTATALKAQFPSVAVEASGGITLDNLPQFCGPHIDVISMGMLTQAVPALDFSLKLFKEVAPVPKIH

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FIGURE 381

TAACGGTCTAAGGTAGCGAGATGATGCGAGGGGAAAACCCGAGCAGTGTGCCAAGAGGAGGAAATAGGCCAATGT
GGTCTGGGACGGTTGGATATACTTAAACATCTTAATAATCAGAGTAATTTTCATTTACAAAGAGAGGTGCGTACT
TAAAATAACCCGTGAAAAATAACACTGGAATTCCTTTTCTAGCATTATATTTATTCCTGATTIGCCTTTGCCATAT
AATCTAATGCTTGTTTTATATAGTGTCTGGTATTGTTTAAACAGTTCTGTCTTTCTATTTAAATGCCACTAAATTT
TAAATTCATACCTTTCCATGATTCAAAATTCAAAAGATCCCATGGGAGATGGTTGGAAAAATCTCCACTTCATCCT
CCAAGCCATTCAAGTTTCCTTTCCAGAAGCAACTGCTACTGCCTTTTCATTCATATGTTCTTCTAAAGATAGTCTA
CATTTGGAAATGTATGTTAAAAGCACGTATTTTTTAAAATTTTTTTCCTAAATAGTAACACATTGTATGTCTGCTG
TGTAATTTGCTATTTTTTATTTATTTTAGTGTCTTCTATATAGCAGATGGAATGAATTTGAAGTTCCAGGGCTGA
GGATCCATGCCTTCTTTGTTTCTAAGTTATCTTTCCCATAGCTTTTCATTATCTTTTCATATGATCCAGTATATGT
TAAATATGTCCTACATATACATTTAGACAACCACCATTGTGTTAAGTATTTGCTCTAGGACAGAGTTTGGATTTGT
TTATGTTTGCTCAAAAGGAGACCCATGGGCTCTCCAGGGTGCACTGAGTCAATCTAGTCCTAAAAAGCAATCTTA
TTATTAACCTCTGTATGACAGAATCATGTCTGGAACTTTTGTTTTCTGCTTTCTGTCAAGTATAAACTTCACTTTG
ATGCTGTACTTGCAAAATCACATTTTCTTTCTGGAAATTCGGGCAGTGTACCTTGACTGCTAGCTACCCTGTGCC
AGAAAAGCCTCATTCGTTGTGCTTGAACCCTTGAAATGCCACCAGCTGTCACTACACAGCCCTCCTAAGAGGC
TTCCTGGAGGTTTCGAGATTCAGATGCCCTGGGAGATCCAGAGTTTCCTTTCCCTCTTGCCCATATTCTGGTGT
CAATGACAAGGAGTACCTTGCTTTGCCACATGTCAAGGCTGAAGAAACAGTGTCTCCAACAGAGCTCCTTGTGT
TATCTGTTTGTACATGTGCATTTGTACAGTAATTGGTGTGACAGTGTCTTTGTGTGAATTACAGGCAAGAATTG
TGGCTGAGCAAGGCACATAGTCTACTCAGTCTATTCTAAGTCCTAACTCCTCCTTGTGGTGTGGATTTGTAAG
GCACTTTATCCCTTTTGCTCATGTTTCATCGTAAATGGCATAGGCAGAGATGATACCTAATTCTGCATTTGATT
GTCACTTTTTGTACCTGCATTAATTTAATAAAATATCTTATTTATTTTGTACTTGGTACACCAGCATGTCCAT
TTTCTTGTTTATTTTGTGTTTAAATAAAATGTTTCAGTTTAAACATCCCAGTGGAGAAAGTTAAAAAA

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FIGURE 382

MFSLTSQWRKL

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FIGURE 383

CCCAAATATATATTTAATCTTGTGGTTCAAATAAGCTTTTGGCTCACATCTAAGCACATCATAAAGAACGCTGTA
GAAGAGGTGACATGATGAGGCGGGAAGACGAGGAAGAGGAGGGAACAATGATGAAGGCAAAAGGGGACTTAGAGA
TGAAGGAGGAGGAAGAGATTAGTGAGACAGGAGAACTGGTTGGCCCTTTTGTGAGTGCTATGCCCCTCCAATGC
CCCACAACAAGGGCACCCTGGTCTCTGAGGCATGGGAATATTTCCACCTAGCTCCTGCTCGTGCTGGGCACCATC
CCAACCAGTATGCCACCTGCCGCTGTGTGGCAGGCAGGTGAGCCGTGGCCCTGGGGTCAACGTGGGCACCACTG
CACTGTGGAAGCATCTGAAAAGCATGCACAGAGAGGAGCTGGAGAAGAGTGCCATGGTCAGGCTGGGCAGCGCC
AGGATCCAAGGCCCCACGGGCCCCAGCTCCCCACAGGCATTGAGGGTAACCTGGGGTAGGCTCCTGGAGCAGGTGG
GCACCATGGCTTTGTGGGCCAGCCAAAGGGAAAAGGAGGTGCTTAGGAGGGAAAGGGCAGTGGAATGGCGGGAGA
GGGCTGTGGA AAAAAGGGAGCGAGCCCTGGAGGAGGTGGAAAGGGCCATCCTGGAGATGAAGTGGAAGGTGAGGG
CTGAGAAGGAGGCATGCCAGCGGGAGAAAGAGCTGCCTGCAGCAGTACATCCCTTCCATTTTGTTAAATTGGGC
TTGGAGAATCTATTCTGAAAACATTGACTCTAGACTTGTAGAAAAGAGCCATTTTAGTTTCAACTCAAATGTAAA
GCAAAGTAGTTTGGTGACATTTTGCTTTTATGTGAAATAGTGACAGTATGAGTTAATCTGAGCAGGTCTGAATT
GACCAAATGCTTATCTACGAGGTTCTTAGAGCTCTGCTGACCTTGGCCGAACTCTAAAAATGTACCTATTAAAG
ATAAATGCTTCTACCAAAGTAAACTCTGTGAGTTGTTTCAGGGCAGAATGTACCAGCCAGTCAGCGTTGTTTAA
CAAAATAATCAGATTTTTGCCTAGCACTCGGTTTTGGTGGAGCTGACGATTTTGAGGGCTGAGGCTGGTTAGGTA
GCTGGAATGTGCCTATGTGACCAGCTCACTTGACAGACCCCTGCCGGAAGCAGAGCTTAATCTTCTAGGACTGA
GGTCTTAGCACATGTACTGGTGGAGTTCCAGACCACCAGTATGAATAAAAGCTTGTCTGTGTGACCCAGCAAG
TGGAAGGACAAAGAACTGTGAGCCTCAGATCTTTGGACCTTTCCAATGCGTCTCTTCTCCTGTTATTGTGCAA
TGTATTTTCTTGCTTATATTAAAGTTGTTTCATCAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 384

MRREDEEEEGTMMKAKGDLEMKEEEEISETGELVGPFVSAMPTPMPHNKGTRFSEAWYFHLAPARAGHHPNQYA
TCRLCGRQVSRGPGVNVGTTLWKHLKSMHREELEKSGHGQAGQRQDPRPHGPQLPTGIEGNWGRLLLEQVGTMAL
WASQREKEVLRERAVEWRERAVEKRERALEEVERAILEMKWKVRAEKEACQREKELPAAVHPFHFV

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FIGURE 385

GGCCGGAGGGAGCCCGCGCTCGGGGCGGCGGCTGGAGGCAGCGCACCGAGTTCCCGCGAGGATCCATGACCTGAC
GGGGCCCCGGAGCCCGCTGCCTCTCGGGTGTCTGGGTGCGGTGGGGAGCCAGTGCTCGCAGGCCGGCGGGCGG
GCCGGAGGGCTGCAGTCTCCCTCGCGGTGAGAGGAAGGCGGAGGAGCGGGAACCGCGGCGGCGCTCGCGCGGCGC
CTGCGGGGGGAAGGGCAGTTCCGGGCGGGCCGCGCCTCAGCAGGGCGGCGGCTCCCAGCGCAGTCTCAGGGCCC
GGGTGGCGGCGGCGACTGGAGAAATCAAGTTGTGCGGTGCGGTGATGCCCCAGTGAGCGGGGGGCTGGGCCTCTG
CCCTTAGGAGGCAACTCCACGCAGGCCGCAAAGGCTCTCGCGGCCGAGAGGCTTCGTTTCGGTTTCGCGGCGG
CGGCGGCGTTGTTGGCTGAGGGGACCCGGGACACCTGAATGCCCCGGCCCCGGCTCCTCCGACGCGATCGGGAA
GGTGTATCCAAAATCTTCGGGAACAAGGAAATGCGGATCCTCATGTTGGGCTGGACGCGGCCGCAAGACAAC
AATCCTGTACAAGTTGAAGCTGGGCCAGTCGGTGACCACCATTCCTACTGTGGGTTTCAACGTGGAGACGGTGAC
TTACAAAATGTCAAGTTCAACGTATGGGATGTGGGCGGCCAGGACAAGATCCGGCCGCTCTGGCGGCATTACTA
CACTGGGACCCAAGGTCTCATCTTCGTAGTGGACTGCGCCGACCGCGACCGCATCGATGAGGCTCGCCAGGAGCT
GCACCGCATTATCAATGACCGGGAGATGAGGGACGCCATAATCCTCATCTTCGCCAACAAGCAGGACCTGCCCCA
TGCCATGAAACCCACGAGATCCAGGAGAACTGGGCCTGACCCGGATTTCGGGACAGGAACTGGTATGTGCAGCC
CTCCTGTGCCACCTCAGGGGACGGACTCTATGAGGGGCTCACATGGTTAACCTCTAACTACAAATCTTAATGAGC
ATTCTCCACCCATCCCCTGGAAGGAGAGAAATCAAAAACCCATTTCATAGGATTATCGCCACCATCACCTCTTTCA
ATTGCCACTTTCTCTTTCTTTTGAATTTGAACTCTGGAGTTACTGTTCTACAGTTTGGCGGGGACGGGCTTGGGG
GTTTTCTCTTTTGTGTTTCCCTTTCTTTTTCCTTTTTTTTTTTTTTTTTTGTGGCTTTGCGTTAGGATGGC
TCTGATCTGACATTTGACATGAACACAAAGTTGCCAAGATGCTCCTTGTTGACTTCCAGCAGAATGGGAATGGG
GAAACACAGCAGTTCTTGGGTAAAAGTCCCTTTGTAATAATAGGTTTGGGATTTTTTTATTTTCGAGAGAATCTTT
CATTTTCCTATGTATGCTTTTTTCCTTTTTTGCCCAGTTTCCTTATCACTTGCTGTAGATGGCTTATTTTGATT
CATGCAGACTATGTTGCAAGTCTGTTTCATCTAGTAACTGAAAATTATTGCTTAATCAAATGCGGTTTGTCTT
TTATATTTAAGGCCTTCCCCCCCCTTCCTTATGAGTTCTAACTTAGTAATTTCAAATGTGACCTTTTATATCTAA
GACCAGTATAGTAACTTAGCCACAGTGGCAAATAATGAGTAATATTGTAATATGTTCCAGTTGCACCTCAGTA
TGTTAAACAGGTAATGTAAGAAGTTCTCTGAAATGTCAGCAAGTAAGTTCTGAAACACATCATGCATGAGTAGGA
ATAAAC

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FIGURE 386

MGKVLISKIFGNKEMRILMLGLDAAGKTTILYKLKLGQSVTTIPTVGFNVETVITYKNVKFNVWDVGGQDKIRPLWR
HYTGTQGLIFVVDCAADRDRIDEARQELHRIINDREMRDAIILIFANKQDLPDAMKPHEIQEKLGLTRIRDRNWY
VQFSCATSGDGLYEGLTWLTSNYKS

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FIGURE 387

CGGCAGTGCGCCTGCGCAAGTTACGCGAAAGCTAACAGAATCTGCGGTGCTCTGCTGGCGACTGGCAGGACGCGG
TGCAGAGAGCGGACTTCCGCGACGCGGGTCCTACAGTGTAGGGGAAGCAATGGAAGAACTTCTACCTGATGGACA
AATATGGGCTAATATGGATCCAGAAGAACGAATGTTGGCAGCTGCTACAGCTTTTACCCACATCTGTGCAGGGCA
GGGTGAAGGAGATGTCAGGAGAGAAGCCCAATCTATCCAATATGATCCCTACAGTAAAGCTTCAGTAGCCCCAGG
GAAGCGACCTGCTCTTCCTGTGCAACTACAGTACCCACATGTAGAAAAGTAATGTCCCTTCAGAAACAGTCTCTGA
GGCCTCCCAAAGACTCCGAAAGCCAGTGATGAAGAGAAAAGGTGCTGCGCAGAAAGCCAGATGGGGAAGTATTAGT
AACAGATGAGTCGATTATCAGTGAATCAGAATCTGGTACAGAAAATGATCAGGATCTCTGGGACTTAAGACAAAG
GCTGATGAATGTACAGTTCCAGGAAGACAAGGAATCTTCATTTGATGTTTCACAAAAATTTAACCTACCACATGA
ATACCAAGGAATTTCTCAAGATCAGCTCATTGCTCTCTACAAAGAGAAGGAATGGGCTCTCCAGCTTACGAACA
AGACCTGATTGTTGCCAGCAGACCCCAAGTCCTTTATTCTCCCAAAGCTGGACCAGTTAAGCCGAAACCGGGGCAA
GACAGACCGGGTAGCCCGGTATTTTGAGTACAAACGGGACTGGGACTCAATACGTTTACCTGGTGAAGATCATAG
AAAGGAATTACGCTGGGGTGTCCGAGAGCAGATGCTTTGTGCGAGCAGAACCCCAATCCAAACCTCAGCATATATA
TGTCCTCAAACAATTATCTAGTACCAACAGAGAAGAAAAGGTCTGCACTCCGTTGGGGTGTTCGTTGTGACCTTGC
AAATGGTGTATACCCAGGAAGCTTCCCTTCCCTCTTTCTCCTTCTTAAATCTTTTAACTTCTTTACAGGAT
TGTTTGAGATAACCTAGCTCTTTATATCTTCCCTTTTAAATAGAAACAACCTGTCTTGAGAAGCTCTTCGAAACAT
TTTATGGTAAGGACTTCACCTATCATTGGTCTTTCCTAGCTATATATCACATTGGTATCAGATGATACTTCCAAA
TTGCCACTCAAATCCAGCAATTGCAAGATAAATCATATCAGAGAAAGAACAACAGACCTGGTCTTTCTATTTTGT
CAAATTAGTAAGGGCCCTTTGTGTCCTGTAACCTTTTACCTATCAATATGAGTTGCTGTGCTTCAGTGTGTGT
TTTTTAAGTTGCTGGGCATTACACTTACCAATTAAAGAATTTTGGAATTCAAAAAA

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FIGURE 388

GSAPAQVTRKLTESAVLCWRLAGRGAEGLPRRGSYSVGEAMEELLPDGQIWANMDPEERMLAAATAFTHICAGQ
GEGDVRREAQSIQYDPYSKASVAPGKRPALPVQLQYPHVESNPSETVSEASQRLRKPVMKRKVLRRKPDGEVLV
TDESIISESESGTENDQDLWDLRQRLMNVQFQEDKESSFDVSQKFNLPHHEYQGISQDQLICSLQREGMGSPAYEQ
DLIVASRPKSFILPKLDQLSRNRGKTDRVARYFEYKRDWDSIRLPGEDHRKELRWGVREQMLCRAEPQSKPQHLY
VPNNYLVPTEKKRSALRWGVRCDLANGVIPRKLPFPLSPS

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FIGURE 389

TGGAAGACTTCGAGACCCATTTAGGATCACGGCGCTACGGATGACCTGAGAATTAATTTATGGCACTTAGAAATC
ACAGATAGAAGCTTTAACATCGTGGACATCAAGCCTGCTAACATGGGAGGAGCTGACCGAAGTCATCACTGCAGCC
GAGTTCCACCCGCACCACTGCAACGTGTTTCGTCTACAGCAGTAGCAAAGGGACCATCCGCCTGTGTGACATGCGC
TCCTCGGCCCTGTGCGACAGACACTCCAAGTTTTTTGAAGAGCCTGAAGATCCCAGCAGTAGGTCCTTCTTCTCA
GAAATAATTTTCATCCATATCCGATGTAAAATTCAGTCATAGTGGGCGGTACATGATGACCAGAGACTTACCTGTC
GGTGAAGGTGTGGGACCTCAACATGGGAGAGCAGGCCGGTGGAGACCCACCAGGTCCACGAGTACCTGCGCAGCA
AGCTCTGCTCTCTCTATGAGAACGACTGCATCTTTGACAAGTTTGAGTGTGCTGGAACGGTTTCGGATAGCGCCA
TCATGAACCGGGTCCTATAACAACCTTCTTCAGGATGTTTGATAGAGACACGCGGAGGGATGTGACCTTGAGGCCT
CGAGAGAGAGCAGCAAACCGCGCGCCAGCCTCAAAACCCGGAAGGTGTGTACGGGGGGTAAGCGGAGGAAAGACG
AGATCAGTGTGGACAGTCTGGACTTCAACAAGAAGATCCTGCACACAGCCTGGCACCCCGTGGACAATGTCATTG
CCGTGGCTGCCACCAATAACTTGTACATATTCCAGGACAAAATCAACTAGAGACGCGAACGTGAGGACCAAGTCT
TGTCTTGATAGTTAAGCCGGACATTTTTCTGTGTCAGAGAAAAGGCATCATTGTCCGCTCCATTAAGAACAGTGAC
GCACCTGCTACTTCCCTTCACAGACACAGGAGAAAGCCGCTCCGCTGGAGGCCCGGTGTGGTTCCGCCTCGGCG
AGGCGCGAGACAGGCGCTGCTGCTCACGTGGAGACGCTCTCGAAGCAGAGTTGACGGACACTGCTCCCAAAGGT
CATTACTCAGAATAAATGTATTTATTTCAAAAAA

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FIGURE 390

MEELTEVITAAEFHPHCNVFVYSSSKGTIRLCDMRSSALCDRHSKFFEEPEDPSSRSFFSEIISSISDVKFSSHS
GRYMMTRDLPVGEVGPQHGRAGRWRPTRSTSTCAASSALSMRTTASLTSLSVAGTVRIAPS

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FIGURE 391

GCGCCGAGCGCCGCGCCGCGCCGCGCCGCGCTCCGCTGCCGCGCCGCGCCGCGGCTCCCGATGGAGACTGA
CGCGCCCCAGCCCGGCTCGCCTCCCCGACTCGCCGCACGACCCCTGCAAGATGTTTCATCGGGGGACTCAGTTG
GCAGACTACGCAGGAAGGGCTGCGCGAATACTTCGGCCAGTTCGGGGAGGTGAAGGAGTGTCTGGTGATGCGGGGA
CCCCCTGACCAAGAGATCCAGGGGTTTCGGCTTCGTCACTTTTCATGGACCAGGCGGGGGTGGATAAAGTGCTGGC
GCAATCGCGGCACGAGCTCGACTCCAAAACAATTGACCTAAGGTGGCCTTCCCTCGGCGAGCACAGCCCAAGAT
GGTGACTCGAACGAAGAAGATCTTTGTGGGGGGGCTGTCTGGTGAACACCACGGTGGAGGACGTGAAGCAATATTT
TGAGCAGTTTGGAAGGTGGACGACGCCATGCTGATGTTTGACAAAACCACCAACCGGCACCGAGGGTTCGGGTT
TGTCACGTTTGAGAGTGAGGACATCGTGGAGAAAGTGTGTGAAATTCATTTTCATGAAATCAACAACAAAATGGT
GGAATGTAAGAAAGCTCAGCCAAAGGAGGTGATGTGCCAACGGGCTCAGCCCGGGGGAGGTCTCGAGTCATGCC
CTACGGAATGGACGCCCTTCATGCTGGGCATCGGCATGCTGGGTTACCCAGGTTTCCAAGCCACAACCTACGCCAG
CCGGAGTTATACAGGCCTCGCCCTGGCTACACCTACAGTTCCCCGAATTCGTGTAGAGCGGACCCCTCTCCC
GAGCGCCCCAGTCTCCCCGAGCTTACAGCCATTCCTCTCACTGCCTACGGACCAATGGCGGCGGCAGCGGCGGC
AGCGGCTGTGGTTTCGAGGGACAGGCTCTCACCCCTGGACGATGGCTCCCCCTCCAGGTTCTGACTCCAGCCGCAC
AGGGGGCTTCCCTGGGGACCACCAGCCCCGGCCCCATGGCCGAGCTCTACGGGGCGGCCAACCAGGACTCGGGGGT
CAGCAGTTACATCAGCGCCGCCAGCCCTGCCCCAGCACCGGCTTCGGCCACAGTCTTGGGGGGCCCTTTGATTGC
CACAGCCTTCACCAATGGGTACCACTGAAGCAGGGGACGGTGGCAGGAGCGCCCCAGCCTGCAGCTGACTGAGGA
CCACGAGTGAGCCAGCGAGGGGGCGGGAGACCTCAGCCGACGCCGCCGCCCTCCCCTGCAGCGACTCGGACCC
GCTACTGCCTGCCCCCAACTCCCCGGGCCCGGCCCTGCCCTGCTGCCCCAACAGCGTCTGGCTCCCTACTAA
CGTCCCCCTCTTCGCCCTTGCCCCATCCCCACCCGCCCTCTCCCGGCCCTGCTTTTATTTATTTGGATTAGC
CGGTTGCCACCCAGCCCTCTGGTCCATCCCTCCCTCCGTGCCGCGCCCCCTAGGACCGCCCTCCCCAAAA
GGCTTTTGGATTGTGTCATAGCTGGAGTGAAGGCGGAGGGAGCCTGCTACAGGCCGCAGCCCAACCCCTGTTTTT
TATTCAGATTTCCCCTCCTTTACCCTTTCCCTTTTTTTTTTTTTTTTTTTGTTTAAAGAAACCTTTTTTAA
CTATTTCTAGGTTTGTGAATGTGAAGCCCCAGGCCGAGGGGGCAAGGGGCCAGGTGCCCCCACCAGCTGAGAA
CAAAGTGTCTATCTGGGTGTGGGCCCTGGCCGCCCTCCCTCCAGCCCTGGAGAGGAGGGCAGGGCTGCGGGGAGG
CCAGGCCGAGCCCTGGAACCATCCCGTCTGTATCATATGTAAATACTGTGAGGTGATGTGCCACCCCTCTCT
AAGACCCCTCGGGGGTGAGGGGCTCCCCCTCCCTGTTTCTGTCCCCTCAGACACCGTTACTGT

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FIGURE 392

METDAPQPGLASPDSPHDPCKMFIGGLSWQTTQEGFREYFGQFGEVKECLVMRDPLTKRSRGFGFVTFMDQAGVD
KVLQSRHELDSTIDPKVAFPRRAQPKMVTRTKKIFVGGLSVNTTVEDVKQYFEQFGKVDDAMLMFDKTTNRHR
GFGFVTFESEDIVEKVCEIHFHEINNKMVECKKAQPKVMSPTGSARGRSRVMPYGMDAFMLGIGMLGYPGFQAT
TYASRSYTG LAPGYTYQFPEFRVERTPLPSAPVLPELTAIPLTAYGPMAAAAAA AVVGTGSHFWTMAPPPGST
PSRTGGFLGTTSPGPMAELYGAANQDSGVSSYISAASPAPSTGFGHSLGGPLIATAFTNGYH

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FIGURE 393

CGCGTGAAGTCTTCCTGCAGGCTGGCCATGGCGCTTCACGTTCCCAAGGCTCCGGGCTTTGCCAGATGCTCAA
GGAGGGAGCGAAACACTTTTCAGGATTAGAAGAGGCTGTGTATAGAAACATACAAGCTTGCAAGGAGCTTGCCCA
AACCCTCGTACAGCATATGGACCAAAAGGAATGAACAAAATGGTTATCAACCACTTGGAGAAGTTGTTTGTGAC
AAACGATGCAGCAACTATTTTAAGAGAAGTAGAAGTACAGCATCCTGCTGCAAAAATGATTGTAATGGCTTCTCA
TATGCAAGAGCAAGAAGTTGGAGATGGCACAACCTTTGTTCTGGTATTTGCTGGAGCTCTCCTGGAATTAGCTGA
AGAACTTCTGAGGATTGGCCTGTCAGTTTCAGAGGTCATAGAAGGTTATGAAATAGCCTGCAGAAAAGCTCATGA
GATTCTTCCTAATTTGGTATGTTGTTCTGCAAAAAACCTTCGAGATATTGATGAAGTCTCATCTCTACTTCGTAC
CTCCATAATGAGTAAACAATATGGTAATGAAGTATTTCTGGCCAAGCTTATTGCTCAGGCATGCGTATCTATTTT
TCCTGATTCCGGCCATTTCAATGTTGATAACATCAGAGTTTGTAATAATCTGGGCTCTGGTATCAGTTCTCTCTTC
AGTATTGCATGGCATGGTTTTTAAGAAGGAAACCGAAGGTGATGTAACATCTGTCAAAGATGCAAAAATAGCAGT
GTACTCTTGTCCTTTTGTATGGCATGATAACAGAACTAAGGGAACAGTGTTGATAAAGACTGCTGAAGAATTGAT
GAATTTTAGTAAGGGAGAAGAAAACCTCATGGATGCACAAGTCAAAGCTATTGCTGATACTGGTGCAAATGTGCT
AGTAACAGGTGGCAAAGTGGCAGACATGGCTCTTCATTATGCAAATAAATATAATATCATGTTAGTGAGGCTAAA
CTCAAAATGGGATCTCCGAAGACTTTGTAAAACCTGTTGGTGCTACAGCTCTTCCTAGATTGACACCTCCTGTCTT
TGAAGAAATGGGACACTGTGACAGTGTTTACCTCTCAGAAGTTGGAGATACTCAGGTGGTGGTTTTTAAGCATGA
AAAGGAAGATGGCGCCATTTCTACCATAGTACTTCGAGGCTCTACAGACAATCTGATGGATGACATAGAAAGGT
AGTAGACGATGGTGTTAATACTTTCAAAGTTCTTACAAGGGATAAACGTCTTGTAACCGGAGGTGGAGCAACAGA
AATTGAATTAGCCAAACAGATCACATCATATGGAGAGACATGTCTGGACTTGAACAGTATGCTATTAAGAAGTT
TGCTGAGGCATTTGAAGCTATTTCCCGCGCACTGGCAGAAAACCTCTGGAGTTAAGGCCAATGAAGTAATCTCTAA
ACTTTATGCAGTACATCAAGAAGGAAATAAAAACGTTGGATTAGATATTGAGGCTGAAGTCCCTGCTGTAAAGGA
CATGCTGGAAGCTGGTATTCTAGATACTTACCTGGGAAAATATTGGGCTATCAAACCTCGCTACTAATGCTGCAGT
CACTGTACTTAGAGTGGATCAGATCATCATGGCAAAACAGCTGGTGGGCCCAAGCCTCCAAGTGGGAAGAAAGA
CTGGGATGATGACCAAAATGATTGAATTTGGCTTAATTTTTACTGTAGGTGAAGGCTGTATTTGTAGTAGTACTC
AAGAATCACCTGATGTTTTCTTATTCTCCTTAAATTAAGAGTTATTTTGTGTTGTATTCTTGGCTGGATGTTAT
AATAACATATTGTTACTGTC

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FIGURE 394

MALHVPKAPGFAQMLKEGAKHFSGLEEAVYRNIQACKELAQTTRTAYGPKGMNKMVINHLEKLFVTNDAATILRE
LEVQHFAAKMIVMASHMQEQEVGDGTNFVLVVFAGALLELAEEELLRIGLSVSEVIEGYEIACRKAHEILPNLVCCS
AKNLRDIDEVSSLLRTSIMSKQYGNEVFLAKLIAQACVSIFPDSGHFNVDNIRVCKILGSGISSSSVLHGMVFKK
ETEGDVTSVKDAKIAVYSCFPDGMITETKGTVLIKTAELMNF SKGEENLMDAQVKAIADTGANVVVTGGKVADM
ALHYANKYNIMLVRLNSKWDLRRLCKTVGATALPRLTPPVLEEMGHCD SVYLSEVGDTQVVVFKHEKEDGAISTI
VLRGSTDNLMDDIERVVDDGVNTFKVLTRDKRLVP GGGATEIELAKQITSYGETCPGLEQYAIKKFAEAFEAI PR
ALAENSGVKANEVISKLYAVHQEGNKNVGLDIEAEVPAVKDMLEAGILD TYLGKYWAIKLATNAAVTVLRVDQII
MAKPAGGPKPPSGKKDWDDQND

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FIGURE 395

AGTCCTGCGATTTTCGGTGTAGAGGAGCAGGGGCTGCGGGACCTGGTGTGGGTGGAGTGGGACAAGCGGTGGAGAA
GGGTACGCCAGGGTCGCTGAGAGACTCTGTTCTCCCTGGAGGGACTGGTTGCCATGAGAGCAGCCGTCTGAGGGG
ACGCAGCCTGCACTACGCGCCCCAAGAGGGCTGTGCGTGGCGAGCAGGTCACGTGACGGGAGCGCGGGCTTTGGAA
GGCGGCTGAACGTCAGGCCACCCGCCGCTAAGCTGAGAAGGGAGAGCGAGCTTAGGACCGCCTGCCCCGGGCAAC
CCCGAACCAAGCTTTAGCCGCCGAGGCCGCGTGTCCAAAGGCCAGTCATCCCTCCTCTGTGTTGCCATGGGAAT
TCAAGGCCTGGCCAACTAATTGCTGATGTGGCCCCAGTGCCATCCGGGAGAATGACATCAAGAGCTACTTTGG
CCGTAAGGTGGCCATTGATGCCTCTATGAGCATTATCAGTTCCGTATTGCTGTTGCCAGGGTGGGGATGTGCT
GCAGAATGAGGAGGGTGAAGACCAGCCACCTGATGGGCATGTTCTACCGCACCATTGCGATGATGGAGAACGG
CATCAAGCCCCTGTATGTCTTTGATGGCAAGCCGCCACAGCTCAAGTCAGGCGAGCTGGCCAAACGCAGTGAGCG
GCGGGCTGAGGCAGAGAAGCAGCTGCAGCAGGCTCAGGCTGCTGGGGCCGAGCAGGAGGTGGAAAAATTCATAA
GCGGCTGGTGAAGGTCATAAGCAGCACAAATGATGAGTGCAAACATCTGCTGAGCCTCATGGGCATCCCTTATCT
TGATGCACCCAGTGAGGCAGAGGCCAGCTGTGCTGCCCTGGTGAAGGCTGGCAAAGTCTATGCTGCGGCTACCGA
GGACATGGACTGCCTCACCTTCGGCAGCCCTGTGCTAATGCGACACCTGACTGCCAGTGAAGCCAAAAAGCTGCC
AATCCAGGAATTCACCTGAGCCGATTCTGCAGGAGCTGGGCCTGAACCAGGAACAGTTTGTGGATCTGTGCAT
CCTGCTAGGCAGTGACTACTGTGAGAGTATCCGGGGTATTGGGCCCCAAGCGGGCTGTGGACCTCATCCAGAAGCA
CAAGAGCATCGAGGAGATCGTGCGGCGACTTGACCCCAACAAGTACCCTGTGCCAGAAAATTGGCTCCACAAGGA
GGCTCACCAGCTCTTCTTGGAACCTGAGGTGCTGGACCCAGAGTCTGTGGAGCTGAAGTGGAGCGAGCCAAATGA
AGAAGAGCTGATCAAGTTCATGTGTGGTGAAGAGCAGTTCTCTGAGGAGCGAATCCGCAGTGGGGTCAAGAGGCT
GAGTAAGAGCCGCCAAGGCAGCACCCAGGGCCGCCGATGATTTCTTCAAGGTGACCGGCTCACTCTCTTCAGC
TAAGCGCAAGGAGCCAGAACCCAAGGGATCCACTAAGAAGAAGGCAAAGACTGGGGCAGCAGGGAAGTTTAAAG
GGGAAAATTAATGTGTTTCCCCATTATACCTCCTTCACCCCAAGATATTTGCCGTCTTGTACCCTTAAGAGCTAC
AGCTAGAGAAACCTTCACGGGGTGGAGAGAGGATTCTAAGGCTTTTCTAGCGTGACCCCTTTTCAGTAGTGCTAGT
CCCTTTTTTACTTGATCTTAATGGCAAGAAGGCCACAGAGGTACTTTTCCTTTTTTTAGCTCAGGAAAATATGTC
AGGCTCAAACCACTTCTCAGGCAGTTTAAATGG

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FIGURE 396

MGIQGLAKLIADVAPSAIRENDIKSYFGRKVAIDASMSIYQFLIAVRQGGDVLQNEEGETTSHLMGMFYRTIRMM
ENGIKPVYVFDGKPPQLKSGELAKRSERRAEAEKQLQQAQAAGAEQEVEKFTKRLVKVTKQHNDCKHLLSLMGI
PYLDAPSEAEASCAALVKAGKVYAAATEDMDCLTFGSPVLMRHLTASEAKKLP IQEFHLSRILQELGLNQE QFVD
LCILLGSDYCESIRGIGPKRAVDLIQKHKSIEEIVRRDPNKYPVPENWLHKEAHQLFLEPEVLD PESVELKWSE
PNEEELIKFMCGEKQFSEERIRSGVKRLSKSRQGSTQGRLLDFFKVTGSLSSAKRKEPEPKGSTKKKAKTGAAGK
FKRGK

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FIGURE 397

CCTAAGATGAGCTTTCCATGTAAATTTGTAGCCAGCTTCCTTCTGATTTTCAATGTTTCTTCCAAAGGTGCAGTC
TCCAAAGAGATTACGAATGCCTTGGAAACCTGGGGTGCCTTGGGTCAGGACATCAACTTGGACATTCCTAGTTTT
CAAATGAGTGATGATATTGACGATATAAAATGGGAAAAAACTTCAGACAAGAAAAAGATTGCACAATTCAGAAAA
GAGAAAGAGACTTTCAAGGAAAAAGATACATATAAGCTATTTAAAAATGGAACCTCTGAAAATTAAGCATCTGAAG
ACCGATGATCAGGATATCTACAAGGTATCAATATATGATACAAAAGGAAAAAAATGTGTTGGAAAAAATATTTGAT
TTGAAGATTCAAGAGAGGGTCTCAAAACCAAGATCTCCTGGACTTGTATCAACACAACCCCTGACCTGTGAGGTA
ATGAATGGAAC TGACCCCGAATTAAACCTGTATCAAGATGGGAAACATCTAAACCTTTCTCAGAGGGTCATCACA
CACAAGTGGACCACCAGCCTGAGTGCAAAATTCAAGTGCACAGCAGGGAACAAAGTCAGCAAGGAATCCAGTGTC
GAGCCTGTGAGCTGTCCAGAGAAAGGTCTGGACATCTATCTCATCATTGGCATATGTGGAGGAGGCAGCCTCTTG
ATGGTCTTTGTGGCACTGCTCGTTTTCTATATCACAAAAGGAAAAAACAGAGGAGTCGGAGAAATGATGAGGAG
CTGGAGACAAGAGCCACAGAGTAGCTACTGAAGAAAGGGGCGGGAAGCCCCAACAAATCCAGCTTCAACCCCT
CAGAATCCAGCAACTTCCCAACATCCTCCTCCACCACCTGGTCATCGTTCACAGGCACCTAGTCATCGTCCCCG
CCTCCTGGACACCGTGTTGAGCACCAGCCTCAGAAGAGGCCTCCTGCTCCGTCGGGCACACAAGTTCACCAGCAG
AAAGGCCCCGCCCTCCCCAGACCTCGAGTTCAGCCAAAACCTCCCCATGGGGCAGCAGAAAACCTATTGTCCCCT
TCCTCTAATTAAGATAGAACTGTCTTTTTCAATAAAAAGCACTGTGGATTCTGCCCTCCTGATGTGCAT
ATCCGTACTTCCATGAGGTGTTTTCTGTGTGCAGAACATTGTACCTCCTGAGGCTGTGGGCCACAGCCACCTCT
GCATCTTCGAACTCAGCCATGTGGTCAACATCTGGAGTTTTTGGTCTCCTCAGAGAGCTCCATCACACCAGTAAG
GAGAAGCAATATAAGTGTGATTGCAAGAATGGTAGAGGACCGAGCACAGAAATCTTAGAGATTTCTGTCCCCTC
TCAGGTGATGTGTAGATGCGATAAATCAAGTGATTGGTGTGCCTGGGTCTCACTACAAGCAGCCTATCTGCTTAA
GAGACTCTGGAGTTTCTTATGTGCCCTGGTGGACACTTGCCACCATCCTGTGAGTAAAAGTGAAATAAAAGCTT
TGAC

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FIGURE 398

MSFPCKFVASFLLIFNVSSKGAVSKEITNALETWGALGQDINLDIPSFQMSDDIDDIKWEKTSDDKKKIAQFRKEK
ETFEKEDTYKLFKNGTLKIKHLKTDDQDIYKVSIDYDTKGKNVLEKIFDLKIQERVSKPKISWTCINTTLTCEVMN
GTDPELNLYQDGKHLKLSQRVITHKWTTSLSAKFKCTAGNKVSKESSVEPVSCPEKGLDIYLIIGICGGGSLLMV
FVALLVFYITKRKKQRSRRNDEELETTRAHRVATEERGRKPQQIPASTPQNPA TSQHPPPPPGHRSQAPSHRPPPP
GHRVQHQPQKRPPAPSGTQVHQKGPFLPRPRVQPKPPHGAAENSLSPSSN

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FIGURE 399

CTGGTGTGAGCCACCACGCCCAGCTCAAAAACAATTTTTTTAGGGGCACTTCTACAAATCATGAAAGGGGGATAA
AAGCACTGACTTTAAAAAGCCATGTTTAAAGATGCTATAAATGTTCTCCCCCTTTTCATTGATTGGAGAGTTGTAGA
GGACCTTAGAGATCATTGTTGCTAACTCCCTCATCCCAAAGATAAACTGAGGCCTAGAGATCGTTCAGGGTGTG
TAACTGGGAACATCTGAATGCTGAGGCCTAGAGATCGTTCAGGGTGTGTAAGTGGGAACATCTGAATGCTGAGG
CCTAGAGATCGTTCAGGGTGTGTAAGTGGGAACATCTGAATGCTGAGGCCTAGAGATCGTTCAGGGTGTGTAA
CTGGGAACATCTGAATGCTGAGGCCTAGAGATCGTTCAGGGTGTGTAAGTGGGAACATCTGAATGCTGAGGCCT
AGAGATCGTTCAGGGTGTGTAAGTGGGAACATCTGAATGCTGAGGCCTAGAGATCGTTCAGGGTGTGTAAGT
GGAACATCTGAATGCTGAGGCCTAGTCCAGTGTCTCTCTCCCTTACCACTCCTCTTCCCCTTCCCTCTATAATG
GCAGTACCCAGGGCCCCGGTCCATAGACTACTATCGAGTGCTCCTATGTGCATCTTAGTACGTATCATTTTCCCTT
GCCTTTTTCTTCTATCCTTTCAGTGGTAGCAACTGCCCTTGCTAATCACCGTAACCTCGGCTGAGAAAGAAGAG
GAAGCGAAATCCAAGATGCAGCTCAGTTCATCAAAGCCTAGCAGGTCCCCTCAGCTGCCTTTTCATGCCTGCCAC
AGACTACAGTAGGACAAAACCTGACCTGGTCTTTGAAGTTAAGAGCTAAGAAAGCTTCCTATAGTAGTATCTCCC
ATGGCACTTACCACATTCTATCTGGTATTACAATTATTTGTATGCAATTAATCACTCTTAGATTGTATGTTCTG
GAGGGCAGAATATGCCCATTCATATTTGTATCTTCTTCTTCTGCTCTTGGCACCTAACACAGTGCCTTGCACAC
AAACAATAAATGATTGTTGAGTGAATAAGTAAACCTGATTGTGGTGTCTATTGCTTTTTTCAGCAAGAAGTCAAA
CTGATGGCCTTTAAGTCAGAGAAGCAGCAATGGAGCAAC

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FIGURE 400

GVSHHAQLKNNFFRGITSTNHERGIKALTLKSHV

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FIGURE 401

GGCGGCGACGGATCGAGCTCACCGCGCCGAGCGCGCCGGCACCGCCTGCACCGCCCTTCCGCCCCGCCCTCCGGAC
GGCCGCAGCCTGCGGTCTCCGTCCAGACCCACCCCGCCCCACCCCGCGCCCTCTGCCGCTCTTCCAGAGACC
CAGCTTGCCGAGCGGCCCGCGCTGCCGTGTGCGCGCCGCGCCGCCACCGCGCCAGGTTCCGGCCGCGGCCACCC
TCCGCCGTCCAGGGCCTCTCCGTCTCGGCCCCGGGACCCCGCCTCCCCGCCAGCCCCGGCCCCGGCCCCGGCACC
ATGTCGGAGAAAAGCGTGGAGGCAGCGCCGAGTTGAGCGCCAAGGACCTGAAGGAGAAGAAGGAGAAGGTGGAG
GAGAAGGCAAGCCGAAAGAGCGAAAGAAAGAAGTGGTGGAGGAGGAGGAGAACGGGGCTGAGGAGGAAGAAGAA
GAAACTGCCGAGGATGGAGAGGAGGAAGATGAAGGGGAAGAAGAAGATGAGGAAGAAGAAGAAGAGGATGATGAA
GGGCCCCGCGCTGAAGAGAGCTGCCGAAGAGGAGGATGAAGCGGATCCCAAACGGCAGAAGACAGAAAATGGGGCA
TCGGCG**TGA**CGCCTGCCAACAGGCTGGGTTGGGAGGCCTCTCTGGGCTGGAGGTGGGGGTGGGGGCAGCCAAGTC
CAGCCACTCTTACCTGGCTCCCTGCTCTGGGCCC TGACCGAGAGCTGCCACCCTCTTCTTTCTCCCCAGCCTT
CTCATTTCCGCCTCTCCAGACACTGCGCCCTCCACCCTCACTCTGCCATTGTTCCACCTCCTGACCTGCTCCATC
TGAGCTCTCCAGCTGGCCCCCAATTGCTCCTCTCTCTCTTTGCTCTCTTTCTCCCTCCCTACCAGCCTCATTCT
TCTCCGGTAGCCTCTCCACCTAACCTCTGCATCCCCAGCGTCAIGTCCTGCCCCATCCCTATCCTGCCTGATC
CCTGGATCTCCCTCAGATCCCTCTTCTCAGACAGCGCCAGGCCGGGGTGGGGCCGGGGTTGCCGAGCCCCACAG
CTGCCCCCTCCCTCCCTTTTGTATAATTTAATAAAGAAATGGTCGCGCTTCIGTTT

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FIGURE 402

MSEKSVEAAAELSAKDLKEKKEKVEEKASRKERKKEVVEEEEENGAEETAEDEGEDEDEDEDEDEDEDE
GPALKRAAEEDEADPKRQKTENGASA

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FIGURE 403

GGCACGAGGGGGAAGGCAAGATGGCGGCGCCCATGGAGGTGGCCGTGTGTACGGACTCGGCGGCCCCGATGTGGA
GCTGCATCGTGTGGGAACCTTCACTCGGGCGCCAACCTGCTCACCTACCGCGGCGGCCAGGCGGGACCCCGCGGCC
TGGCGCTGCTCAATGGCGAGTATCTGCTGGCGGCGCAGCTGGGCAAGAACTACATCAGCGCCTGGGAGCTGCAGC
GGAAGGACCAGCTCCAGCAGAAGATCATGTGCCCCGGGCCTGTACCTGTCTGACTGCATCACCCAATGGTCTCT
ACGTCCTGGCAGGAGTTGCAGAAAGCATCCACCTGTGGGAGGTCTCCACCGGGAACCTTCTGGTCATCCTGAGTC
GACACTACCAGGACGTCTCCTGCCTTCAGTTCACAGGGGACAGCAGCCACTTCATCTCAGGGGGCAAGGACTGCC
TGGTGCTGGTTTGGAGCCTCTGCAGCGTGCTGCAGGCCGACCCCTCCAGGATTCCGGCGCCCAGGCACGTCTGGT
CTCACCACACGCTCCCCATCACGGACCTGCACTGCGGCTTTGGGGGCCCCCTGGCCCCGGGTGGCCACCTCCTCAC
TGGACCAGACGGTGAAGCTATGGGAGGTCTCCTCGGGGGAGCTGCTGCTCTCCGTCTCTTTGACGTGTCCATCA
TGGCAGTGACCATGGACCTGGCTGAGCACCATATGTTCTGCGGGGGCAGTGAGGGCTCCATCTTCCAGGTGACCC
TCTTCACTGGCCCCGACAGAGGGAGAGGAGCTTCACCCAGAGCAGGACGCCGGGAAGGTCTTCAAAGGGCACA
GGAACCAGGTGACTTGCTGTGAGTGTCCACTGACGGCAGCGTGCTGCTCTCAGGCTCCACGACGAGACCGTGC
GCCTCTGGGACGTGCAGAGCAAGCAGTGATCCGGACGGTGGCCCTCAAAGGCCCAGTCACCAATGCCGCCATCC
TGCTGGCGCCCCGTGAGCATGCTGAGCTCAGACTTCAGGCCCAGCCTGCCGCTGCCCCACTTCAACAAGCACCTGC
TGGGCGCCGAGCACGGGGACGAGCCGCGCCACGGGGGCTCACTCTGCGCCTGGGCCTCCACCAGCAGGGCTCGG
AGCCCAGCTACCTGGACCGCACGGAGCAGCTGCAGGCCGTCTGTGTCAGCACCATGGAGAAGAGCGTGCTCGGCG
GCCAGGACCAGCTGCGCGTCCGTGTGACGGAGCTGAGGACGAGGTGCGCAACCTGCGCAAGATCAATCGGGACC
TGTTGACTTCTCCACGCGCTTCATCACGCGCCGSCCAAGTTGAGGCCCGGAGACCCCGGCCCCGAGGCGCCCAGG
CCTGAGCCCCATGCCTCCAGCAACCAGGGCCCGCGGGTGTGGCCCCACCAGCCAGGCCTGGACTCTCCTCAG
TTCTGTGTCGTGTTTCGGGTTTTTCTCTGTGACTGGGCCGTCTTGGTGTCTCGTGGCACGCGTCACAGTGGTGCT
AGTCTGTTTTTAACAAAAGAGGATGAAAAGCCAAAAAAAAAAAAAAAAAAAA

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FIGURE 404

HEGEGKMAAPMEVAVCTDSAAPMWSCIVWELHSGANLLTYRGGQAGPRGLALLNGEYLLAAQLGKNYISAWELQR
KDQLQQKIMCPGPVTCLTASPNGLYVLAVAGVAESIHLWEVSTGNLLVILSRHYQDVSCLOFTGDSSHFISGGKDCL
VLVWSLCSVLQADPSRIPAPRHVWSHHTLPITDLHCGFGGPLARVATSSLDQTVKLWEVSSGELLLSVLF'DVSIM
AVTMDLAEHHMFCCGSEGSIFQVDLFTWPGQRRERSFHPEQDAGKVFKGHRNQVTCLSVSTDGSVLLSGSHDETNR
LWDVQSKQCIRTVALKGPVTNAAILLAPVSMSSDFRPSLPLPHFNKHLGAEHGDEPRHGGLTLRLGLHQQGSE
PSYLDRTQLQAVLCSTMEKSVLGGQDQLRVRVTELEDEVNLRKINRDLDFSTRFITRPAK

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FIGURE 405A

ATGCTGGGGAAGAGCCATGGTAGGACCACTCATGGCCCTCTTCCTTTGGCGGACCTTGGAATCCACCTTCCCTGC
 GTTAAAGTGCTCCACCAGGTGACGCCGGAAGAGAAGCCAGCAGGCGGCGGCGGCGTCAGCATCAGCGGCCTCCTG
 CCCGTATCTATCGTGGCGGCGACGGGACCCGCCCTCCCTGGGCGCCGGAGTCATGTGACCCACACAATGGCTGAGT
 GGCTACTCTCGGCTTCCTGGCAACGCCGAGCGAAAGCTATGACTGCGGCCGCGGGTTCGGCGGGCCGCGCCGCGG
 TGCCCTTGCTGCTGTGTGCGCTGCTGGCGCCCGGCGGCGGTACGTGCTCGACGACTCCGACGGCTGGGCGGGG
 AGTTCGACGGCATCGGCGCGGTGACGGCGGCGGGCAACCTCCCGACTTCTAGTAAATTACCCAGAGCCCTATC
 GTTCTCAGATATTGGATTATCTCTTTAAGCCGAATTTGGTGCCTCTTTGCATATTTTAAAAGTGGAATAGGTG
 GTGATGGGCAGACAACAGACGGCACTGAGCCCTCCACATGCATTATGACTAGATGAGAATTATTTCCGAGGAT
 ACGAGTGGTGGTTGATGAAAGAAGCTAAGAAGAGGAATCCCAATATTACACTCATTGGGTTGCCATGGTCATTCC
 CTGGATGGCTGGGAAAAGGTTTCGACTGGCCTTATGTCAATCTTCAGCTGACTGCCTATTATGTCGTGACCTGGA
 TTGTGGGCGCCAAGCGTTACCATGATTGGACATTGATTATATTGGAATTTGGAATGAGAGGTCATATAATGCCA
 ATTATATTAAGATATTAAGAAAAATGCTGAATTATCAAGGCTCTCCAGCGAGTGAAAATCATAGCAAGTGATAATC
 TCTGGGAGTCCATCTCTGCATCCATGCTCCTTGATGCCGAACCTCTTCAAGGTGGTTGATGTTATAGGGGCTCATT
 ATCCTGGAACCCATTTCAGCAAAAGATGCAAGTTGACTGGGAAGAAGCTTTGGTCTTCTGAAGACTTTAGCACTT
 TAAATAGTGACATGGGTGCAGGCTGCTGGGGTCGCATTTTAAATCAGAATTATATCAATGGCTATATGACTTCCA
 CAATCGCATGGAATTTAGTGGCTAGTTACTATGAACAGTTGCCTTATGGGAGATGCGGGTTGATGACGGCCCAAG
 AGCCATGGAGTGGGCACTACGTGGTAGAATCTCCTGTCTGGGTATCAGCTCATACCACTCAGTTTACTCAACCTG
 GCTGGTATTACCTGAAGACAGTTGGCCATTTAGAGAAAGGAGGAAGCTACGTAGCTCTGACTGATGGCTTAGGGA
 ACCTCACCATCATCATTGAAACCATGAGTCATAAACATTCTAAGTGCATACGGCCATTCTTCCTTATTTCAATG
 TGTCACAACAATTTGCCACCTTTGTTCTTAAGGGATCTTTTAGTGAAATACCAGAGCTACAGGTATGGTATACCA
 AACTTGGA AAAACATCCGAAAGATTCTTTTTAAGCAGCTGGATTCTCTATGGCTCCTTGACAGCGATGGCAGTT
 TCACACTGAGCCTGCATGAAGATGAGCTGTTCAACTCACCCTCTCACCCTGGTCGCAAGGCAGCTACCCGC
 TTCTTCCAAAATCCCAGCCCTTCCCAAGTACCTATAAGGATGATTTCAATGTTGATTACCCATTTTTTAGTGAAG
 CTCCAAACTTTGCTGATCAAACCTGGTGATTTTGAATATTTTACAAATATTGAAGACCTGGCGAGCATCACTTCA
 CGCTACGCCAAGTTCTCAACCAGAGACCCATTACGTGGGCTGCCGATGCATCCAACACAATCAGTATTATAGGAG
 ACTACAACCTGGACCAATCTGACTATAAAGTGTGATGTTTACATAGAGACCCCTGACACAGGAGGTGTGTTTATTG
 CAGGAAGAGTAAATAAAGGTGGTATTTGATTAGAAGTGCCAGAGGAATTTTCTTCTGGATTTTTCGAAATGGAT
 CTTACAGGGTTACAGGTGATTTAGCTGGATGGATTATATATGCTTTAGGACGTGTTGAAGTTACAGCAAAAAAT
 GGTATACACTCACGTTAACCTATTAAGGGTCATTTGCCTCTGGCATGCTGAATGACAAGTCTCTGTGGACAGACA
 TCCCTGTGAATTTTCCAAAGAATGGCTGGGCTGCAATTGGAACCTCACTCCTTTGAATTTGCACAGTTTGCACACT
 TTCTTGTGGAAGCCACACGCTAATACTTAACAGGGCATCATAGAATACTCTGGATTTTCTTCCCTTCTTTTTGGT
 TTTGGTTACAGAGCCAATTCTTGTTCATTGGAACAGTATATGAGGCTTTTGAGACTAAAAATAATGAAGAGTAAA
 AGGGGAGAGAAATTTATTTTTAATTTACCCTGTGGAAGATTTTATTAGAATTAATTCCAAGGGGAAAACTGGTGA
 ATCTTTAACATTACCTGGTGTGTTCCCTAACATTCAAACCTGTGCATTGGCCATACCCTTAGGAGTGGTTTTAGTA
 GTACAGACCTCGAAGCCTTGCTGCTAACACTGAGGTAGCTCTCTTCATCTTATTGCAAGCGGCTCTGTAGATGG
 CAGTAACTTGATCATCACTGAGATGTATTTATGCA TGCTGACCGTGTGTCCAAGTGAGCCAGTGCTCTTCATCACA
 AGATGATGCTGCCATAATAGAAAGCTGAAGAACAC TAGAAGTAGCTTTTTGAAAACCACTTCAACCTGTTATGCT
 TTATGCTCTAAAAAGTATTTTTTATTTTCTTTTTTAAGATGATACTTTTGAAATGCAGGATATGATGAGTGGGA
 TGATTTTAAAAACGCCTCTTTAATAAACTACCTCTAACACTATTTCTGCGGTAATAGATATTAGCAGATTAATTG
 GGTATTTGCAATTATTTAATTTTTTGATTCCAAGTTTGGTCTTGTAACCACTATAACTCTCTGTGAACGTTTT
 TCCAGGTGGCTGGAAGAAGGAAGAAAACCTGATATAGCCAATGCTGTTGTAGTCGTTTCTCAGCCTCATCTCAC
 TGTGCTGTGGTCTGTCTCACATGTGCACTGGTAA CAGACTCACACAGCTGATGAATGCTTTTCTCTCCTTATGT
 GTGGAAGGAGGGGAGCACTTAGACATTTGCTAACTCCCAGAATTGGATCATCTCCTAAGATGTACTTACTTTTTTA
 AAGTCCAAATATGTTTATATTTAAATATACGTGAGCATGTTTCATCATGTTGTATGATTTATACTAAGCATTAAATG
 TGGCTCTATGTAGCAAAATCAGTTATTCATGTAGGTAAAGTAAATCTAGAATTATTTATAAGAATTACTCATTGAA
 CTAATCTACTATTTAGGAATTTATAAGAGTCTAACATAGGCTTAGCTACAGTGAAGTTTGCATTGCTTTTGAA
 GACAAGAAAAGTGCTAGAAATAAATAAGATTACAGAGAAAATTTTTGTTAAAACCAAGTGATTTCCAGCTGATGT
 ATCTAATATTTTTTAAAACAAACATTATAGAGGTGTAATTTATTTACAATAAAATGTTCTACTTTAAATATACA

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FIGURE 405B

ATTCAGTGAGTTTTGATAAATTGATATACCCATGTAACCAACACTCCAGTCAAGCTTCAGAATATTTCCATCACC
CCAGAAGGTTTCTTTGTATACCTGCTCAGTCAGTTCCTTTCACTCCCAATTGTTGGCAGCCATTGATAGGAATTC
TATCACTATAGGTTAGTTTTCTTTGTTCCAGAACATCATGAAAGCGGCGTCATGTACTGTGTATTCTTATGAATG
GTTTCTTTCCATCAGCATAATGATTTGAGATTGGTCCATGTTGTGTGATTCAGTGGTTTGTTCCCTTCTTATTTCT
GAAGAGTTTTCCATTGTATGAATATACCACAATTTGTTTCCTCCCCACCAGTTTCTGATACTACAATTAAACTG
TCTACATTTAC

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FIGURE 406

MTAAAGSAGRAAVPLLLCALLAPGGAYVLDDSDGLGREFDGIGAVSGGGATSRLLVNYPEPYRSQILDYLFKPNF
GASLHILKVEIGGDGQTTDGTEPSHMHYALDENYFRGYEWWMKEAKRNPNTLIGLPWSFPGWLKGFDWPYV
NLQLTAYYVVTWIVGAKRYHDLDDIDYIGIWNERSYNANYIKILRKMLNYQGLQRVKIIASDNLWESISASMLLDA
ELFKVVDVIGAHYPGTHSAKDAKLTGKKLWSSEDFSTLNSDMGAGCWGRILNQNYINGYMTSTIAWNLVASYEQ
LPYGRCLMTAQEPWSGHYVVEPVVWSAHTTQFTQPGWYYLKTIVGHLEKGGSYVALTDGLGNLTII IETMSHKH
SKCIRPFLPYFNVSQQFATFVLKGSFSEIPELQVWYTKLGKTSEFLFKQLDSLWLLSDSGSFTLSLHEDELFTL
TTLTTGRKGSYPLPPKSQFPSTYKDDFNVDYPFFSEAPNFADQTGVFEYFTNIEDPGEHHFTLRQVLNQRPIW
AADASNTISIIGDYNWTNLTIKCDVYIETPDITGGVFIAGRVKNKGILIRSARGIFFWIFANGSYRVTDLAGWII
YALGRVEVTAKKWTTLTLTIKGFASGMLNDKSLWTDIPVNFKNGWAAIGTHSFEFAQFDNFLVEATR

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FIGURE 407

ACGAACAGGCCAATAAGGAGGGAGCAGTGCGGGGTTTAAATCTGAGGCTAGGCTGGCTCTTCTCGGCGTGCTGCG
GCGGAACGGCTGTTGGTTTTCTGCTGCTGTTGTAGGTCCTTGGCTGGTCGGGCCTCCGGTGTTCTGCTTCTCCCCGCT
GAGCTGCTGCCTGGTGAAGAGGAAGCCATGSCGCTCCGAGTCACCAGGAACTCGAAAATTAATGCTGAAAATAAG
GCGAAGATCAACATGGCAGGCGCAAAGCGCGTTCTACGGCCCCCTGCTGCAACCTCCAAGCCCGGACTGAGGCCA
AGAACAGCTCTTGGGGACATTGGTAACAAAGTCAGTGAACAACTGCAGGCCAAAATGCCTATGAAGAAGGAAGCA
AAACCTTCAGCTACTGGAAAAGTCATTGATAAAAACTACCAAAACCTCTTGAAAAGGTACCTATGCTGGTGCCA
GTGCCAGTGTCTGAGCCAGTGCCAGAGCCAGAACCTGAGCCAGAACCTGAGCCTGTTAAAGAAGAAAACTTTTCG
CCTGAGCCTATTTTGGTTGATACTGCCTCTCCAAGCCCAATGGAAACATCTGGATGTGCCCTGCAGAAGAAGAC
CTGTGTCAGGCTTTTCTCTGATGTAATTCTTGCACTAAATGATGTGGATGCAGAAGATGGAGCTGATCCAAACCTT
TGTAAGTGAATATGTGAAAGATATTTATGCTTATCTGAGACAACCTTGAGGAAGAGCAAGCAGTCAGACCAAAATAC
CTACTGGGTCGGGAAGTCACTGGAAACATGAGAGCCATCCTAATTGACTGGCTAGTACAGGTTCAAATGAAATTC
AGGTTGTTGCAGGAGACCATGTACATGACTGTCTCCATTATTGATCGGTTTCATGCAGAATAATTGTGTGCCCAAG
AAGATGCTGCAGCTGGTTGGTGTCACTGCCATGTTTATTGCAAGCAAATATGAAGAAATGTACCCTCCAGAAATT
GGTGACTTTGCTTTTGTGACTGACAACACTTATACTAAGCACCAAATCAGACAGATGGAAATGAAGATTCTAAGA
GCTTTAAACTTTGGTCTGGGTCGGCCTCTACCTTTGCACTTCCTTCGGAGAGCATCTAAGATTGGAGAGGTTGAT
GTCGAGCAACATACTTTGGCCAAATACCTGATGGAACAACTATGTTGGACTATGACATGGTGCACTTTCTCTCT
TCTCAAATTGCAGCAGGAGCTTTTGTGCTTAGCACTGAAAATTCTGGATAATGGTGAATGGACACCAACTCTACAA
CATTACCTGTCATATACTGAAGAATCTCTTCTCCAGTTATGCAGCACCTGGCTAAGAATGTAGTCATGGTAAAT
CAAGGACTTACAAAGCACATGACTGTCAAGAACAAGTATGCCACATCGAAGCATGCTAAGATCAGCACTCTACCA
CAGCTGAATTCTGCACTAGTTCAAGATTTAGCCAAGGCTGTGGCAAAGGTGTAACTTGTAACCTTGAGTTGGAGT
ACTATATTTACAAATAAAATTGGCACCATGTGCCATCTGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

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FIGURE 408

MALRVTRNSKINAENKAKINMAGAKRVPTAPAATSKPGLRPRTALGDIGNKVSEQLQAKMPMKKEAKPSATGKVI
DKKLPKPLEKVPMLVPVPVSEPVPEPEPEPEPEPVKEEKLSPPEILVDTASPSMETSGCAPAEEDLCQAFSDVI
LAVNDVDAEDGADPNLCSEYVKDIYAYLRQLEEEQAVRPKYLLGREVTGNMRAILIDWLQVQMKFRLLQETMYM
TVSIIDRFMQNNCVPKKMLQLVGVTAMFIASKYEEMYPPEIGDFAFVTDNTYTKHQIRQMEMKILRALNFGGLGRP
LPLHFLRRASKIGEVDVEQHTLAKYLMELTMDYDMVHFPPSQIAAGAFCLALKILDNGEWTPTLQHYLSYTEES
LLPVMQHLAKNVVMVNQGLTKHMTVKNKYATSKHAKISTLPQLNSALVQDLAKAVAKV

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FIGURE 409

AGAGAGCTGTTTACTAGGCACGACTGCGAAGGCAAGGGGGCACCAGCTCAGGACTGCATCTGCCTGCCATTTCCC
TTCCACTCCTCCTTTCTGGAGTCTGACATTAGAAAAGCCAGCGAGAAGGAAGATTCAAACAACCAACCCTGATTTCC
CTGCTTCTCCTTTTTCATGAGTGTTCCTGTGGTCTCTGCACCTCCTTTCTGTCCCCCGGCAGAGGGCAGTAGAGAT
GGCCGGCCCAAGGCCTCGGTGGCGCGACCAGCTGCTGTTTCATGAGCATCATAGTCCTCGTGATTGTGGTCACTG
CCTGATGTTATACGCTCTTCTCTGGGAGGCTGGCAACCTCACTGACCTGCCCCAACCTGAGAATCGGCTTCTATAA
CTTCTGCCTGTGGAATGAGGACACCAGCACCTACAGTGTACCCAGTTCCTGAGCTGGAAGCCCTGGGGGTGCC
TCGGGTGGCCTGGGCCTGGCCAGGCTTGGCGTGTACGGGTCCCTGGTCCCTACCCCTCTTTGCCCCCAGCCTCT
CCTCCTAGCCCAGTGCAACAGTGATGAGAGAGCGTGGCGGCTGGCAGTGGGCTTCTGGCTGTGTCTCTGTGCT
GCTGGCAGGCGGCCTGGGCCTCTTCCTCTCCTATGTGTGGAAGTGGGTCAGGCTCTCCCTCCCGGGGCTGGGTT
TCTAGCTCTGGGCAGCGCCAGGCCCTTACTCATCTCTTGCTTATAGCCATGGCTGTGTTCCCTCTGAGGGCTGA
GAGGGCTGAGAGCAAGCTTGAGAGCTGCTTAAAGGCTTACGTGATTGCAAGGGTTCAATTCCAACCATAGTCAGAG
GTGGCACATCTGCTCAGCCATCTCATTTTACAGCTAACGCTGATCTCCAGCTCCAGCGATGGAACCCACTACAGA
GGAGGTGGGGCCCTGTGTCAAAGAGGCGAGGGGAGCAAGGGCAGCCAGGGCACCTGTGACTTCTTAGTACAA
GATTGTCTGTCTTCAGGACTTCCAAGGCTCCCAAAGACTCCCTAAACCATGCAGCTCATTGTACACCAATTCC
TGCTTTAATTAATGGATCTGAGCAAATCTTCCTCTAGCTTCAGGAGGGTGGGGAGGGAGTGATTGCCGTATGGG
GCCAGACTTCCAGGCTGATTTGCCAAATGCCAAATGAAACCTAGCAAAGAACTTACGGCAACAAACGAGGACAT
TAAAAGAGCGAGCACCTCAGTGTCTCTGGGGACATGGTTAAGGAGCTTCCACTCAGCCCACCATAGTGAGTGGGC
CGCCATAAGCCATCACTGGAATCCAACCCAGAGGTCCAGGAGTGATCTCTGAGTGACTCAACAAAGACAGGAC
ACATGGGGTACAAAGACAAGGCTTGACTGCTTCAAAGCTTCCCTGGACCTGAAGCCAGACAGGGCAGAGGCGTCC
GCTGACAAATCACTCCCATGATGAGACCTGGAGGACTCCAAATCCTCGCTGTGAACAGGACTGGACGGTTGCCG
ACAAACAAACGCTGCCACCTCCACTTCCCAACCCAGAACTTGGAAAGACATTAGCACAACCTTACGCATTGGGGA
ATTGTGTGATTTTCTAGCACTTGTGTATTGGAACCTGTATGGCAGTGATTATTTCATATATTCTGTCCAAA
GCCCACTGAAAACAGAGGCAGAGACATGT

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FIGURE 410

MAGPRPRWRDQLLFMSIIVLVIVVICLMLYALLWEAGNLTDLPNLRIGFYNFCLWNEDTSTLQCHQFPELEALGV
PRVGLGLARLGVGSLVLTTFAPQPLLLAQCNSEDAWRLAVGFLAVSSVLLAGGLGLFLSYVWKVRLSLPGPG
FLALGSAQALLILLLIAMAVFPLRAERAESKLESC

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FIGURE 411

CTGGTCCCGAGCACGAGCTGTGAGGGGATTCACTTGTGTGCGGAACCTCCTCGGAACCATGGCGTCCCTTTCCCTT
GCACCTGTAAACATCTTTAAGGCAGGAGCTGATGAAGAGAGAGCAGAGACAGCTCGTCTGACTTCTTTTATTGGT
GCCATCGCCATTGGAGACTTGGTAAAGAGCACCTTGGGACCCAAAGGCATGGACAAAATTCTTCTAAGCAGTGGA
CGAGATGCCCTCTCTTATGGTAACCAATGATGGTGCCACTATTCTAAAAACATTGGTGTGACAATCCAGCAGCT
AAAGTTTTAGTTGATATGTCAAGGGTTCAAGATGATGAAGTTGGTGTGCGCACTACCTCTGTTACCGTTTTAGCA
GCAGAATTATTAAGGGAAGCAGAATCTTTAATTGCAAAAAAGATTCTCCACAGACCATCATAGCGGGTTGGAGA
GAAGCCACGAAGGCTGCAAGAGAGGCGCTGTTGAGTTCTGCGAGTTGATCATGGTTCCGATGAAGTTAAATTCCGT
CAAGATTTAATGAATATTGCGGGCACAACATTATCCTCAAACTTCTTACTCATCACAAAGACCACTTTACAAAG
TTAGCTGTAGAAGCAGTTCTCAGACTGAAAGGCTCTGGCAACCTGGAGGCAATTCATATTATCAAGAAGCTAGGA
GGAAGTTTGGCAGATTCTATTTAGATGAAGGCTTCTGTTGGATAAAAAAATTGGAGTAAATCAACCAAAACGA
ATTGAAAATGCTAAATTTCTTATTGCAAATACTGGTATGGATACAGACAAAATAAGATATTTGGTTCCCGGGTA
AGAGTTGACTCTACAGCAAAGGTTGCAGAAATAGAACATGCGGAAAAGGAAAAAATGAAGGAGAAAGTTGAACGT
ATTCTTAAGCATGGAATAAATTGCTTTATTAAACAGGCAATTAATTTATAATTATCCTGAACAGCTCTTTGGTGCT
GCTGGTGTGATGGCTATTGAGCATGCAGATTTTGAGGTGTGGAACGCCTAGCTCTGTGCACAGGTGGTGAAATT
GCCCTACCTTTGATCACCCAGAACTGGTGAAGCTTGGAAGTTGCAAACTTATCGAGGAAGTCATGATTGGAGAA
GACAAACTCATTCACTTTTCTGGGGTTGCCCTTGGTGAGGCTTGTACCATTGTTTTGCGTGGTGCCACTCAACAA
ATTTTAGATGAAGCAGAAAGATCATTGCATGATGCTCTTTGTGTTCTTGCGCAAACTGTAAAGGACTCTAGAACA
GTTTATGGAGGAGGCTGTTCTGAGATGTTGATGGCTCATGCTGTGACACAGCTTGCCAATAGAACACCAGGCAAA
GAAGCTGTTGCAATGGAGTCTTATGCTAAAGCACTGAGAATGTTGCCAACCATCATAGCTGACAATGCAGGCTAT
GACAGTGACAGACCTGGTGGCACAGCTCAGGGCTGCTCACAGTGAAGGCAATACCACTGCTGGATTGGATATGAGG
GAAGGCACCATTGGAGATATGGCTATCCTGGGTATAACAGAAAGTTTTCAAGTGAAGCGACAGGTTCTTCTGAGT
GCAGCTGAAGCAGCAGAGGTGATTCTGCGTGTGGACAACATCATCAAAGCGGCACCCAGGAAACGTGTCCCTGAT
CACCACCCCTGTTAAGCATTCCCACGTGCTGTGATCTTTGGACCAAGTTTCTAGCAAAGTTGTGTTTGAAAGATA
CTCTATTAAAGAAGACTGTGGAATCTGTTTATCGGTGCCCATATATCCTTAAGTTTGGATATTTAGCTGACCTT
CGCTTTAACATAGGTCTAATTTATTTGCCGTGTCATTTCCATACAAATCAGTTGATTTAAAGGAGTTCAATTCG
CATACTGGGCATTAAATAAAAAATTTGAACAATGAAAGGAAAAAAGGAGAAAAA

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FIGURE 412

MASLSLAPVNIFKAGADEERAETARLTSFIGAIAIGDLVKSTLGPKGMDKILLSSGRDASLMVTNDGATILKNIG
VDNPAAKVLVDMRSRVQDDEVGDGTTSTVTLAAELLREAESLIAKKIHPQTIIAGWREATKAAREALLSSAVDHGS
DEVKFRQDLMNIA GTTLSSKLLTHHKDHFTKLAVEAVLRLKSGNLEAIHIIKKLGGS LADSYLDEGFLLDKKIG
VNQPKRIENAKILIAN TGMDTDKIKIFGSRVRVDSTAKVAEIEHAEKEKMKEKVERILKHGINCFINRQLIYNYP
EQLFGAAGVMAIEHADFA GVERLALVTGGEIASTFDHPELVKLG SCKLIEEVMIGEDKLIHFSGVALGEACTIVL
RGATQQILDEAERSLHDALCVLAQTVKDSRTVYGGGCSEMLMAHAVTQLANRTPGKEAVAMESYAKALRMLPTII
ADNAGYDSADLVAQLRAAHSEGNTTAGLDMREGTIGDMAILGITESFQVKRQVLLSAAEAAEVILRVDNIIKAAP
RKRVPDHHPC

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FIGURE 413

CGGCTTCTCCCGCTTTTTCTTCTCTCTCCTTGCGGTCTGAAGATGCCCTCGGCCACCAGCCACAGCGGGAGCGC
AGCAAGTCGTCGGGACCGCCACCGCGCTCGGGTTCTCTCGGGAGTGAGGCGGCCGCGGGAGCCGGGGCCCGCG
CCGGCTTCTCAGCACCCCGCAACCGGCACCGGCGCTGTCCAGACCGAGGCCATGAAGCAGATTCTCGGGGTGATC
GACAAGAACTTCGGAACCTGGAGAAGAAAAAGGGTAAGCTTGATGATTACCAGGAACGAATGAACAAAGGGGAA
AGGCTTAATCAAGATCAGCTGGATGCCGTTTCTAAGTACCAGGAAGTCACAAATAATTTGGAGTTTGCAAAGAA
TTACAGAGGAGTTTCATGGCACTAAGTCAAGATATTAGAAAACAATAAAGAAGACAGCACGTCGGGAGCAGCTT
ATGAGAGAAGAAGCTGAACAGAAACGTTTAAAACTGTACTTGAGCTACAGTATGTTTTGGACAAATTGGGAGAT
GATGAAGTGGGACTGACCTGAAACAAGGTTTGAATGGAGTGCCAATATTGTCCGAAGAGGAGTTGTCATTGTTG
GATGAATTCTATAAGCTAGTAGACCCTGAACGGGACATGAGCTTGAGGTTGAATGAACAGTATGAACATGCCTCC
ATTCACCTGTGGGACCTGCTGGAAGGGAAGGAAAAACCTGTATGTGGAACCACTATAAAGTTCTAAAGGAAATT
GTTGAGCGTGTTTTTCACTCAAACTACTTTGACAGCACCCACAACCACCAGAATGGGCTGTGTGAGGAAGAAGAG
GCAGACTCAGCACCTGCAGTTGAAGACCAGGTACCTGAAGCTGAACCTGAGCCAGCAGAAGAGTACACTGAGCAA
AGTGAAGTTGAATCAACAGAGTATGTAATAGACAGTTTCATGGCAGAAACACAGTTCACCAGTGGTGAAAAGGAG
CAGGTAGATGAGTGGACAGTTGAAACGGTTGAGGTGGTAAATTCCTCCAGCAGCAACCTCAGGCTGCATCCCCCT
TCAGTACCAGAGCCCCACTCTTTGACTCCAGTGGCTCAGGCAGATCCCCCTTGAGAAGACAGCGAGTACAAGAC
CTTATGGCACAATGCAGGGTCCCATAATTTACATACAGGATTCAATGCTGGATTTGAAAATCAGACACTTGAT
CCTGCCATTGTATCTGCACAGCCTATGAATCCAACACAAAACATGGACATGCCCCAGCTGGTTTGCCCTCCAGTT
CATTCTGAATCTAGACTTGCTCAGCCTAATCAAGTTCCCTGTACAACAGAAAGCGACACAGGTTCCCTTGGTATCA
TCCACAAGTGAGGGGTACACAGCATCTCAACCCCTGTACCAGCCTTCTCATGCTACAGAGCAACGACCACAGAAG
GAACCAATTGATCAGATTCAGGCAACAATCTCTTTAAATACAGACCAGACTACAGCATCATCATCCCTTCTGCT
GCGTCTCAGCCTCAAGTATTTCAAGCTGGGACAAGCAAACCTTTACATAGCAGTGGAAATCAATGTAAATGCAGCT
CCATTCCAATCCATGCAAACGGTGTTCAATATGAATGCCCCAGTTCCCTGTTAATGAACCAGAACTTTAAAA
CAGCAAAATCAGTACCAGGCCAGTTATAACCAGAGCTTTTCTAGTCAGCCTCACCAAGTAGAACAACAGAGCTT
CAGCAAGAACAGCTTCAAACAGTGGTTGGCACTTACCATGGTTCCCCAGACCAGTCCCATCAAGTGACTGGTAAC
CACCAGCAGCCTCCTCAGCAGAACTGGAATTTCCACGTAGCAATCAGCCCTATTACAATAGTCGTGGTGTGTCT
CGTGGAGGCTCCCGTGGTGCTAGAGGCTTGATGAATGGATACCGGGGCCCTGCAATGGATTACAGAGGAGGATATG
ATGGTTACCGCCCTTCATTCTTAACACTCCAAACAGTGGTTATACACAGTCTCAGTTCAAGTGTCCCCGGGATT
ACTCTGGCTATCAACGGGATGGATATCAGCAGAATTTCAAGCGAGGCTCTGGGCAGAGTGGACCACGGGGAGCCC
CAGGAGGTGCTGGAGGGCCCCCAAGACCCCAACAGAGGGATGCCGCAATGAAACTCAGCAAGTGAATTAATCTG
ATTCACAGGATTATGTTTAATCGCCAAAAACACACTGGCCAGTGTACCATAATATGTTACCAGAAGAGTTATTAT
CTATTTGTTCTCCCTTTTCAAGAACTTATTGTAAAGGGACTGTTTTCATCCATAAAGACAGGACTACAATTGTC
AGCTTTCTATTACCTGGATATGGAAGGAACTATTTTACTCTGCATGTTCTGTCTTAAGCGTCATCTTGAGCCT
TGCACATGATACTCAGATTCTCACCCTTGCTTAGGAGTAAACAATATACTTTACAGGGTGATAATAATCTCCA
TAGTTATTTGAAGTGGCTTGAAAAAGCAAGATTGACTTTTATGACATTGGATAAAATCTACAAATCAGCCCTCG
AGTTATTCATGATAACTGACAACTAAATTATTTCCCTAGAAAGGAAGATGAAAGGAGTGGAGTGTGGTTTGGC
CAGAACAACATGATTTTACAGCTTTTCCAGTTAAATTGGAGCACTGAACGTTTCAGATGCATACCAATATGCTAT
GGGTCTTAATCACACATATAAGGCTGGCTACCAGCTTTGACACAGCACGTTCATCTGGCCAAACAACCTGTGGTT
AAAAACACATGTAAATGGCTTTTAAACAGCTGATACTGTATAAGACAAAGCCAAGATGCAAAATTAGGCTTTGA
TTGGCACTTTTTGAAAAATATGCAACAAATATGGGATGTAATCCGGATGGCCGCTTCTGTACTTAATGTGAAATA
TTTAGATACCTTTTTGAACACTTAACAGTTTCTTTGAGACAATGACTTTGTAAGGATTGGTACTATCTATCATTC
CTTATGACATGTACATTGTCTGTCTACTAATCCTTGGATTTTGTCTGATTGTACCCGGGATTGGTACAGGTACTGA
TGAAATCTCTAGTGGATAATCATAACACTCTCGGTCACATGTTTTTCCCTCAGCTTGAAAGCTTTTTTAAAG
GAAAAGATACCAATGCCTGCTGCTACCACCCTTTTCAATTGCTATGTTTTGAAAGGCACCAGTATGTGTTTTAG
ATTGATTTCCCTGTTTTCAGGGAAATCACGGACAGTAGTTTCCG

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FIGURE 414

MKQILGVIDKKLRNLEKKKGKLLDDYQERMNKGERLNQDQLDAVSKYQEVTTNNLEFAKELQRSFMALSQDIQKTIK
KTARREQLMREEAEQRLKTVLELQYVLDKLGDDDEVRTDLKQGLNGVPILSEEEELSLLDEFYKLVDPERDMSLRRL
NEQYEHASIHLDLLEGEKEKPVCGTTYKVLKEIVERVFQSNYFDSTHNNHQNGLCEEEEAADSAPAVEDQVPEAEPE
PAEEYTEQSEVESTHEYVNRQFMAETQFTSGEKEQVDEWTVETVEVVNSLQQPQAASPSVPEPHSLTPVAQADPL
VRRQRVQDLMAQMGPDNFIQDSMLDFENQTLDPALVSAQPMNPTQNMDMPQLVCPVHSESRLAQPNOVPVQPE
ATQVPLVSSTSEGYTASQPLYQPSHATEQRPOKEPIDQIQATISLNTDQTTASSSLPAASQPQVFQAGTSKPLHS
SGINVNAAPFQSMQTVFNMNAPVPPVNEPETLKQONQYQASYNQSFSSQPHQVEQTELQQEQLOTVVGYHGSPP
QSHQVTGNHQPPQONTGFPRSNQPYNSRGVSRGGSRGARGLMNGYRGPAMDSEEDMMVTALHSLTLQTVVIHS
LSSVLPGITLAINGMDISRISSEALGRVDHGEPHEVVEGPDPTGCRK

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FIGURE 415

ATGGAAGGAGACTTCTCGGTGTGCAGGAACTGTAAAAGACATGTAGTCTCTGCCAACTTCACCCTCCATGAGGCT
TACTGCCTGCGGTTCCCTGGTCCTGTGTCCGGAGTGTGAGGAGCCTGTCCCCAAGGAAACCATGGAGGAGCACTGC
AAGCTTGAGCACCAGCAGGTTGGGTGTACGATGTGTGACGAGCATGCAGAACTCCTCGCTGGAGTTTCATAAG
GCCAATGAGTGCCAGGAGCGCCCTGTTGAGTGTAAGTTCTGCAAAGCTGGACATGCAGCTCAGCAAGCTGGAGCTC
CACGAGTCCTACTGTGGCAGCCGGACAGAGCTCTGCCAAGGCTGTGGCCAGTTCATCATGCACCGCATGCTCGCC
CAGCACAGAGATGTCTGTGCGAGTGAACAGGCCAGCTCGGGAAAGGGGAAAGAATTCAGCTCCTGAAAGGGAA
ATCTACTGTCAATTATTGCAACCAAATGATTCCAGAAAATAAGTATTTCCACCATATGGGTAAATGTTGTCCAGAC
TCAGAGTTTAAGAAACACTTTCCTGTTGGAAATCCAGAAATTCTTCCTTCATCTCTTCCAAGTCAAGCTGCTGAA
AATCAAACCTCCACGATGGAGAAAGATGTTTCGTCCAAAGACAAGAAAGTATAAACAGATTTCTCTTCATTCTGAA
AGTTCATCAAAGAAAGCACCAAGAAGCAAAAACAAACCTTGGATCCACTTTTGATGTGAGAGCCCAAGCCCAGG
ACCAGCTCCCCTAGAGGAGATAAAGCAGCCTATGACATTCTGAGGAGATGTTCTCAGTGTGGCATCCTGCTTCCC
CTGCCGATCCTAAATCAACATCAGGAGAAATGCCGGTGGTTAGCTTCATCAAAAAGGAAAACAAGTGAGAAATTT
CAGCTAGATTTGGAAAAGGAAAGGTACTACAAATTCAAAGATTTCACTTTTTAACACTGGCATTCTGCCTACTT
GCTGTGGTGGTCTTGTGAAAGGTGATGGGTTTTATTTCGTTGGGCTTTAAAAGAAAAGGTTTGGCAGAACTAAAA
CAAACTCACGTATCATCTCAATAGATACAGAAAAGGCTTTTGATAAAATTCAACTTGACTTCATGTTAAAAACC
CTCAACAAACCAGGCGTCGAAGGAACATACCTCAAAATAATAAGAGCCATCTATGACAAAACCACAGCCAAACATC
ATACTGAATGAGCAAAAGCTGGAGCATTACTCTTGAGAAGTAGAACAAGGCACCTTCAGTCCTATTCAACATAGTA
CTGGAAGTCTCGCCACAGCAATCAGGCAAGAGAAAAGTAAAAGGCACCC

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FIGURE 416

MEGDFSVCRNCKRHVVSANFTLHEAYCLRFLVLCPECEEPVPKETMEEHCKLEHQQVGCTMCQQSMQKSSLEFHK
ANECQERPVECKFCKLDMQLSKLELHESYCGSRTELCQGCQFIMHRMLAQHRDVCRSEQAQLGKGERISAPERE
IYCHYCNQMIPENKYFHHMGKCCPDSEFKKHFPVGNPEILPSSLPSQAAENQTSTMEKDVRPKTRSINRFPLHSE
SSSKKAPRSKNKTLDP LLMSEPKPRTSSPRGDKAAYDILRRCSQCGILLPLPILNQHQEKCRWLASSKRKTSEKF
QLDLEKERYYKFKRFHF

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FIGURE 417

AAACTGGGAGAGGGAGGAAGGGAGAAAGTGAGAAGGGAAATCGGAAAGAGAAAAGGGAGGAAACGGCAGAGCCAG
AGAGAAAGAGGAAGAGACTGAGTGTGAAGGAGAGAGGACACAGGGGATGACTGAGAGACAGAGAGAGAGAGAGAG
AGAGAATGAGACAGAGACTTAAGGAAGAGACCCTGTGAGTCTGACAATAAAAGATTTGGACAGAAACAGAAAGAT
TGGAGAGAGAGAGAGAGGGAGAGAATGAGTGAGAGAGAGACTGGAAGAGACAGAGATCAGAGGGAGACACAGAAA
GTGAGAGTGGGGAGAGAGGTAGTGTAAAAGGAAGAGAGAGAGAGAGAGACCCTAAGAGACAGGAGACAAAGAGAC
AAAAAGTGTGAGTGAGCAGGTGAGGAGAGAGATTGAGAATATGAGAGACAGCAGCTAAGAGACAAAGGAGGCGG
GAGACTGCCTAGGTGCCGAGCACCACACCGTCTCTTGCCCCCGTCACTGGGACCCAGAGCTGGCCCTTG
ATGGAGGGGAGCCGACCTCGCAGCAGCCTGAGCCTGGCCAGCAGCGCCTCCACCATCTCTCTCGCTCAGCAGCCTG
AGCCCCAAGAAGCCACCCGGGCAGTAACAAGATCCACGCCTTTGGGAAGAGAGGCAATGCGCTCAGGAGGGAT
CCCAACCTTCCCGTGCACATCCGAGGCTGGCTTTCATAAGCAGGACAGCTCGGGGCTCCGTCTCTGGAACGCCGC
TGGTTCTGCTCTCTCGGCCATTGCCTCTTTTATTACAAGGACAGCCGCGAGGAGAGTGTCTTAGGCAGCGTCTTG
CTCCCCAGCTACAATATTAGACCAGATGGGCGGGAGCCCCCGAGGGCGGCGCTTCACCTTCACCGCAGAGCAC
CCGGGCATGAGGACCTACGTTTTGGCCGCTGACACCTTAGAAGACCTGCGGGGCTGGCTACGGGCGCTGGGCCGG
GCCTCCCGTGCGGAGGGGGACGACTATGGGCAACCCAGGTACCTGCACGACCCAGCCCGGGAGGGCCCCGGC
GGCCCCGCTGGTCCCCCGAGGTGAGCAGAGGGGAAGAGGGGCGCATCTCAGAATCACCGGAAGTGACTCGACTC
TCCAGAGGTCTGGTAGACCCAGGCTGCTCACTCCAGCCCCACAACCGACCTCCACTCTGGACTCCAGATGCGG
AGGGCGAGGAGCCCCGACCTGTTACCCCCCTCTCTCGCCCTCCCTCGCCTCTGAGCCTCCCCCGTCCCGTTCT
GCCCCTGCGCGCGACCCCCCTGCCCCCTCAGGAGACACAGCACCCTGCCCCGACCTCACACCCCGTTGAGTCGC
ATTGATGTCCGACCTCCTCTGGATTGGGGCCCCAACGCCAGACCTCTCCCGACCCCTACTCCCCGCCGAGGA
CCTCCCTCTGAGGCTGGGGGAGGAAAGCCCCCAGGAGTCCCCAGCACTGGAGTCAGGAGCCCAGAACACAGGCA
CACTCTGGCTCCCCCACTTATCTCCAGCTCCCCCGCGGCCCTTGGGACCCGGGCTCCATGGTTTTATTGCCG
GGTCTCTCCCTGGAGTCAACTTTCCACCAAAGCTTGGAGACAGATACGCTGCTGACCAAGTTGTGCGGGCAGGAC
CGGCTTCTGCGGAGGCTGCAGGAGGAGATAGACCAGAAGCAGGAGGAGAAGGAGCAACTAGAAGCAGCTCTGGAG
TTGACCCGGCAACAGCTGGGCCAAGCCACCAGGGAGGCTGGGGCTCCCGGGAGGGCCTGGGGTTCGCCAGCGCCTC
TTGAGGACCGGCTGGTCACTGTGAGGGCCACCCTCTGTCACTTGACTCAGGAGCGAGAGAGGGTTTGGGACAG
TACAGTGGCCTGGAGCAGGAGCTGGGCACCTTAAGAGAGACGCTGGAGTACCTGCTGCACCTTGGTTCTCCCCAG
GACAGAGTGTCTGCTCAGCAGCAGCTGTGGATGGTGAAGACACGCTGGCAGGTCTGGGTGGCCCCCAGAAACCG
CCCCACACACTGAGCCTGACTCCCCATCTCCCGTCTCCAGGGCGAGGAGTCTCAGAGAGGGAGAGCCTGCCA
GAGTCTTGGAACTGAGCTCCCCCTAGGTCCCCCGAGACTGACTGGGGCGGCCTCCTGGAGGCGACAAAGACCTC
GCCAGCCCTCACTTAGGTCTTGGGTCTCCGAGGGTCTCCCGGGCTTCCAGCCCTGAGGGTTCGCCACCTCCCTTCC
CCACAGCTAGGAACCAAGGCCCCGGTGGCCCGGCCCGGATGAATGCCAGGAGCAGCTGGAGCGGATGCGCAGA
AACCAGGAATGTGGACGGCCCTTCCCTCGCCCCGACCTCCCCCGGCTTCTCACCTTGGGAAGGACACTGTCCCCA
GCCAGACGCCAGCCTGACGTGGAGCAAAGGCCTGTCTAGGACACTCGGGAGCCCAGAAATGGCTCAGAAGCTCT
GGGTCTTGGAGTAGTCCAAGGAACACCACCCCTTACTTGCCGACTTCCGAAGGTACCCGGGAGCGGGTTCTCAGC
CTCTCCCAAGCCCTGGCTACTGAGGCGTCGAGTGGCACAGAATGATGACAGGTGGAAATTTGGACTCCCAGGGA
GACCTCTTCCCGGTGTCCGCTGCCTCCTTCGGACCCACGCGCCAGGAGACCCCTCCCCCAGATCTCCCCCG
GTGGCTAATTCGGGTTCACGGGGTTCTCTCGCCGAGGGAGTGGGCGTGGAGGAGGTCCACCCCTGGGGGGCC
GCGTGGGATGCCGGGATCGCCCCCTCCGGTCTGCCACAAGACGAGGGGGCATGGCCTCTGCGAGTCACTCTGCTA
CAATCCAGCTTGTAATCCGCCCAAAGCGGCAGCCAATCGGAGCGGAGGACGTGGTCTGGAGGTACCGCCGAAG
ATCTGGGACCACTCAGGGCATCAGGGGGCGTGGTCTGGTCCCCATTGCGGGCCCGGAGGGGAATGGTTTCTATG
GCCAAAGTTGGTTTTCTCAACACTGTCTAAATTTGGATTAAACCTTTGAACCTTT

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FIGURE 418

MEGSRPRSSLSLASSASTISSLSLSPKKPTRAVNKIHAFGKRGNALRRDPNLPVHIRGWLHKQDSSGLRLWKRR
WFLVLSGHCLFYYKDSREESVLGSVLLPSYNIRPDGPGAPRGRRFTFTAHPGMRTYVLAADTLEDIRGWLRLALGR
ASRAEGDDYQPRSPARPQPGEGPGGPGGPPPEVSRGEEGRISSESPEVTRLSRGRGRPRLLTPSPTTDLHSGLQMR
RARSDDLFTPLSRPPSPLSLPRPRSAPARRPPAPSGDTAPPARPHTPLSRIDVRPPLDWGPGRQTLSPPTPRRG
PPSEAGGGKPPRSPQHWSQEPRTQAHSGSPTYLQLPPRPPGTRASMVLLPGPPLESTFHQSLETDLLTKLCGQD
RLRLRLQEEIDQKQEEKEQLEAALELTRQQLGQATREAGAPGRAWGRQRLQDRLVSVRATLCHLTQERERVWDT
YSGLEQELGTLRETLEYLLHLGSPQDRVSAQQQLWMVEDTLAGLGGPQKPPPHTEPDSPSPVLQGEESSERESLP
ESLELSSPRSPETDWGRPPGGDKDLASPHLGLGSPRVSRASSPEGRHLPSPQLGTKAPVARPRMNAQEQLERMRR
NQECGRPFPRPTSPRLTLGRTLSPARRQPDVEQRPVVGHSGAQKWLSSGSWSSPRNTTPYLPTSEGHRERVL
LSQALATEASQWHRMMTGGNLDSQGDPLPGVPLPPSDPTRQETPPPRSPPVANSGSTGFSRRGSGRGGGPTPWGP
AWDAGIAPPVLPQDEGAWPLRVTLQSSL

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FIGURE 419

GGCACGAGGGGGACCCAACCGCGGCGACCGGACGTGCACTCCTCCAGTAGCGGCTGCACGTCGTGCCAATGGCCC
GCTATGAGGAGGTGAGCGTGTCCGGCTTCGAGGAGTTCCACCGGGCCGTGGAACAGCACAATGGCAAGACCATTT
TCGCCTACTTTACGGGTTCTAAGGACGCCGGGGGGAAAAGCTGGTGCCCCGACTGCGTGCAGGCTGAACCAGTCG
TACGAGAGGGGCTGAAGCACATTAGTGAAGGATGTGTGTTTCATCTACTGCCAAGTAGGAGAAAAGCCTTATTGGA
AAGATCCAAATAATGACTTCAGAAAAAACTTGAAAGTAACAGCAGTGCCTACACTACTTAAGTATGGAACACCTC
AAAAACTGGTAGAATCTGAGTGTCTTCAGGCCAACCTGGTGAAATGTTGTTCTCTGAAGATTAAGATTTTAGGA
TGGCAATCATGTCTTGATGTCCTGATTGTCTAGTATCAATAAACTGTATACTTGCTTTGAATTCATGTTAGCA
ATAAATGATGTTAAA

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FIGURE 420

MARYEEVSVSGFEEFHRAVEQHNGKTIFAYFTGSKDAGGKSWCPDCVQAEPPVREGLKHISEGCVFIYCQVGEKP
YWKDPNNDFRKNLKVTAVPTLLKYGTPQKLVESECLQANLVEMLFSED

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FIGURE 421

GAAAAATGTTTATATAAGCGTAAAGCTGGTAGGACAGGAAAGGAAGCCGAAACAAAAAGTAAAGAAAAATCCACA
AGGACAACTTTTGGAGCTAGTGCCTGAGATTTTGGATTTCTGAGTCCCAGGAGGTGCTGATATCATTATCTGCG
GACTCGTATTATGAAGCGCAAGGTCCTAGAGCGTGTGATTTTACAGGCATAAGGAATATAAGATGAAGGCTGAGA
CAAAATAGGATGGGTGGCCTAATTTTCTTCCCCACCTCTCGTCCCTCCCATACACATAACAACCTGACAACCTAA
AAGGGCCGCACTCCATGGAAGAAGCTCCTGCAGAGTTGGACTCCCCACCGGCAACAGGAGGAGGCTATGAAGAAA
CTTGCCTGTCTCCGATTTTCTTGGGAATTGAAAAAATAAAATTTTAAAGCCTTTCATGAAAA

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FIGURE 422

KNVYISVKLVGQERKPKQKVKKNPQGQLLELVPEILDF

FIGURE 423

CTCAGCTTGC GCCCGCCGCCGCCGCCGCCGCCGCCGCGCACGCCATGGGAGCCGTGACTGACGACGAAGTTATACG
GAAGCGTCTCCTCATTGATGGAGATGGTGGTGGAGGTGATCGGAGAATTAATCTGCTAGTGAAGAGTTTCATTAA
ATGGTGCAACTCTGGGTCCCAGGAGGAGGGATATAGCCAGTACCAACGTATGCTGAGCAGCTGTCTCAATGTGA
ATTTTCAATGGGCAAACTTTACTAGTATATGATATGAATCTCAGAGAAATGGAAAATTATGAAAAATTTACAA
GGAAATAGAATGTAGCATAGCTGGAGCACATGAAAAATTGCTGAGTGCAAAAAGCAAATTCCTCAAGCAAAACG
AATACGAAAAAATCGCCAAGAATATGATGCTTTGGCAAAAGTGATT CAGCACCATCCAGACAGGCATGAGACATT
AAAGGAACTAGAGGCTCTGGGAAAAAGAATTAGAGCATCTTTCACACATTAAAGAAAAGTGTGGAAGATAAGCTGGA
ATTGAGACGGAACAGTTTCATGTTCTTCTTAGTACCATCCATGAACTTCAGCAAACATTGGAAAATGATGAAAA
ACTCTCAGAGGTAGAAGAAGCTCAGGAAGCAAGCATGGAATCAGATCCTAAGCCATAGACAGGCTAATTGCCCAC
CACTCCCAGGAATATTGAAATAGCTACATGACCATAATGTGTTTAAAATGTGGTATGCTCTTGAGATATTTAAAG
TTTTGGCAGTAAATACTCTGTTTTTAAGTATGAATGTATTTTCATT CATATTTCTCTCACAAAGGAAAATGACT
TCAGTATAGATTTGTTTTTATTAAATGCATTTTTTATTCTTAAAGTGGTAGGAAGCAACATCCAAAATGCTTAA
TAAATGCTTTTAAAGCTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 424

MGAVTDDEVIRKRLIDGDGAGGDRRINLLVKSFIKWCNSGSQEEGYSQYQRLSTLSQCEFSMGKTLLVYDMNL
REMEYKIIYKEIECSIAGAHEKIAECKKQILQAKRIKRNQEYDALAKVIQHHPDRHETLKELEALGKELEHLS
HIKESVEDKLELRRKQFHVLLSTIHELQQTLENDEKLSEVEEAQEASMESDPKP

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FIGURE 425

CCGAGCGCCAGCGCGGGGAACCGGGAAAAGGAAACCGTGTGTGTACGTAAGATTCAGGAAACGAAACCAGGAGC
CGCGGGTGTGGCGCAAAGGTTACTCCCAGACCCTTTTCCGGCTGACTTCTGAGAAGGTTGCGCACAGCTGTGCC
CGGCAGTCTAGAGGCGCAGAAGAGGAAGCCATCGCCTGGCCCCGGCTCTCTGGACCTTGCTCGCTCGGGAGCGG
AAACAGCGGCAGCCAGAGAAGTGTTTTAATCATGAGACAAACAAAACCTCACAGATGAATGCTTCTACCCGGAAAC
AACTTGCCAGTTGGGTATCCTCCTCAGTATCCACCGACAGCATTCCAAGGACCTCCAGGATATAGTGGCTACCC
TGGGCCCCAGGTCAGCTACCCACCCCCACCAGCCGGCCATTTCAGGTCTGGCCAGCTGGCTTTCCTGTCCCAA
TCAGCCAGTGTATAATCAGCCAGTATATAATCAGCCAGTTGGAGCTGCAGGGGTACCATGGATGCCAGCGCCACA
GCCTCCATTAAACTGTCCACCTGGATTAGAATATTTAAGTCAGATAGATCAGATACTGATTTCATCAGCAAATTGA
ACTTCTGGAAGTTTTTAACAGGTTTTGAACTAATAACAAATATGAAATTAAGAACAGCTTTGGACAGAGGGTTTA
CTTTGCAGCGGAAGATACTGATTGCTGTACCCGAAATTGCTGTGGGCCATCTAGACCTTTTACCTTGAGGATTAT
TGATAATATGGGTCAAGAAGTCATAACTCTGGAGAGACCACTAAGATGTAGCAGCTGTTGTTGTCCTGTCTGCC
TCAGGAGATAGAAATCCAAGCTCCTCCTGGTGTACCAATAGGTTATGTTATTTCAGACTTGGCACCCTATGTCTACC
AAAGTTTACAATTCAAATGAGAAAAGAGAGGATGTACTAAAAATAAGTGGTCCATGTGTTGTGTGCAGCTGTTG
TGGAGATGTTGATTTTGAGATTAAATCTCTTGATGAACAGTGTGTGGTTGGCAAAATTTCCAAGCACTGGACTGG
AATTTTGAGAGAGGCATTTACAGACGCTGATAACTTTGGAATCCAGTTCCTTTAGACCTTGATGTTAAATGAA
AGCTGTAATGATTGGTGCCTGTTTCCTCATTGACTTCATGTTTTTTGAAAGCACTGGCAGCCAGGAACAAAAATC
AGGAGTGTGGTAGTGGATTAGTGAAAGTCTCCTCAGGAAATCTGAAGTCTGTATATTGATTGAGACTATCTAAAC
TCATACCTGTATGAATTAAGCTGTAAGGCCTGTAGCTCTGGTTGTATACCTTTTGCTTTTCAAATTATAGTTTATC
TTCTGTATAACTGATTTATAAAGGTTTTTGTACATTTTTTAATACTCATTGTCAATTTGAGAAAAAGGACATATG
AGTTTTTGCATTTATTAATGAACTTCCTTTGAAAACTGCTTTGAATTATGATCTCTGATTCAATTGTCCATTTT
ACTACCAAATATTAATAAGGCCTTATTAATTTTTATATAAATTATATCTTGTCTATTAAATCTAGTTACAATT
TATTTTCATGCATAAGAGCTAATGTTATTTTGCAAATGCCATATATTCAAAAAGCTCAAAGATAATTTTCTTTAC
TATTATGTTCAAATAATATTCAATATGCATATTATCTTTAAAAAGTTAAATGTTTTTTAATCTTCAAGAAATCA
TGCTACACCTTAACCTCTCCTAGAGCTAATCTATACCATAATATTTTCATATTCACAAGATATTAAATTACCAAT
TTTCAAATTATTTGTTAGTAAAGAACAAAATGATTCCTCCCAAAGAAAGACACATTTTAAATACTCCTTCACTCT
AAAACCTCTGGTATTATACTTTTGAAAGTTAATATTTCTACATGAAATGTTTAGCTCTTACACTCTATCCTTCCT
AGAAAATGGTAATTGAGATTACTCAGATATTAATTAATACAATATCATATATATATTACAGAGTATAAACCTA
AATAATGATCTATTAGATTCAAATATTTGAAATAAAAACCTTGATTTTTTTGT

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FIGURE 426

MDKQNSQMNASHPETNLPVGYPPQYPPTAFQGPPGYSGYPGPQVSYP PPPAGHSGPGPAGFPVPNQPVYNQPVYN
QPVGAAGVPWMPAPQPPLNCPGLEYSQIDQILIHQQIELLEVLTGFETNNKYEIKNSFGQRVYFAAEDTDCCT
RNCCGPSRPFTLRIIDNMGQEVITLERPLRCSSCCCPCLQEIEIQAPPGVPIGYVIQTWHPCLPKFTIQNEKRE
DVLKISGPCVVCSCCGDVDFEIKSLDEQC VVGKISKHWTGILREAF TDADNFGIQFPLDL DVKMKAVMIGACFLI
DFMFFESTGSQEQKSGVW

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FIGURE 427

GTTTTCTTCGAAGATTTGGGGCTCCGCGATACAGTTAGGATGCTGTAGTACCTCTGCTGTTGTTGGGGGGTTTG
TGGAGCGCTGTGGGAGCGTCCAGCCTGGGTGTCGTTACTTGGCGCTCCGTGGTGAAGCTACTCAATACGCGCCAC
AACGTCCGACTGCACCTCACACGACGTGCGCTATGGGTCAAGTAGTGGGCAGCAGTCAGTGACAGGTGTAACCTCT
GTGGATGACAGCAACAGTTACTGGAGGATACGGCGGAAGAGTGCCACAGTGTGTGAGAGGGGAACCCCCATCAAG
TGTGGCCAGCCCATCCGGCTGACACATGTCAACACTGGCCGAAACCTCCATAGTCACCACTTCACCTCACCTCTT
TCTGGAAACCAGGAAGTGACTGCTTTTGGTGAAGAAGGTGAAGGTGATTATCTGGATGACTGGACAGTGCTCTGT
AATGGACCCTACTGGGTGAGAGATGGTGAGGTGCGGTTCAAACACTCTTCCACTGAGGTACTGCTGTCTGTCACA
GGAGAACAATATGGTCGACCTATCAGTGGGCAAAAAGAGGTGCATGGCATGGCCCAGCCAAGTCAGAACAACCTAC
TGGAAGCCATGGAAGGCATCTTCATGAAGCCCAGTGAGTTGTTGAAGGCAGAAGCCCACCATGCAGAGCTGTGA

ATCTTGAGGCTCTGAGGCACTGTTAACGCACAATGTTACAGACATCTGTTGCTGCCTCACCTTGGGATCCCTGC
CACAAGTTTCCTTGGGCAGTGGCCATGTCACCATGAGATGAAGATATACAACAGAGAAATAGTGGCTGTGTTTGG
GAAGCTTCAGCCCTGCACATTTTGAAGTACTACTCTCCAGACTTGGCGGTGGGTGAGTTCTTTTCTGAGTAGA
GGACTTGCTGGTAAAAGGGGCAGATGCTTTTTATTAGTACTGATTAAACCACACTGAGGGAAACATCCCTCTTAG
CTGGGAAACTGTTTACTCTTCAGGAGCTTGGCATCATGGACTGTTAATGTATGTGATTTTCCCCCTATTTTCTCT
CCCCACAATGATAAAAAACAATAATTTTATTATGA

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FIGURE 428

MAVVPLLLLGGLWSAVGASSLGVVTCGSVVKLLNTRHNVRLHSHDVRYGSSSGQQSVTGVTSVDDSNSYWRIRRK
SATVCERGTPIKCGQPIRLTHVNTGRNLHSHHFTSPLSGNQEVTAFGEEGEGDYLDDWTVLCNGPYWVRDGEVRF
KHSSTEVL LSVTGEQYGRPI SGQKEVHGMAQPSQNNYWKAMEGIFMKPSELLKAEAHHAEL

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FIGURE 429

TGCGAACGGCGAGCAGCGGGCGGCGGAGAGACGCAGCGGAGGTTTTCTGGTTTCGGACCCCAGCGGCCGG
ATGGTGAAATCCTCCCTGCAGCGGATCCTCAATAGCCACTGCTTCGCCAGAGAGAAGGAAGGGGATAAACCCAGC
GCCACCATCCACGCCAGCCGCACCATGCCGCTCCTTAGCCTGCACAGCCGCGGCGGCAGCAGCAGTGAGAGTTCC
AGGGTCTCCCTCCACTGCTGTAGTAACCCGGGTCCGGGGCTCGGTGGTGCTCCTGATGCCCCTCACCCACCCCT
GAAGATCCCAGGTGGGCGAGGGAATAGTCAGAGGGATCACAAATCTTTCAGCTAACTTATTCTACTCCGATGATCG
GCTGAATGTAACAGAGGAACCTAACGTCCAACGACAAGACGAGGATTCTCAACGTCCAGTCCAGGCTCACAGACGC
CAAACGCATTAACTGGCGAACAGTGCTGAGTGGCGGCAGCCTCTACATCGAGATCCCCGGGCGGCGCTGCCCGA
GGGGAGCAAGGACAGCTTTGCAGTTCTCCTGGAGTTCGCTGAGGAGCAGCTGCGAGCCGACCATGTCTTCATTTG
CTTCCACAAGAACC GCGAGGACAGAGCCGCCTTGCCTCGAACCTTCAGCTTTTTGGGCTTTGAGATTGTGAGACC
GGGGCATCCCCTTGTCCCAAGAGACCCGACGCTTGCTTCATGGCCTACACGTTTCGAGAGAGAGTCTTCGGGAGA
GGAGGAGGAGTAGGGCCGCCTCGGGGCTGGGCATCCGGCCCCCTGGGGCCACCCCTTGTGAGCCGGGTGGGTAGGA
ACCGTAGACTCGCTCATCTCGCCTGGGTTTGTCCGCATGTTGTAATCGTGCAAATAAACGCTCACTCCGAATTAG
CGGTGTATTTCTTGAAGTTTAATATTGTGTTTGTGATACTGAAGTATTGCTTTAATTCTAAATAAAAATTTATA
TTTTACTTTTT

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FIGURE 430

MVKSSLQRILNSHCFAREKEGDKPSATIHASRTMPLLSLHSRGGSSSESSRVSLHCCSNPGGPRWCSDAPHPPL
KIPGGRGNSQRDHNLSANLFYSDDRLNVTEELTSNDKTRILNVQSRLTDAKRINWRTVLSGGSLYIEIPGGALPE
GSKDSFAVLLEFAEEQLRADHVFICFHKNREDRAALLRTFSFLGFEIVRPGHPLVPKRPDACFMAYTTERESSGE
EEE

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FIGURE 431

GATTGGAAGCAGAGGAAGCTGAAGAAAAGTAATGTAGTTTCCTTAAAGGCATACAAAGGACTGGCAGAAGTCGCT
GTGAAGAGCTTGTGTGAGCTGTTGGTGGCACTACCTCATTTTAACTTTTACAACAACATCATCGTATTGATTGTC
CCTCTCATGAATGACATGTCAAAATTGATATCTGAAATGTGTTGTGAAGCTGTGAAGAACTCTTTAAGCAAGAT
AAATTAGGCCAAGCTTCTCTTGGTGTAAATTAAAGTGATTCTGGTTTTGTGAAGGGCAGAAATTACGAAGTTAGG
CCAGAGATGTTAAAAACATTTTTATGCCTAAGAATCAAGGAAGTAGAAGTGAAAAAGATACAGAAGACATTAAAT
AAACCAAAAAAATTTATGACTTTCAAAGAAAAGAGAAAAATCTCTATCAAGAATGCAGAGAAAGTGAAGAAAGCA
GAAGAGAACTAGCGCGAGAGCTTCGAGAGGCAGAAGCTTCAGAGAGTACTGAGAAAAAACTTAAACTGCACACA
GAGACTCTGAATATTGTGTTGTAACTTCTCAGAATATTGAAGAAGGCCAGAGGTCACCTCTCCTGCCAGCA
GTTCTAGAAGGTCTTGCCAAGTTTGCTCACCTTATAAATGTGGAATTTTTTGTATGATCTGTTAGTAGTTCTTCAT
ACTCTCATTGAGTCTGGTGACCTAAGCTATCAAGAAAGTCTTCACTGTGTCCAGACTGCTTTTCATATTCTTTCT
GGACAAGGTGATGTTCTGAATATTGATCCATTGAAATTCTACACACATCTCTACAAAACACTGTTCAAATTACAT
GCAGGTGCTACCAATGAAGGTGTGAGATTGTACTCCAGTGCCTTGATGTGCTAAGCGCAGAAAGCAA
GTTTCTCAGCAGCGAGCTCTTGCCCTTCATCAAACGCCCTTTGTACCCTTGCTCTTCATGTTCTTCCAAATTCAGT
ATTGGCATTTTAGCAACTACCAGAATATTAATGCATACTTTCCCCAAAACAGATCTACTGCTTGACAGTGAATCT
CAGGGAAGTGGAGTTTTCTTCTGAACTGGATGAGCCTGAGTACTGCAATGCTCAGAACACTGCTCTGTGGGAA
CTGCATGCTCTGCGGAGGCATTATCATCCCATAGTGCAGAGATTTGCAGCCACCTGATCGCTGGAGCACCTTCT
GAAGGCTCTGGAGCACTCAAACCAGAGTTGAGTGAAGATCTGCTACTGAACTTTTTGAGGCATATAGCATGGCA
GAAATGACATTCAATCCTCCTGTTGAATCTTCAAACCCCAAAATAAAGGGTAAATTTTTACAAGGGGATTCAATT
TTGAATGAAGATTTAAATCAGCTAATCAAAAGATACTCCAGTGAAGTTGCTACTGAATCGCCTCTGGATTTCACG
AAATATTTGAAAACATCACTACACTAGTAGAGGAATGAAGTCAGTGGACTTTCTTGTATATTGTGTGTGCAGAT
GTACATAAAGATGAGTTGTTAACTTAGGATCTTTTCTTTTTATACAAGGAAAGCTTCCTAAGAATGTCTAGGAAG
AAGAGGAAGAATGACCCTTTGCATGGCACAGGGTTCTGCCCCATTCTGAATATGTCATTCCATCAAGGAGATCA
AAAGCCTTTTTTTCTCCCCAGTATTTGGAATTACTTTCTTGAIGATGCTGCCTTTTAAAGCTTCACGTACATT
ATAGTTTTTTAAAAAAATCTTTGGACTGGATCTTACTGAAGTGCAGTTGCTATATTAAAATTAGGGCATAGAGCA
CAGAAAAATCAAGACCATGAGAAGACATTTTACCATTTAGCTACTTTTTATACTAAATACTCTTTAAATATTTT
TATTTCAATACTGTGGATGGAAATGAGAAGCATTCTAAATTTGAGTTAATATATTTTTATGAAGATATTTGAGAA
AAGAAAAAATAGCTTGTATTGAGTTTCTTTGCTGATGATCCACCTAAAGAAGTTACCTAATTTGGC
CTTTTAAAAAAGGTGTTAGTGTATTATTATAGCTACTTTCAAGGAAAGTTTGAATATGATTCTAGTCTCTAAAGTT
CTTCACGTTTTCTGACATTCCCTGGAGGGTGACTGGGGAAGAATTGCTCCAGGGTAGAAGAACCAGGCCCAAGAC
TTTACCATTCTGATCTAGAGACAAAGGATACTCAATGAGGAGCTTTTTTCCCCTCTTGAACAGGTAAAATGCTT
TTTCTTATTAATATAATTATAAACAGTATTTTATGTAACAGCTATTCCCATATTCTAGGAGTGGCCTAAGAAAT
GCGTGTTCAGTGACTAGATTATAAATATTCTCTATTGTGAATAGTTGAATAAACAGCTGTTTTTTCTGCTTC
T

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FIGURE 432

MNDMSKLI SEMCCEAVKKLFKQDKLGQASLGVIKVISGFVKGRNYEVRPEMLKTFCLCRIKEVEVKKDTEDINKP
KKFMTFKEKRKSLSRMQRWKKAEEKLARELREAEASESTEKKLKLHTETLNIVFVITYFRILKKAQRSPLLPVL
EGLAKFAHLINVEFFDDLLVVLHTLIESGDLSYQESLHCVQTAFHILSGQGDVLNIDPLKFYTHLYKTLFKLHAG
ATNEGVEIVLQCLDVMLTKRRKQVSQQRALAFIKRLCTLALHVLNPNSSIGILATTRILMHTFPKTDLLDSESG
SGVFLPELDEPEYCNAQNTALWELHALRRHYHPVQRFAAHLIAGAPSEGSALKPELSRRSATELFEAYSMAEM
TFNPPVESSNPKIKGKFLQGDSFLNEDLNQLIKRYSSEVATESPLDFTKYLKTS LH

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FIGURE 433

GGTGGCCCTGAGCGCCGGCGACACCTTTCCTGGACTATAAATTGAGCACCTGGGATGGGTAGGGGGCCAAACGCAG
TCACCGCCGTCCGCAGTCACAGTCCAGCCACTGACCGCAGCAGCGCCCTTGCGTAGCAGCCGCTTGCAGCGAGAA
CACTGAATTGCCAACGAGCAGGAGAGTCTCAAGGCGCAAGAGGAGGCCAGGGCTCGACCCACAGAGCACCCCTCAG
CCATCGCGAGTTTCCGGGCGCCAAAGCCAGGAGAAGCCGCCCATCCCGCAGGGCCGGTCTGCCAGCGAGACGAGA
GTTGGCGAGGGCGGAGGAGTGCCGGGAATCCCGCCACACCGCTATAGCCAGGCCCCAGCGCGGGCCTTGGAGA
GCGCGTGAAAGGCGGGCATCCCCTTGACCGCGCCGACCATCCCCGTGCCCTGCGTCCCTGCGCTCCAACGTCCGC
GCGGCCACCATGATGCAAATCTGCGACACCTACAACCAGAAGCACTCGCTCTTTAACGCCATGAATCGCTTCATT
GGCGCCGTGAACAACATGGACCAGACGGTGATGGTGCCAGCTTGCTGCGCGACGTGCCCTGGCTGACCCCGGG
TTAGACAACGATGTTGGCGTGGAGGTAGGCGGCAGTGGCGGCTGCCCTGGAGGAGCGCACGCCCCAGTCCCCGAC
TCGGGAAGCGCCAATGGCAGCTTTTCGCGCCCTCTCGGGACATGTACAGCCACTACGTGCTTCTCAAGTCCATC
CGCAACGACATCGAGTGGGGGCTCTGCAACAGCCGCCTCCACCGGCTGGGAGCGAGGAGGGCAGTGCCTGGAAG
TCCAAGGACATCCTGGTGGACCTGGGCCACTTGGAGGGTGGCGACGCCGCGGAAGAAGACCTGGAACAGCAGTTC
CACTACCACCTGCGCGGGCTGCACACTGTGCTCTCGAAACTCACGCGCAAAGCCAACATCCTCACTAACAGATAC
AAGCAGGAGATCGGCTTCGGCAATTGGGGCCACTGAGGCGTGGCGCCCGTGGCTGCCAGCACCTTCTTCGACCC
ATCTCACCTCTCTCATTCCCTCAAAGCTTTTTTTTTTCTTGGCTGGGGGGCGGGAAGGGCAGACTGCAAACCT
GGGGGGCTGCGTACGTGCAGGAGGCGCGGTGGGGCTGCGTGGAGGAGGGGGCCACGTGTGAGAGAGAAGAAAATG
GTGGCCGAGATGGGAGGGGCCCCAAGGAACCTCCTGGGAGGGGGCTGCATTCTATGTTGGTGGGAATGGGACTGG
GCTGACGCCCTGCATTGACCTGTGCCCTTCTGCGGGTTCTTTTCTGTTCTTTTCGGAGGAGAGGGCCCGAGAA
GGGGCCATACCAGGGCGCGCGCTGGGTTGCCACACTTGGGAAAGCAGCCCGGAGCTGGGTGCTGGGGAAGCGG
GGCGCGTAGCCTCCCGCCGCCCTGCGGTTGGGCCGTTGGAGGCCAGGCGTTGCTAGGATTGCATCAGTTTTCCT
GTTTGCACTATTTCTTTTGTAACTTGGCCCTGTGTGAAGTATTTTGAATCTCCTCCTTGCTCTGAACTTCAG
CGATTCCATTGTGATAAGCGCACAAACAGCACTGTCTGTGCGTAATCGGTACTACTTTATTAATGATTTTCTGTT
ACACTGTATAGTAGTCTATGGCACCCCCACCCCATCCCTTCGTGCCACTCCCGTCCCCACCCCCACCCAGTG
TGTATAAGCTGGCATTTCGCCAGCTTGTACGTAGCTTGCCACTCAGTGAATAATAACATTATTATGAGAAAGT
GGACTTAACCGAAATGGAACCAACTGACATTCTATCGTGTGTACATAGAATGATGAAGGGTTCCACTGTTGTTG
TATGTCTTAAATTTATTTAAACTTTTTTAAATCCAGATGTAGACTATATTCTAAAAATAAAAAAGCAAATGTG
TCAACT

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FIGURE 434

MMQICDTYNQKHSLEFNAMNRFIGAVNNMDQTMVPSLLRDVPLADPGLDNDVGVEVGSGGCLEERTPPVPDSGS
ANGSFFAPSRDMYSHYVLLKSIRNDIEWGVLHQPPFPAGSEEGSAWKSKDILVDLGHLEGADAGEEDLEQQFHYH
LRGLHTVLSKLTRKANILTNRYKQEIGFGNWGH

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FIGURE 435

GGCACGAGGCTCCAGC**ATG**GAGGAGGCCACCGGCTGTGCAGGGTTCAATCTCATCCACTTGGTGGCCACGGGCAT
CTCCTGCTTCTTGGGCTCTGGGCTCCTGACCCTAGCAGTGTACCTGTCTTGCCAGCACTGCCAGCGTCAGTCCCA
GGAGTCCACACTGGTCCATCCTGCCACCCCCAACCAATTTGCACTACAAGGGCGGAGGCACCCGAAGAATGAAAA
GTACACACCCATGGAATTCAAGACCCTGAACAAGAATAACTTGATCCCTGATGACAGAGCCAACCTTCTACCCATT
GCAGCAGACCAATGTGTACACGACTACTTACTACCCAAGCCCCCTGAACAAACACAGCTTCCGGCCCCGAGGCCTC
ACCTGGACAACGGTGCTTCCCCAACAGC**TGAT**ACCGCCGTCCTGGGGACTTGGGCTTCTTGCCTTCATAAGGCAC
AGAGCAGATGGAGATGGGACAGTGGAGCCAGTTTGGTTTTCTCCCTCTGCACTAGGCCAAGAAGTTGCTGCCTTG
CCTGTGGGGGGTCCCATCCGGCTTCAGAGAGCTCTGGCTGGCATTGACCATGGGGGAAAGGGCTGGTTTCAGGCT
GACATATGGCCGCAGGTCCAGTTCAGCCCAGGTCTCTCATGGTTATCTTCCAACCCACTGTACGCTGACACTAT
GCTGCCATGCCTGGGCTGTGGACCTACTGGGCATTTGAGGAATTGGAGAATGGAGATGGCAAGAGGGCAGGCTTT
TAAGTTTGGGTTGGAGACAACTTCCTGTGGCCCCACAAGCTGAGTCTGGCCTTCTCCAGCTGGCCCCAAAAAG
GCCTTTGCTACATCCTGATTATCTCTGAAAGTAATCAATCAAGTGGCTCCAGTAGCTCTGGATTTTCTGCCAGGG
CTGGGCCATTGTGGTGCTGCCCCAGTATGACATGGGACCAAGGCCAGCGCAGGTTATCCACCTCTGCCTGGAAGT
CTATACTCTACCCAGGGCATCCCTCTGGTCAGAGGCAGTGAGTACTGGGAAGTGGAGGCTGACCTGTGCTTAGAA
GTCCTTTTAATCTGGGCTGGTACAGGCCTCAGCCTTGCCCTCAATGCACGAAAGGTGGCCCAGGAGAGAGGATCAA
TGCCATAGGAGGCAGAAGTCTGGCCTCTGTGCCTCTATGGAGACTATCTTCCAGTTGCTGCTCAACAGAGTTGTT
GGCTGAGACCTGCTTGGGAGTCTCTGCTGGCCCTTCATCTGTTTCAGGAACACACACACACACACTCACACACG
CACACACAATCACAATTTGCTACAGCAACAAAAAGACATTGGGCTGTGGCATTATTAATTAAAGATGATATCCA
GTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 436

MEEATGCAGFNLIHLVATGISCF LGSGLLT LAVYLSCQHCQRQSQESTLVHPATPNHLHYKGGGTPKNEKYTPME
FKTLNKNLIPDDRANFYPLQQTINVYTTTTYYPSPLNKHSFRPEASPGQRCFPNS

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FIGURE 437

GAAAAATGAAACGTCTTTGTGGTCCGGGGCTGAGACCCACGAGGAGACTGGGCGGGATTCTGGCGTTAGGAGGC
GGGGCCCTTTTCGGCTTTGGGCGCGAGTGGT**TAA**AAGACAGTTGGTGTGCGTTTCGGCTTCTCGGGTCGGATTCCGCG
GTCCCAACCCCTTCCCATGGCCGACCCTGAGGAGTTGCAGGTTTCTTCGCCGCCCCCGCCCTCCCTCTTCTCC
CTCCTCTTCAGACGCCTCTGCAGCATCTTCCCCGGGCGGCCAGTGAGTTTGGGCTGGCCAGTTCCGAGCAGGAG
CAGCGGCCCAACGGTGGACCAGCTGGAGGAAGTGGAGCTGCAGATCGGAGACGCAGCCTTTTCATTAACCAA
TCTTGAAGCCACATCTGCAGTATCAGCTCAAGTGAAGAAGTGCCTTCAAATGTACAGAAAATGCACGTTTCCT
TAAACGTGGCGGGACCTCTTGAAAGAAGGCTATGATTCTTTGAAACCTGATGACTGATTTGGCATACTTCGTTG
GTCCAGCAGTTCTGTATATACTCAGAAATGAAATTTTCTTGGTTTTCTTGGTTTTTGTGAAAGCAGAATACCGAT
GCTATTTTTTGTGCGGACCACTTGTTCCTTAAATACTTTATGCCTCTGAACCTTTCATAGAATCCTTTAT
GAAAGTTAACTTCATCAATAGACGGTTAATATTAATAGAGCCACAGTGCTACCAGTAGCAAAGTGTAGACCAT
TATTTGTTTTGCAACAAGATGCTAAGCATGGCAGACTTTGAAGTTGCGTTTCATCTTAAGGACCAAGGGAGGTAA
CTTTAAGGTTGCCAGTGGTGGATCCAGCTCCGTTAGGCTAAGTTGCTACAGCTAATGATTGTGTCTTTATTCTA
TATCCCCAGCACCTAAACAGGGTCACACAACATTCACTAAATGTTTGTGAATAAAAGAGTTAACAAACATAAT
TGAAAGCTTTTTTCTTCCCTATATTTAGCATGAAGACTGTCATTGTTTCTCTAGGAAATGTATGAATCTGAACCT
TTTTGACTTGAAGAAAAACATTCTTTTTTACAGAGATTTGGACTTTGATGATAGGTTTTAAAAATATATGATAA
ATATTTTTTGTACTTGTGTTTTTTTTTAAAGACTTTACTTCAGAAAGGGAAAGACTGTTTAGAAAGAAATGC
ATATTTTTTCCCTATTTATTTCTGTGGTTACTGCTTTTGAGTTTAAACAGTGTTTGTATTTGATATTTGTATATG
TTTGATTGCTATCTTTAAAGTGCCCTATCAGATTTATGGGCTCTGTGCTATTACTTTTTGAGCTTTGCAAGTTGT
GTACATAATAATTCTAAAGAAGTTACTTTGTTTGCATGCATCAAATTTAAATGATGTGATTTTTTTGTATTAT
TTGATCTTAGTGACAGTGTTCTATTTTGCATCCTGTATCTTATGTTGCTTTTGGTGTGTTGTGTGTCAAC
GATTAAGCCAACTAATCTCTACCATATATACTTCTGGACATTTTTTGATACAACATCTTAATCTTTGTAGATA
TGGAGATAGGTACAGAACTATATTCTAATGCCCCACAATGGGGCTATGAGAGGGGACAGATGGATGGGCAAAGAA
TAGTTTTGTTTAAACATATTAGGTCATAGTTCTTGATTAGTTTTTTTAGTTAAAGATAAACACATAGGGTGTGATT
TCTATACCAAAGATATGCTTATTTAGTATTAGAAAAATATTCTTCTTACATCTCCTGAAAAATTGCAATTTTTAA
AATGTGTAAAAATAAATTATTATTAAGACACATTTTATTTCCATTTGTTTGGATTCAATACCTTAAACCTTTAT
TGACATATTTCAAAGATATAGGAAAGGTAAATGATTTCAAGAAAAATCCGTGTATTTCTACCATGCAGATGTAATA
AATGTTAGCATTGGCTATATTTTCTTCAGACACACATATGCATGTAATTGCAAATGTTAGATACATTTGAAGTT
TGCTTTGTTACCTGTTTGATCCTGTCCCGTTCTCCTCCCTCCCGAGAGTCCCGAGAGGTAACTAGAGGGGGCAT
AATATAGCATGTGTTTTTATATTTTAAATACAAATATATTTTTTAAAGCGCTACAAAATATTGTTTTATATATG
TGGTAGCCAGCTTCCAGATGGCCCCAGTGATCCCTGGCCTCCTGGTGTTCATGCCCCAGTATAGCCTTCTCCTGC
ATTTTACAGTGCTGACTTTTGTAACTACCAGGATATTGAGCAAATGCAGTGTTGATTCTGAGGCCATANNNNN
NN
NNNAAGCACTGGGAGTACAGGC
ATTTTGTCTATTTTCTATGTTGTTTTTTTACTTGTCAGTTTTTAGATATTACATATTTGAATACTAATGAT
CTGTTATGTATGTTCCAATTATCTTTTTTAGTCTGGTTTGTCTTCATATTTTGGTTATGAAATCTTGAATTTTTA
AAACGTAATTTTACCAATCTTTCATAATGATTGCTTTTTCTGGTTTTTGTATAGGAAATGTCATAAAAAATAGT
CCTATTCAGCCTTCCAAAAGTTACAAAATTTTGGTTTTTAAACATTTAGATGTTTAGTCCAAGTGGAAATGGTT
TCCTTTTATGGCATGATTTTGGAACTGTGTTTTAATTATTTTACATATTTATAGCTGTTTCTCCAAAGTATCAAT
TTTTCAAGTGCAACATCTGTATGCAGTTACTATGTAAGGGCCAGATTCTGACCTTTCGTGTTCTTTTATCTGAA
GGAAATTTGAACATGCCACCCCAAATATGCCGATTTGGCATACTGATTATTCGAGCTAAAGGTGCTTGACTAA
CAGTAGTTGCAGAAAATGGCTATTTTAACTGTCTTTCCTACCTGTAGCAAGCCATACAACTTCTTTGATAAAGA
TGCTTTCTGATACCAAGATGAGAAGATGGCTCTAATCAGCTGAGACAGCACCAGAGGAATCTACAAACAAGAAA
CTATTAGTTTCTTAACATATATTTACCTCCACAGTTTCTGCCTCTGGAAGCCTAAACCTGCTTTCCTTCGTCTT
GTCACACTTCTCTGAAATGTATTCTTTGTGGAAGATGCTATATAGTCCAGAGTTGTAAGCCACTACTTGTGTTA
CCTTTTCATTGAGTTTTCTCCTGTGTGATGACGTGTCATATATTAATAAAATTACTTGTTTTTCTCTT

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FIGURE 438

KMKRLCGPGLRPTRRLGGISGVRRRGLSALGASG

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FIGURE 439

ACAGAGATGGCACTGATGCAGGAAGTGTATAGCACACCAGCCTCCAGGCTGGACTCCTTCGTGGCTCAGTGGCTG
CAGCCCCACCGGGAGTGGAAGGAAGAGGTGCTAGACGCTGTGCGGACCGTGGAGGAGTTTCTGAGGCAGGAGCAT
TTCCAGGGGAAGCGTGGGCTGGACCAGGATGTGCGGGTGTGAAGGTAGTCAAGGTGGGCTCCTTCGGGAATGGC
ACGGTTCTCAGGAGCACCAGAGAGGTGGAGCTGGTGGCGTTTCTGAGCTGTTTCCACAGCTTCCAGGAGGCAGCC
AAGCATCACAAAGATGTTCTGAGGCTGATATGGAAAACCATGTGGCAAAGCCAGGACCTGCTGGACCTCGGGCTC
GAGGACCTGAGGATGGAGCAGAGAGTCCCCGATGCTCTTGTCTTACCATCCAGACCAGGGGGACTGCGGAGCCC
ATCACGGTCACCATTGTGCCTGCCTACAGAGCCCTGGGGCCTTCTCTTCCAACTCCCAGCCACCCCTGAGGTC
TATGTGAGCCTGATCAAGGCCTGCGGTGGTCTTGGAAATTTCTGCCATCCTTCAGCGAGCTGCAGAGAAATTC
GTGAAACATCGGCCAACTAAGCTGAAGAGCCTCCTGCGCCTGGTGAACACTGGTACCAGCAGTATGTGAAAGCC
AGGTCCCCCAGAGCCAATCTGCCCCCTCTCTATGCTCTTGAACCTTAACCATCTATGCCTGGGAAATGGGTACT
GAAGAAGACGAGAAATTCATGTTGGACGAAGGCTTCAACCTGTGATGGACCTGCTCCTGGAGTATGAAGTCATC
TGTATCTACTGGACCAAGTACTACACACTCCACAATGCAATCATTGAGGATTGTGTCAGAAAACAGCTCAAAAAA
GAGAGGGCCCATCATCCTGGATCCGGCCGACCCACCCCTCAACGTGGCAGAAGGGTACAGATGGGACATCGTTGCT
CAGAGGGCCTCCCAGTGCCTGAAACAGGACTGTTGCTATGACAACAGGGAGAACCCCATCTCCAGCTGGAACGTG
AAGAGGGCACGAGACATCCACTTGACAGTGGAGCAGAGGGGTTACCCAGATTTCAACCTCATCGTGAACCCCTTAT
GAGCCCATAGGAAGGTTAAAGAGAAAATCCGGAGGACCAGGGGCTACTCTGGCCTGCAGCGTCTGTCCTTCCAG
GTTCTGAGCAGTGAGAGGCAGCTTCTCAGCAGCAGGTGCTCCTTAGCCAAATATGGGATCTTCTCCCACTCAC
ATCTATCTGCTGGAGACCATCCCCCTCCGAGATCCAGGTCTTCGTGAAGAATCCTGATGGTGGGAGCTACGCCTAT
GCCATCAACCCCAACAGCTTCATCCTGGGTCTGAAGCAGCAGATTGAAGACCAGCAGGGGCTTCCTAAAAAGCAG
CAGCAGCTGGAATTCCAAGGCAAGTCTGCAGGACTGGTGGGTCTGGGGATCTATGGCATCCAAGACAGTGAC
ACTCTCATCCTCTCGAAGAAGAAAGGAGAGGCTCTGTTCCAGCCAGTTAGTTTTCTCTGGGAGACTTCTCTGTA
CATTTCTGCCATGTACTCCAGAAGTCTCCTGTCAATCACTCTGTCCCATTTGTCTACTGGGAAGGTCCCAGGTCT
TCACCAGTTTTACAATGAGTTATCCAGGCCAGACGTGGTAGCTCACACCTGTAATCCCAGAAGTTTGGGAGGCC
GAGGTGGGAGGAGCGCTTGAGCCGAGGAGTTCAAGACCAGCCTGGGTATCATAGGGAGACCCCGTCTCTACAAAA
TAAAAAATAATTCACTGGG

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FIGURE 440

MALMQELYSTPASRLDSFVAQWLQPHREWKEEVLDVRTVEEF LRQEHFQGKRGLDQDVRVLKVVKVGSFGNGTV
LRSTREVELVAF LSCFHSFQEA AKHKDVLRLIWKTMWQSQDLLDLGLEDLRMEQRVPDALVFTIQTRGTAEPIT
VTIVPAYRALGPSLPNSQPPPEVYVSLIKACGGPGNFCPSFSELQRNFVKHRPTKLKSLRLVKHWYQQYVKARS
PRANLPPLYALELLTIYAWEMGTEEDENFMLDEGFTTVMDLLEYEVICIYWTKYYTLHNAI IEDCVRKQLKKER
PIILDPADEPTLNVAEGYRWDIVAQRASQCLKQDCCYDNRENPISSWNVKRARDIHLTVEQRGYPDFNLIVNPYEP
IRKVKEKIRRTRGYSGLRLSFQVPGSERQLLSSRCSLAKYGIFSHTHIYLLETIPSEIQVFVKNPDGGSYAYAI
NPNSFILGLKQQIEDQQGLPKKQQQLEFQGOVLQDWLGLGIYGIQDSDTLILSKKKGEALFPAS

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FIGURE 441

CTTCCGTCGCCCTTGCTTCGTCTTCGCTTTTCTTTCTACTTATTCTTATCTGTGTCTTTCGCTTTGTTTGCCCTCT
CCGTCTGTTTTCCCTCAGGGCCCCCTTCTTTCCTCGACCTTTTCAAATCGCAAATATGGCGCCGGAGCGGCTGCG
GAGCCGGGCGCCCTCCGCCTTCAAGTTGCGGGGCTTGCTGCTCCGTGGTGAAGCTATTAAGTACCTCACAGAAGC
TCTTCAGTCTATCAGTGAATTAGAGCTTGAAGATAAACTGGAAAAGATAATTAATGCAGTTGAGAAGCAACCCTT
GTCATCAAACATGATTGAACGATCTGTGGTGAAGCAGCAGTCCAGGAATGCAGTCAGTCTGTTGATGAACTAT
AGAGCACGTTTTCAATATCATAGGAGCATTGATATTCCACGCTTTGTGTACAATTCAGAAAGAAAAAATTTCT
TCCTCTGTTAATGACCAACCACCCTGCACCAAATTTATTTGGAACACCAAGAGATAAAGCAGAGATGTTTCGTGA
GCGATATACCATTTTGACCAGAGGACCCACAGGCATGAATTATTTACTCCTCCGGTGATAGGTTCTCACCCCTGA
TGAAAGCGGAAGCAAATTCAGCTTAAACAATAGAAACCTTATTGGGTAGTACAACCAAAATCGGAGATGCGAT
TGTTCTTGGAATGATAACGCAGTTAAAGAGGGAAAATTTTTCTGGAAGATCCTACTGGAACAGTCCACTAGA
CCTTAGTAAAGCTCAGTTCCATAGTGGTTTATACACAGAGGCATGCTTTGTCTTAGCAGAAGGTTGGTTTGAAGA
TCAAGTGTTTCATGTCAATGCCTTTGGATTTCCACCCACTGAGCCCTCTAGTACTACTAGGGCATACTATGGA
TATTAATTTTTTTGGAGGTCCTTCTAATACATCTGTGAAGACTTCTGCAAACTAAAACAGCTAGAAGAGGAGAA
TAAAGATGCTATGTTTGTGTTTTATCTGATGTTTGGTTGGACCAGGTGGAAGTATTGAAAAACTTCGCATAAT
GTTTGCTGGTTATTACCAGCACCTCCAACCTGCTTTATTCTGTGTGGTAATTTTTCATCTGCACCATATGGA
AAATCAAGTTCAAGCTTTGAAAGATTCCCTAAAAAATTTGGCAGATATAATATGTGAATACCCAGATATTCACCA
AAGTCGTTTTGTGTTTGTACCTGGTCCAGAGGATCCTGGATTTGGTTCCATCTTACCAAGGCCACCACTTGCTGA
AAGCATCACTAATGAATTCAGACAAAGGGTACCATTTTCAGTTTTTACTACTAATCCTTGCAGAATTCAGTACTG
TACACAGGAAATTAAGTCTTCCGTGAAGACTTAGTAAATAAAATGTGCAGAACTGCGTCCGTTTTCTTAGCAG
CAATTTGGCTATTCCCTAATCACTTTGTAAAGACTATCTTATCCCAAGGACATCTGACTCCCTTACCTCTTTATGT
CTGCCCAGTGTATTGGGCATATGACTATGCTTTGAGAGTGTATCCTGTGCCCGATCTACTTGTGATTGCAGACAA
ATATGATCCTTTCACTACGACAAATACCGAATGCCTCTGCATAAACCCCTGGCTCTTTTCCAAGAAGTGGATTTTC
ATTCAAAGTTTTTTATCCTTCTAATAAGACAGTAGAAGATAGCAAACCTTCAAGGCTTTTGAGATTCTTAAAGATC
ATCTGAAGAAAATTCATCAGTTTTCTGCTTAACTCTATATCTTATGTGATTCTGATATTACAATAAAATATGGT
AAACTTT

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FIGURE 442

MAPERLRSRAPSAFKLRGLLLRGEAIKYLTEALQSISELELEDKLEKIINAVEKQPLSSNMIERSVVEAAVQECS
QSVDETIEHVFNIIGAFDIPRFVYNSEKFLPLLMTNHPAPNLFGTPRDKAEMFRERYTILHQTRHELFTPP
VIGSHPDESGSKFQLKTIETLLGSTTKIGDAIVLGMITQLKEGKFFLEDPTGTVQLDLSKAQFHSGLYTEACFVL
AEGWFEDQVFHVNAFGFPPTEPSSTTRAYYGNINFFGGPSNTSVKTSAKLKQLEEENKDAMFVFLSDVWLDQVEV
LEKLRFAGYSPAPPTCFILCGNFSSAPYGNQVQALKDSLKTLADIICEYPDIIHQSRFVFPVPEDPGFGSIL
PRPPLAESITNEFRQRPFSVFTTNPCRIQYCTQEITVFREDLVNKMCRNCVRFPSSNLAI PNHFVKTILSQGHL
TPLPLYVCPVYWAYDYALRVYPVPDLLVIADKYDPFTTNTECLCINPGSFPRSGFSFKVFYPSNKTVEDSKLQG
F

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FIGURE 443

GCGGCTCTCTGATCCAGCCCCGGGAGAGGACCGAGCTGGAGGAGCTGGGTGTGGGGTGCGTTGGGCTGGTGGGGAG
GCCTAGTTTGGGTGCAAGTAGGTCTGATTGAGCTTGTGTTGTGCTGAAGGGACAGCCCTGGGTCTAGGGGAGAGA
GTCCCTGAGTGTGAGACCCGCCCTTCCCCGGTCCCAGCCCCTCCAGTTCCCCCAGGGACGGCCACTTCCTGGTCC
CCGACGCAACCATGGCTGAAGAACAACCGCAGGTGCAATTGTTCTGTGAAGGCTGGCAGTGATGGGGCCAAGATTG
GGAAGTGGCCATTCTCCCAGAGACTGTTTCATGGTACTGTGGCTCAAGGGAGTCACCTTCAATGTTACCACCGTTG
ACACCAAAAAGGCGGACCGAGACAGTGCAGAAGCTGTGCCCAGGGGGGCAGCTCCCATTCTGCTGTATGGCACTG
AAGTGCACACAGACACCAACAAGATTGAGGAATTTCTGGAGGCAGTGCTGTGCCCTCCCAGGTACCCCAAGCTGG
CAGCTCTGAACCCTGAGTCCAACACAGCTGGGCTGGACATATTTGCCAAATTTTCTGCCTACATCAAGAATTCAA
ACCCAGCACTCAATGACAATCTGGAGAAGGGACTCCTGAAAGCCCTGAAGGTTTTAGACAATTACTTAACATCCC
CCCTCCCAGAAGAAGTGGATGAAACCAGTGCTGAAGATGAAGGTGTCTCTCAGAGGAAGTTTTTGGATGGCAACG
AGCTCACCTTGGCTGACTGCAACCTGTTGCCAAAGTTACACATAGTACAGGTGGTGTGTAAGAAGTACCGGGGAT
TCACCATCCCCGAGGCCTTCCGGGGAGTGCATCGGTACTTGAGCAATGCCTACGCCCGGGAAGAATTCGCTTCCA
CCTGTCCAGATGATGAGGAGATCGAGCTCGCCTATGAGCAAGTGGCAAAGGCCCTCAATAAGCCCCCTCCTGGGA
CTCCCTCAACCCCTCCATTTTCTCCACAAAGGCCCTGGTGGTTTCCACATTGCTACCCAATGGACACACTCCAA
AATGGCCAGTGGGCAGGGAATCCTGGAGCACTTGTTCGGGATGGTGTGGTGAAGAGGGGATGAGGGAAAGAAA
TGGGGGGCCTGGGTGAGATTTTTATTGTGGGGTGGGGTGAGTAGGACAACATATTTAGTAATAAAATACAGAAT
AAAAATCAAGTGTTTTTAAAAAAA

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FIGURE 444

MAEEQPQVELFVKAGSDGAKIGNCPFSQRLFMVLWLKGVTFNVTTVDTKRRTETVQKLCPPGGQLPFLLYGTEVHT
DTNKIEEFLEAVLCPPRYPKLAALNPESNTAGLDIFAKFSAYIKNSNPALNDNLEKGLLKALKVLDNYLTSPLPE
EVDETSAEDEGVSRKFLLDGNELTLADCNLLPKLHIVQVVCKKYRGFTIPEAFRGVHRYLSNAYAREEFASCPD
DEEIELAYEQVAKALK

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FIGURE 445

GATATCAATTCCGCCGGGAAGTGGAGGAAGGAGACCCTGGCTTCGCAGGGGCCCCGGCTGGGGCAGAGGCGAGGG
GCCTGGGGGGGCGCTGGCTTTGGCCCCGCTGGGGCAGGATGGIGAATCTGGAGTCCATGCACACAGATATCAAG
ATGAGTGGGGATGTAGCCGATTCCACGGATGCTCGCAGCACTCTCAGCCAGGTGGAGCCAGGAAATGATCGAAAT
GGCCTAGATTTCAACAGGCAGATTAAACCGAAGATCTCAGTGACTCCCTGCAGCAGACCCTCTCCCATCGGCCA
TGCCACCTGAGTCAAGGACCTGCCATGATGTCCGGAACCAAATGTCTGGGCTAAATGCCAGCCCATGTCAGGAC
ATGGCTTCCCTCCATCCGCTCCAGCAGCTTGTGCTGGTTCCCGGCCACTTACAGTCTGTATCCCAGTTCCTGCTA
TCTCAGACCCAGCCTGGGCAGCAAGGTCTGCAGCCAAATCTCCTCCCTTTCCACAGCAACAAAGCGGTCTCCTC
CTCCACAGACTGGGCCGGGACTGGCATCCCAGGCATTTGGGCGCCCTGGGCTGCCAGGATCCTCTTTAGAAGCC
CACCTGGAAGCATCCCAGCATCTCCAGTGCCCAAGCATCTACCCAGCTCTGGAGGGGCCGATGAGCCCAGTGAC
CTCGAGGAGCTGGAGAAGTTTGCCAAGACCTTCAAGCAGAGGCGCATTAGCTGGGCTTCACACAGGGAGATGTG
GGGCTGGCGATGGGAAAGCTGTATGGCAACGACTTCAGCCAGACCACCATCTCACGATTTGAGGCCCTCAACCTG
AGCTTCAAGAACATGTGCAAGCTCAAGCCCCTGCTGGAGAAGTGGCTGAATGATGCAGAGTCCTCTCCGTCAGAC
CCCTCAGTGAGCACGCCCAGCTCCTACCCAGCCTCAGTGAAGTATTTGGTAGGAAGAGAAAGAAACGGACCAGC
ATCGAGACCAACATCCGCCTGACTCTGGAGAAGAGGTTTCAAGATAACCCAAAACCCAGCTCGGAGGAGATCTCC
ATGATTGCAGAGCAGTTGTCCATGGAGAAGGAGGTGGTGAGGGTCTGGTTCTGCAACCGACGCCAAAAGGAGAAG
CGAATCAACTGCCCTGTGGCCACACCCATCAAACACCTGACTACAACCTCCCGGCTGGTATCTCCCTCAGGGTCT
CTGGGCCCCCTCTCTGTCCCTCCTGTCCACAGTACCATGCCTGGAACAGTAACGTATCTCTCCCTGGGAAC
AACAGCAGGCCTTCACTCTCCTGGCTCAGGACTCCACGCCAGCAGCCCCACTGCATCTCAAAATAACTCCAAAGCA
GCAGTGAACCTCCGCCTCCAGTTTTAACTCTTCAGGATCTTGGTACCGATGGAATCATTCCACCTACCTCCACTTGA

GACCAAAAAGTTTCTCCTACTCCAGCTGGCCCTGTATTCCCCCTGGAAGGAAGGAATCATGCCTTCTATATACA
GACAGATTGCCTTCAGAAGAGTGGAAGAAAATCTCCACTATCAATGAACCCAGACTCTTGTCTTCTTCAAGAGCA
AGGGCCTCCGGAGATCCAACTGTGATTGAACCAAGTGCAGACTCCTAATGCTCTGAAATACACAGCCCCCTCCT
AGGAGCTTACCATTTTACCTTCCTTGCCTATGCCCTTGCCCTTCTAGTTCCAAATATTTTAGCCAGCTTCACTGT
GGCAATAGTCTTTCAGAGAAAAGACTTCTTGCTGTATTCTCCAACCTCATCCGTGGGCTTCTGGGGACAGCCATT
TGGCTGGGGTGCCAAACACCAGAAGGGGAGATAATAGTTTGTACTCTGAACTTGGCCACAACCCCTGAACTGATC
CCAAAATCTGTGAAAAGATTGAATCTGATATCTCCACCAAAGCCTTGATGTTTTCTCTGTACAGCTAAGTTTTTC
TGATGGAATCTTCATCTCACCCATTTTCTTTTAACTCGCCCCCTTTTCTACAATCAAATCCATTCAATTATTG
CGCCCTCCAGGTCCCTCCTTTTTTGAGAAGGTGTAAAAGAGCTGCCCTTGGTGGGTGCCCTGGGCATGTTGCAA
CGCCTGCTGGTGCCCTTCTGTCTGTCCACGCTGCCTAGGGCTCAGGAGTGCTTGTCTTTCCCTTCTCCTGT
GTTTCTCTTTATCCTGTCCCTCTCCTTTCTCCTGGCAGCAGAAAAGGAAGAACAAGAGCAAACACACAACAA
TGATGGTGGCAAAGTACCTGTATATAGCCCTTTCCATTTTTTGCATTATGTTCTTAACCTCCTTAATGTGAATT
TTCCAGCGAAATGTTTAACTCAGGTGTGATTTTTG

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FIGURE 446

MVNLESMHTDIKMSGDVADSTDARSTLSQVEPGNDRNGLDFNRQIKTEDLSDSLQQTLSHRPCHLSQGPAMMSGN
QMSGNLNASPCQDMASLHPLQQLVLVPGHLQSVSQFLLSQTQPGQQGLQPNLLPFPQQQSGLLLPQTGPGLASQAF
GRPGLPGSSLEPHLEASQHLFVPKHLPSGGADEP SDLEEELEKFAKTFKQRRIKLGFTQGDVGLAMGKLYGNDFS
QTTISRFEALNLSFKNMCKLKPLLEKWLNDAESSP SDPSVSTPSSYPSLSEVFGRKRKKRTSIETNIRLTLEKRF
QDNPKPSSEEISMIAEQLSMEKEVVRVWFCNRRQKEKRINCPVATPIKPPDYNRLVSPSGSLGPLSVPPVHSTM
PGTVTSSCSPGNNSRPSSPGSLHASSPTASQNNKAAVNSASSFNSSGWSYRWNHSTYLH

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FIGURE 447

CAGGAAGGATTTCAGACAACCTCTGCCTGGGAGTGAGGGCTCTGCTCAGCGGCCTAGACCTGGGCACAACGGAGCAG
GCCACTCCGTTTCTCATCACAGACCTGAAGGCAGATGGCCTGGGCGTCGGGCTTCTCTGCTCTCTGGCGGGGCG
ATTTTCACGGTCACCAGGCTGCGGACAGGCTGTGGGGTGGCGGGCGGTCCAAAGCCACCGCTTCACGTAGGCCA
GGGAGCCTTGGAGAAATCAGGCCTGATGTTGCTCAGCAGCGGCAGCCTGTTGGGAAAGCACCTCCAGGCCTCGG
GGACCATCTCTCTCAGGACGCGGATGCGGGCGGGGACCATCTCTCTCTGGATGCAGATGCGGGGTGTAGTCCCAGC
TGGGAGGAGTGGTGCGGAGGGGCCGATGCGGACCCAGTGCTTCTGTGGAAGTAGGTGACCTTGCAGTTCTCCT
GGACCTGGGAGCTGAGGAAGGGCCTGGACTGCAGAACCCAGTGCTTTTGGGCGGGGCGCAGCTTTCTGGCAAGCG
GCTTGGGCCTTCCAGTAGACACTGGGCTGCCAGAAGTTTCCGAAATCTGCGGTCAAGGCCAGAGATCAAATGTCA
GGGCTCAGTGACTAGCGACGGTTGGCATCAAAATGTTGGAAAGTGCACAAGGCGCCGTGTGCCAGGTACGGTCTG
TCCACCAACTGTTGTCATGGGGCAGGAGGCCACGGCCAGGCCACAGCTTTGCCGCGCGCAGCTGCAGAAGGGGCAA
GTAGCGCCCCATGCTGTCTGAGGACCAAGGAGGCTCAAGCCTGTCTCTTCCACTCATGGTCCCAGACACTTAGC
TCTGGGCAGAGGGGCCCTGGCAGCTGTCTCTGCTTTTGTACCTGACCTTTAAAGGCAGAACATAGAAGAATTTCTG
CCAGGTCTTGAAACTGCAGATACCTGTTGACAGAAGGGTGCTCTCTTTGATCAGTGTGAAAATGATCACAATAC
ACTTGGAGGCTCTTTTAAGGAAAAACAAATCATTGCTCATATTTCGTCTAGGATGACTGTTAATATCACTTTTTG
CAATTTTGCTCTTAAGAAAACGGTGAAAGCCATCAGGATTTATGTTTTAGTACCTGTAATGCTGATTTTATGTTG
ACCCTCATAATTTTCAGTGTTACACAGCCATATAACATAATCTTCTCTAAACACTAATGCCATTTCTGTCCTT
TCATTTCTATTGGTAATCCTGGAGTAGAGTGAGGCACATTTTCCACTAATAGCTGAAAAGATCTAAGTTCAAAAA
CAAAGAATCCAAAGGCTGCTTAGTAAGTGTAGTGCCCTAAGTTTAGAGTCTGTTCAAGGTGGTGTGAAAAGTTTTT
TGGGGGGGGGCATTTCCCTCAAAAGCACGTGGAGAAGGAACCTATTGACCCTCTGGAATGCCAGAATCGGGAAG
AGACAAAAAAGTCGCAACCAATTGAAGATTGGGCAATAGATTTGGCCCAGACTGAGGCAGATGGGTGAATAGTAA
AAACAATAATTTGGAAAAACCCATGAAGGTAACCTAACGAAGGAAAAAATAAGAGAATGAAAAGTATTTGCCTCT
GGAAAGAACAACTGGCAGGACTGTTGTTTTTCATTGTAAGACTTTTGGAGCCATTTAATTGTACTTAACCATTTTC
ATCTATTTCTTTAATAAGAACAATTCCATCTTAATAAAGAGTTACACTTGTTAATAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAGCG

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FIGURE 448

MAWASGFLCSLAGRFSRSPGCGQAVGVAGGPKPPLHVGQGSIGEIRPDVAQQRQPVGKAPPGLGDHLSQDADAGG
DHLSLDADAGVVPAGRSGAEGPDADPVLPEVVGDLAVLLDLGAEEGPGLQNPVLLGGAQLSGKRLGPSSRHWAAR
SFRNLRSRPEIKCQGSVTS DGWHQNVGKCTRRRVP GTVCPPTVAWGRRPRPGHSFAARSCRRGK

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FIGURE 449

ACCACCCAGTGAAACCCACAGAACCATGTACACCCTCTAAGTCCCGAAGTGCCAGCTCAGAGGAGGCCTCAGAG
TCACCTACAGCCCGGCAGATCCCCCAGAGGCACGTGGCTCATAGTGAACAAAAATGCTGGTGAGACCCTCCTG
CAGAGGGCGGCGCGTCTTGGCTATAAGGATGTTGTTCTCTACTGCCTCCAGAAAGACAGTGAAGATGTGAATCAC
CGTGACAATGCTGGCTACACAGCCCTGCATGAGGCTTGTTCGGGGCTGGACCGACATCCTGAACATCCTGCTG
GAGCAGGGGGCCAACTGAACTGCAGTGGCAGGACGGCACGAGGCCAGTTCATGATGCGGTGGTCAATGACAAC
CTGGAGACCATCTGGCTCCTGCTGTCTATGGGGCCGATCCACACTGGCTACCTACTCGGGTCAGACAGCCATG

AAGCTGGCCAGCAGCGACACCATGAAGCGCTTTCTCAGTGATCACCTCTCGGATCTTCAGGGCCGGGCAGAGGGT
GATCCCGGTGTATCCTGGGATTTTACAGCAGTTCTGTGTTGGAGGAAAAAGACGGGTTTGCTGTGACCTCCTA
CATAATCCTCCTGGGAGCTCAGATCAAGAAGGAGACGATCCGATGGAGGAGGATGATTTTCATGTTGAACCTCTCA
GACAAGCCTCTTCTCCCTTGCTACAACCTCCAAGTGTGAGTGTCCCGGGGCCCTGCAACTGGTTCTCTTTTCC
GATGTCTTGAAGAGGCTGAAGCTTCTCTGAGGATCTTTCAGGCCCGGTTCCCGCACTTTGAAATCACCACCATG
CCCAAGGCCGAGTTCTACAGGCAGGTGGCCTCCAGTCAGCTGCTGACCCCTGCCGAGAGGCCCTGGAGGCTTGGAC
GACAGATCCCCCAGGCTCCTCTGAGACTGTGGAGCTGGTGGGTACGAGCCAGACCTACTTCGGCTCCTAGGG
TCCGAGGTGGAATTCCAGTCTTGCAACAGTTCAGCCGGGAAAAACAGCCCTCCTCTTCTTTCTCCTTCCGAGTTCCG
CCCTTCCCCACCTCCTTGTCTTTCCCGACCGAGCACCAGACTGCAGAATGAGGCAATAATACGGACCAACAAG
AAGCCGCCTTATCAATGCCAGCATTAGCGACTGGAAGTGTGTTTTGTTTTTGGTTACAATTAGTTCTCATCTCCC
TGTCGTCGTCATTGTTATCGTGGTGTCTGATGGGGGTGGAAGTTGAACTCCATGTCTGAGGACAAGAGGTCCCG
GGGGTGGTGGGAGGTGGCGCCGGGGTCCCTTGGACTGGCCTCCTTGTTCATGACCAAGACCAACCTGGGCCCTG
GATGGCCTTGGCCTGTCCCGAGGAGAAATGAGAAAATCCAGATCTCTGAGCGCCCCCAACTCCATTCCCCTGT
GTTCTTCTGTCTTCTGTAGTATTTATTTTATTAGTATTTAATTTGTATTGTTTCATTGGTTTCTGATAAGTCTGT
ATCACTGTGACGATTTGAGACAACCTGTTGTATTGAGGGACTTTCTGTACCTCCTTTTCTTTTCTTTGTTGATG
AGCTCTGACAAAGCTATTCCCTGGTGTGTTTTTCCCCACTGGGGAGGGGGTGAGGTGGAATGGGTGGGGGAAC
ATGGACTTGTGACTAACGAAGCTGGTTGCTGCTGGCCAGGGCTGGGGGCTTGGGGGTAAATCCTGAGGCTTTGG
TGCTCCCCCACCACCCATTCCCGCCCTTTGCAGCAGCCCCGCTATCTTGAGATTAGTGTGACAGGGAGGGGAG
GATTGTGAGGTGAGGGGTTAATAAGTTACTCTAATAAGGAGCGTGGAGAAGGGATCTGAGGGGTGAGGGTGGCC
CCCCTCCTCACGCCCTTCTTCACTGCCCCCTCAGAGTGCACAATACGAGTTTGTTCCTGCCTCCACTCTCCCACC
CCGTTCTGGCCTCCCTGTCTCAAGATACTGAGCCTCTACCTCCCAGCCCTCAGCCACCCCCATCCCTGCCCTT
CTGAGACTCACAGCACCCTTTCTTCTCTCTCCACCTCCTCCCTCAGCCCTCATTTCTCCTTGGGAATCTG
CAGAGGGCTCTGGGACTCACTGCCGATGTGAAATCCAGGCGTCAGCTGTTTGCTAGGCAAGGGCAGGAAAGTGG
TCTCCAGCCCTTGCTCCACTCATGCCTGGGGGCTGGGGCTGAGTGGTATCCCTACCTGGCCTCCCCCTGGCCTC
TGGGCCTCCAGCGCTGGGTTTGTGAGTGAGAGAGAGAGAGGAGCTTGGGTGCTTCCCTGTCCCCGCCCTCT
GTGGCATTGTCCCTCCCACTCTTATTTTTCTACCAATTGCTATTTTTCCGAACAATCCTGTAGAGTATGTACCA
TCCAAAGGCAGGAGGGCTCGCCGTGGCCGGCTCTGGTTGGAGATGGTACAGTTTTATTGTACAGGTGCTAAAC
AACACAACAACAAAAAGAAAATGG

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FIGURE 450

MKLASSDTMKRFLSDHLSDLQGRAEGDPGVSWDFYSSSVLEEKDGFACDLLHNPPGSSDQEGDDPMEEDDFMFEL
SDKPLLPCYNLQVSVSRGPCNWFLFSDVLKRLKLSRIFQARFPHFEITTMPKAEFYRQVASSQLLTPAERPGGL
DDRSPPGSSETVELVRYEPDLLRLLGSEVEFQSCNS

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FIGURE 451

ATCGAATAGGAGCCATCCGAGACAACCTGAGTGAAACGGCCAGCACCATGGCACTAGCTGGAGCCAGTATAACGG
GGAGTCTGTCAGGAAGTGCCATGGTAACTGTTTTAACAGGTTGGAAGTACAAGCAGATGTACAGAAAGAACGGT
ACAGTCTAAGTGGAGAATCTGGCACAGTCAGCTTGGGAACAGTTAGTGATAATGCCAGCACCAAAGCAATGGCAG
GATCCATTCTGAATTCCTACATCCCATTGGACAAAAGGCAACAGTATGGAGGTGCAAGTAGATATTGAGTCAA
AGCCATCCAAATTCAGGCACAACAGTGAAGCAGTAGTGTGGATGATGGCAGTGCCACCCGAAGTCATGCTGGCG
GTTTCATCCAGTGGCTTGCCTGAAGGTAAATCTAGTGCCACCAAGTGGTCCAAAGAAGCAACAGCAGGGAAAAAAT
CAAAAAGTGGTAACTGAGGAAAAAGGTAACATGAAGATAAATGAGACGAGAGAGGACATGGATGCACAGTTGT
TAGAACACAAAGCACGAACTCAAGTGAATTTGAGGCTCCATCCCTCAGTGACAGTATGCCTTCTGTAGCAGATT
CTCACTCTAGTCATTTTTCTGAATTTAGTTGTTCTGACCTAGAAAGCATGAAAACCTTCTTGTAGTCATGGTTCCA
GTGATTATCACACCCGCTTTGCTACTGTTAACATTCTTCTGAGGTAGAAAATGACCGTCTGGAAAATTCCCCAC
ATCAGTGTAGCATTCTGTGGTTACCCAACTGCTTCTGTTTCAAGTTTCACAGTTGAATCATATTGCTGAAG
AACATGGTAACAATGGAATAAAACCTAATGTTGATTTATATTTTGGCGATGCACTAAAAGAAAACAAATAACAACC
ACTCACATCAGACAATGGAATTAAGTTGCAATTGAGTGAATTTAGGCCATAAATGCTGCAGAATAATTA
CCACTGTACAACCGTGTGTTGAGCTGGTTGAACTACATGTGACTACTTAAGTTTCAGGTTACCAGCAAAAGCCGG
GTTTCATTATCATAATGCAGATACATTTCTGTGTTGAGCAAGGCATTGTGTGTCATGTGGATCTTAGTTACCAA
ACTATGAAGTGAAGGCTTTAAAAGTGCATTATTTTAAGGATAATAAATTTGAAGAGCAAAGCATGTTTTGTGTGT
TTGCCACAAAACATTGCTTGAAGCACATACTTAGATAGAAATGGTCTTAATTTATATAATCAATATAAAATACT
AATGCAATTCTACAGCATTCAAATGAAGAAAACCTGAGGCTTTAGGGATAAGTGGTTAGTGATATTTTATTGAAA
CCACTAAAGAGATAAGTTTAAAAGAACTGCATAGGTTACTCTCAGTATATGATACTCTGTAACATTTCTATTTAT
ATCGGCATAAATTTCATTTTTTTTCTTCATATGCAATGTGGTTATATAAAGCTTAATGCAGCTCATTGCTACCA
TTTGGATACTTAGACACTTTGAGCAAGATTGTGGCAGTTTTTGCACACTTTGAAATAGAAATACCTGGTACTCT
ATCTTGTTTTATTGTTGATGCCATCTTAGAGGAAAAAATGTAAAGGTAAGTAATTAAGCATATGACAGCAACAAAT
AAGATACATAAACTACAAAATAAAGTCCCATTAGGTTATAAGTATTACAAAAATCCACCTTTCTCTAAGGGGA
AGTTTGTACCCCATTGATTCTTGGTGCCTTTGGGATCGACTGGGTTTTAATGGCCTAGTTATTTGAGGATTTTGC
TGTGTTGTTTTCCATGTCTTCTGCTCACCTTGGATTATATAAAAAATACAGGAAATAGATAAACATGAATGT
GATTAATAATGCTGAAAAAGTATTAGCCTACCAAAGACACACTCAGGCTTTAGTGAATAACTTTACATAACCTCA
GTTTTTAACACATGCATATCTTCTCAACCATGAAATCAAAGCACGGTGCAGAACTTGTACCAAGTACAAAAGGT
CCATGTATGATTAGCATTATTTCTTTGCTTTTGTGTTATGGACAATGTTTCAAGCTGACATAAGCAGAAGTTGGCC
AAAATACTGCCTGTACTGTTAATTTCTGTATAATTCACTTAAATAAAAGCAGGTTAACCTCAATGATAGCAGTT
AAAATGTTCTATCTTATGTATTTCTTTTAAGT

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FIGURE 452

RIGAIRDNLSETASTMALAGASITGSLSGSAMVNCFNRLVQADVQKERYSLSGESGTVSLGTVSDNASTKAMAG
SILNSYIPLDKEGNSMEVQVDIESKPSKFRHNSGSSSVDDGSATRSHAGGSSSGLPEGKSSATKWSKEATAGKKS
KSGKLRKKGNMKINETREDMDAQLLEQQSTNSSEFEAPSLSDSMPSVADSHSSHFESEFSCSDLESMKTSCHGSS
DYHTRFATVNILPEVENDRENSPHQCSISVVTQTASCSEVSQNLNHIAEEHGNGIKPNVDLYFGDALKETNNNH
SHQTMELKVAIQTEI

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FIGURE 453

CACGAGGCCGCGGGGGCAAGGCCTGGAGCTGTGGTTCGAATTTGTGCAGGCAGCGGGTGCTGGCTTTTAGGGTCC
GCCGCCTCTCTGCCTAATGAGCTGCACCAGAATGATCCAGGTTTTAGATCCACGTCCTTTGACAAGTTCGGTCAT
GCCCGTGGATGTGGCCATGAGGCTTTGCTTGGCACATTACACACCTGTGAAGAGTTTCCTGGGCCCCGTACGATGA
ATTTCAACGACGACATTTTGTGAATAAAATTAAAGCCCCCTGAAATCATGTCTCAATATAAAACACAAAGCCAAATC
ACAGAATGACTGGAAGTGCTCACACAACCAAGCCAAGAAGCGCGTTGTGTTTGCTGACTCCAAGGGCCTCTCTCT
CACTGCGATCCATGTCTTCTCCGACCTCCCAGAAGAACCAGCGTGGGATCTGCAGTTTGATCTCTTGGACCTTAA
TGATATCTCCTCTGCCTTAAACACCACGAGGAGAAAACTTGATTTTAGATTTCCCTCAACCTTCAACCGATTA
CTTAAGTTTCCGGAGCCACTTTTCAAGAAGAACTTTGCTGTCTGGAGAAGTCTCATTGCAAGAGCGAACAGTGAC
AGGGACTGTAAAGTCAAAAATGTGAGTTTGGAGAAGAAAGTTCAGATCCGTATCACTTTTCGATTCTTGGAAAAA
CTACACTGACGTAGACTGTGTCTATATGAAAAATGTGTATGGTGGCACAGATAGTGATACCTTCTCATTGCCCAT
TGACTTACCCCTGTCAATTCCAAGTACGAGAGAAAATTGAGTTCTGCATTTCTTACCATGCTAATGGGCAAGTCTT
TTGGGACAACAATGATGGTCAGAAATTATAGAATTGTTTCATGTTCAATGGAAGCCTGATGGGGTGCAGACACAGAT
GGCACCCAGGACTGTGCATTCCACCAGACGTCTCCTAAGACAGAGTTAGAGTCAACAATCTTTGGCAGTCCGAG
GCTGGCTAGTGGGCTCTTCCAGAGTGGCAGAGCTGGGGGAGAATGGAGAAGTGGCCTCTTATCGATGAATTAA
GCAACAATGTAAGTGGTCTTGACTTGTCAATTTCCCCCATGCAATCCTAGGTCTGTATTGCTCAATTTTAGGAAG
CCTTTGCTACTCCATCAGTAGGTTTAGATTTGA

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FIGURE 454

MSCTRMICVLDPRPLTSSVMPVDVAMRLCLAHSPPVKSFLGPYDEFQRRHFVNKLKPLKSCLNKHKAKSQNDWK
CSHNQAKKRVPFADSKGLSLTAIHVFSDLPEEPAWDLQFDLLDLNDISSALKHHEEKNLILDFPQPSTDYLSFRS
HFQKNFVCLENCILQERTVTGTVKKNVSFEKKVQIRITFDSWKNYTDVDCVYMKNVYGGTSDTFSFAIDLPPV
IPTEQKIEFCISYHANGQVFWDDNDGQNYRIVHVQWKPDGVQTQMAPQDCAFHQTSPKTELESTIFGSPRLASGL
FPEWQSWGRMENLASR

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FIGURE 455A

CGACTCCTTAGAGCATGGCATGGCTCAGAGGTGCTGGTAAACTGATGGGGGTTTTTGCTGTCCCTCCCCTCAGC
GCCGACACC**AT**TGGATCCAGGTTCCGACCATGGACGGGAGGCAGACCCACACGGTGGACTCGCTGTCCAGGCTG
ACCAAGGTGGAGGAGCTGAGGCGGAAGATCCAGGAGCTGTTCCACGTGGAGCCAGGCCTGCAGAGGCTGTCTAC
AGGGGCAAACAGATGGAGGACGGCCATACCTCTTCGACTACGAGGTCCGCTGAATGACACCATCCAGCTCCTG
GTCCGCCAGAGCCTCGTGCTCCCCACAGCACCAAGGAGCGGGACTCCGAGCTCTCCGACACCGACTCCGGCTGC
TGCCTGGGCCAGAGTGAGTCAGACAAGTCTCCACCCACGGCGAGGCGGCCGCCGAGACTGACAGCAGGCCAGCC
GATGAGGACATGTGGGATGAGACGGAATTGGGGCTGTACAAGGTCAATGAGTACGTGATGCTCGGGACACGAAC
ATGGGGGCGTGTTTGGAGGCGAGGTGGTCAGGGTGACGCGGAAGGCCCTCCCGGGACGAGCCCTGCAGCTCC
ACGTCCAGGCCGCGCTGGAGGAGGACGTCAATTAACACGTGAAATACGACGACTACCCGGAGAAGCGCGTGCTC
CAGATGAACTCCAGGGACGTCCGAGCGCGCCCGCACCATCATCAAGTGGCAGGACCTGGAGGTGGGCCAGGTG
GTATGCTCAACTACAACCCGACAACCCCAAGGAGCGGGGCTTCTGGTACGACGCGGAGATCTCCAGGAAGCGC
GAGACCAGGACGGCGCGGGAACCTCTACGCCAACGTGGTGCTGGGGGATGATTCTCTGAACGACTGTCCGATCATC
TTCGTGGACGAAGTCTTCAAGATTGAGCGGCCGGGTGAAGGGAGCCCCATGGTTGACAACCCCATGAGACGGAAG
AGCGGGCCGTCTGCAAGCACTGCAAGGACGACGTGAACAGACTCTGCCGGGTCTGCGCCTGCCACCTGTGCGGG
GGCCGGCAGGACCCCGACAAGCAGCTCATGTGCGATGAGTGCGACATGGCCTCCACATCTACTGCCTGGACCCG
CCCCTCAGCAGTGTTCCAGCGAGGACGAGTGGTACTGCCCTGAGTGCCGGAATGATGCCAGCGAGGTGGTACTG
GCGGGAGAGCGGCTGAGAGAGAGCAAGAAGAAGCGGAAGATGGCCTCGGCCACATCGTCTCACAGCGGGACTGG
GGCAAGGGCATGGCCTGTGTGGGCCGCACCAAGGAATGTACCATCGTCCCGTCCAACCACTACGGACCCATCCCG
GGGATCCCCGTGGGCACCATGTGGCGGTTCCGAGTCCAGGTCCAGGTCCAGCGAGTCGGGTGTCCATCGGCCCCACGTGGCT
GGCATAACAGGCCCGAGCAACGACGAGCGTACTCCCTAGTCTGGCGGGGGGCTATGAGGATGACGTGGACCAT
GGGAATTTTTTACATACACGGGTAGTGGTGGTTCGAGATCTTTCCGGCAACAAGAGGACCGCGGAACAGTCTTGT
GATCAGAACTCACCAACACCAACAGGGCGCTGGCTCTCAACTGCTTTGCTCCCATCAATGACCAAGAAGGGGCC
GAGGCCAAGGACTGGCGGTGGGGGAAGCCGGTCAGGGTGGTGGCAATGTCAAGGGTGGCAAGAATAGCAAGTAC
GCCCCGCTGAGGGCAACCGCTACGATGGCATCTACAAGTTGTGAAATACTGGCCCGAGAAGGGGAAGTCCGGG
TTTCTCGTGTGGCGCTACCTTCTGCGGAGGGACGATGATGAGCCTGGCCCTTGGACGAAGGAGGGGAAGGACCGG
ATCAAGAAGCTGGGGTGACCATGCAGTATCCAGAAGGCTACCTGGAAGCCCTGGCCAACCGAGAGCGAGAGAAG
GAGAACAGCAAGAGGGAGGAGGAGGAGCAGCAGGAGGGGGGCTTCGCGTCCCCAGGACGGGCAAGGGCAAGTGG
AAGCGGAAGTCGGCAGGAGGTGGCCCGAGCAGGGCCGGGTCCCCGCGCCGACATCCAAGAAAACCAAGGTGGAG
CCCTACAGTCTCACGGCCAGCAGAGCAGCCTCATCAGAGAGGACAAGAGCAACGCCAAGCTGTGGAATGAGGTC
CTGGCGTCACTCAAGGACCGGCCGGCGAGCGGCAGCCCGTTCCAGTTGTTCTGAGTAAAGTGGAGGAGACGTTT
CAGTGATCTGCTGTGTCAGGAGCTGGTGTTCGGGCCATCACGACCGTGTGCCAGCACACGTGTGCAAGGACTGC
CTGGACAGATCCTTTCCGGCACAGGTGTTTCAGCTGCCCTGCCTGCCGCTACGACCTGGGCCGAGCTATGCCATG
CAGGTGAACCAGCCTCTGCAGACCGTCTCTCAACCAGCTCTTCCCCGGCTACGGCAATGGCCGGT**CGAT**CTCCAAGC
ACTTCTCGACAGGCGTTTTGCTGAAAACGTGTGCGAGGGCTCGTTTCATCGGCACTGATTTTGTCTTAGTGGGCT
TAACCTAAACAGGTAGTGTTCCTCCGTTCCTTAAAGGTTTGTCTTCCTTTTTTTTTTATTTTATTTTCAA
TCTATACATTTTCAGGAATTTATGTATTCTGGCTAAAAGTTGGACTTCTCAGTATTGTGTTTAGTCTTTGAAA
CATAAAAGCCTGCAATTTCTCGACAAAACAACAAGATTTTTTAAAGATGGAATCAGAACTACGTGGTGTGGA
GGCTGTTGATGTTTCTGGTGTCAAGTTCTCAGAAGTTGCTGCCACCAACTCTTAAAGAAGGCGACAGGATCAGTC
CTTCTCTAGGGTCTGGCCCCAAGGTCCAGAGCAAGCATCTTCTGACAGCATTTTGTCTATCTAAAGTCCAGTGA
CATGGTTCCCCGTGGTGGCCCGTGGCAGCCCGTGGCATGGCGTGGCTCAGCTGTCTGTTGAAGTTGTTGCAAGGA
AAAGAGGAAACATCTCGGGCCTAGTTCAAACCTTTGCCTCAAAGCCATCCCCACCAGACTGCTTAGCGTCTGAG
ATCCGCGTGAAAAGTCTCTGCCCACGAGAGCAGGGAGTTGGGGCCACGCAGAAATGGCCTCAAGGGGACTCTGC
TCCACGTGGGGCCAGGCGTGTGACTGACGCTGTCCGACGAAGGCGGCCACGGACGGACGCCAGCACACGAAGTCA
CGTGCAAGTGCCCTTTGATTGCTTCCTTCTTTCTAAAGACGACAGTCTTTGTTGTTAGCACTGAATTATTGAAAT
GTCAACCAGATTCTAGAACTGCGGTCTATCCAGTTCTTCTGACACCGGATGGGTGCTTGGGAACCGTTTGAGCC
TTATAGATCATTTACATTCAATTTTTTTAACTCAGCAAGTGAGAACTTACAAGAGGGTTTTTTTTTAATTTTTT
TTCTCTTAATGAACACATTTTCTAAATGAATTTTTTTTGTAGTTACTGTATATGTACCAAGAAAGATATAACGTT
AGGGTTTGGTTGTTTTTGTTTTTTGTATTTTTTCTTTTGAAGGGTTTGTAAATTTTTCTAATTTTACCAAAGT

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FIGURE 455B

TTGCAGCCTATACCTCAATAAAACAGGGATATTTTAAATCACATACCTGCAGACAACTGGAGCAATGTTATTTT
TAAAGGGTTTTTTTACCTCCTTATTCTTAGATTATTAATGTATTAGGGAAGAATGAGACAATTTTGIGTAGGCT
TTTTCTAAAGTCCAGTACTTTGTCCAGATTTTAGATTCTCAGAATAAATGTTTTTCACAGATTGAAAAAAAAAAAA
AAA

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FIGURE 456

MWIVRTMDGRQTHTVDSLSRLTKVEELRRKIQELFHVEPGLQRLFYRGKQMEDGHTLFDYEVRLNDTIQLLVRQ
SLVLPHSTKERDSELSDTDSGCCLGQSESDKSSTHGEAAAETDSRPADEDMWDETELGLYKVNEYVDARDTNMGA
WFEAQVVRVTRKAPSRDEPCSSSRPALEEDVIYHVKYDDYPENGVVQMNSRDVVRARARTIIKWQDLEVGVVML
NYPDPNPKERGFWDYDAEISRKRETRTARELYANVVLGDDSLNDCRIIFVDEVFKIERPGEKSPMVDNPMRRKSGP
SCKHCKDDVNRLCRVCACHLCGGRQDPDKQLMCDECDMAFHIYCLDPPLSSVPSEDEWYCPECRNDASEVVLAGE
RLRESKKKAKMASATSSSQRDWGKGMACVGRTECTIVPSNHYGPIPGIPVGTMRFRVQVSESGVHRPHVAGIH
GRSNDGAYSLVLAGGYEDDVHGNFFTYTGSGGRDLSGNKRTAEQSCDQKLTNTNRALALNCFAPINDQEGAEAK
DWRSGKPVVRVVRNVKGGKNSKYAPAEGNRYDGIYKVVKYWPKEGKSGFLVWRYLLRRDDDEPGPWTKEGKDRIKK
LGLTMQYPEGYLEALANREREKENS KREEEEQEGGFASPRTGKWKRRKSAGGGPSRAGSPRRTSKKTKVEPYS
LTAQQSSLIREDKSNAKLWNEVLASLKDRPASGSPFQLFLSKVEETFQCICQELVFRPITTVQCQHNVCCKCLDR
SFRAQVFSCPACRYDLGRSYAMQVNQPLQTVLNQLFPGYGNGR

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FIGURE 457

CTGGGTCTGTGTGTGCCACAGGGGTGGGGTGTCCAGCGAGCGGTCTCCTCCTCCTGCTAGTGCTGCTGCGGCGT
CCCCGCGCCTCCCCGAGTCGGGCGGGAGGGGAGAGCGGGTGTGGATTTGTCTTGACGGTAATTGTTGCGTTTTCCA
CGTCTCGGAGGCCTGCGCGCTGGGTTGCTCCTTCTTCGGGAGCGAGCTGTTCCTCAGCGATCCCCTCCCAGCCGG
GGCTCCCCACACACACTGGGCTGCGTGCGTGTGGAGTGGGACCCGCGCACACGCGTGTCTCTGGACAGCTACGGC
GCCGAAAGAACTAAAATTCCAGATGGCAAACCTCAATGAATGGCAGAAACCCTGGTGGTCGAGGAGGAAATCCCCG
AAAAGGTGCAATTTTGGGTATTATTGATGCTATTCAGGATGCAGTTGGACCCCCTAAGCAAGCTGCCGAGATCG
CAGGACCGTGGAGAAGACTTGGAAGCTCATGGACAAGTGGTAAGACTGTGCCAAAATCCCAAACCTCAGTTGAA
AAATAGCCCACCATATATACTTGATATTTTGCTGATACATATCAGCATTACGACTTATATTGAGTAAATATGA
TGACAACCAGAACTTGCCCAACTCAGTGAGAATGAGTACTTTAAATCTACATTGATAGCCTTATGAAAAAGTC
AAAACGGGCAATAAGACTCTTTAAAGAAGGCAAGGAGAGAATGTATGAAGAACAGTCACAGGACAGACGAAATCT
CACAAAACCTGTCCCTTATCTTCAGTCACATGCTGGCAGAAATCAAAGCAATCTTTCCCAATGGTCAATTCCAGGG
AGATAACTTTTCGTATCACAAAAGCAGATGCTGCTGAATTCCTGGAGAAAGTTTTTTGGAGACAAAACCTATCGTACC
ATGGAAAGTATTTCAGACAGTGCCTTCATGAGGTCCACCAGATTAGCTCTAGCCTGGAAGCAATGGCTCTAAAATC
AACAATTGATTTAATTGCAATGATTACATTTTCTGATTTTGAATTTGATATTTTACCAGGCTGTTTCAGCCTTG
GGGCTCTATTTTGGCGAATTGGAATTTCTTAGCTGTGACACATCCAGGTTACATGGCATTCTCACATATGATGA
AGTTAAAGCAGACTACAGAAATATAGCACCAAACCCGGAAGCTATATTTTCCGGTTAAGTTGCACTCGATTGGG
ACAGTGGGCCATTGGCTATGTGACTGGGGATGGGAATATCTTACAGACCATACTCATAACAAGCCCTTATTTCA
AGCCCTGATTGATGGCAGCAGGGAAGGATTTATCTTATCCTGATGGGAGGAGTTATAATCCTGATTTAACTGG
ATTATGTGAACCTACACCTCATGACCATATAAAGTTACACAGGAACAATATGAATTATATTGTGAAATGGGCTC
CACTTTTCAGCTCTGTAAAGATTTGTGCAGAGAATGACAAAGATGTCAAGATTGAGCCTTGTTGGGCATTTGATGTG
CACCTCTTGCCCTTACGGCATGGCAGGAGTCGGATGGTCAGGGCTGCCCTTTCTGTCTGTTGTGAAATAAAAGGAAC
TGAGCCCATAAATCGTGGACCCCTTTGATCCAAGAGATGAAGGCTCCAGGTGTTGCAGCATCATTGACCCCTTTGG
CATGCCGATGCTAGACTTGGACGACGATGATGATCGTGAGGAGTCCTTGATGATGAATCGGTTGGCAAACGTCCG
AAAGTGCACCTGACAGGCAGAACTCACCAGTCACATCACCAGGATCCTCTCCCTTGCCCAGAGAAGAAAGCCACA
GCCTGACCCACTCCAGATCCCACATCTAAGCCTGCCACCCGTGCCTCCTCGCCTGGATCTAATTCAGAAAGGCAT
AGTTAGATCTCCCTGTGGCAGCCCAACAGGTTACCAAAGTCTTCTCCTTGATGGTGAGAAAACAAGATAAACC
ACTCCCAGCACCACTCCTCCCTTAAGAGATCCTCCTCCACCGCCACCTGAAAGACCTCCACCAATCCCACCAGA
CAATAGACTGAGTAGACACATCCATCATGTGAAAGCGTGCCTTCAGAGACCCGCCAATGCCTCTTGAAGCATG
GTGCCCTCGGGATGTGTTTGGGACTAATCAGCTTGTGGGATGTGCACTCCTAGGGGAGGGCTCTCCAAAACCTGG
AATCACAGCGAGTTCAAATGTCAATGGAAGGCACAGTAGAGTGGGCTCTGACCCAGTGCTTATGCGGAAACACAG
ACGCCATGATTTGCCTTTAGAAGGAGCTAAGGTCTTTCCAATGGTCACCTTGGAAGTGAAGAATATGATGTTCC
TCCCCGGCTTTCTCCTCCTCCTCCAGTTACCACCTCCTCCTTAGCATAAAGTGTACTGGTCCGTTAGCAAATTC
TCTTTCAGAGAAAACAAGAGACCCAGTAGAGGAAGATGATGATGAATACAAGATTCCTTCATCCCACCCTGTTTC
CCTGAATTCACAACCATCTCATTGTCATAATGTAAACCTCCTGTTTCGGTCCCTGTGATAATGGTCACTGTATGCT
GAATGGAACACATGGTCCATCTTCAGAGAAGAAATCAAACATCCCTGACTTAAGCATATATTTAAAGGGTACGTA
TAGAATATAATTTCTTTGTGATGTACATCTTAATGGTCAGAAATTTAAAGGCAAAATTCATGCCATTGTACTGA
AAATACATTAAGGTTTTGTGTTATCCTCTAGGAGATGTTTTTGAATTCAGCCTCTGATCCCGTGCCATTACCACCT
GCCAGGCCTCCAACCTCGGGACAATCCAAAGCATGGTTCTTCACTCAACAGGACGCCCTCTGATTATGATCTTCTC
ATCCCTCCATTAGGTTGAAACCTTTAAAAAGTTTTGAACAACCCACCCCTCCTTCTTTAATTTAGAAATTTTC
AGAATTCAGAGTTCAGTATAACACAGACTCACTGGGTTGTGAATTTGCCTGAAATTTGAATGGGTTCTCCAGGTG
CCGGTGACTCCCAAGTTCACGAGACCATTACTCCATGTAGATGATTAAGGTAGTAGTAGTAGTTGGGCATCAG
TCAGGTTTTAAGCAAGTTGTTTTGTCCATACTAAATGTAGTCTAAAAACACATGAGAGCTTTGTGCTCTAGTAGT
TTTGAAGTGATGACTTGAAGTGTGAGATTTCTTTAAGTATAATAATTCTTAATAAATATGAACCTTGCTTTTCT
TGCAGCATGAGCACCAGTTCCACTTACGCTAATTAATATGCAAAATTAATAGTTGTATGTAGAGAACTGATA
ATAAATCTGTTTTATTCTAATCATTACAACCTGTAACACATTCAAAAAA

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FIGURE 458

MANSMNGRNP GGRGGNPRKGRILGIIDAIQDAVGPPKQAAADRRTVEK TWKLM DKVVRLCQNP KLQLKNSPPYIL
DILPDTYQH LRLILSKYDDNQKLAQLSENEYFKIYIDSLMKKSKRAIRLFKEGKERMYYEQSQDRRNLTKLSLIF
SHMLAEIKAIFPNGQFQGDNFRIKADAAEFWRKFFGDKTIVPWKVFRQCLHEVHQISSSLEAMALKSTIDLTCN
DYISVFEFDIFTRLFQPWGSILRNWNFLAVTHPGYMAFLTYDEVKARLQKYSTKPGSYIFRLSCTRLGQWAIGYV
TGDGNILQTIPHNKPLFQALIDGSREGFYLYPDGRSYNPDLTGLCEPTPHDHIKVTQEYELYCEMGSTFQLCKI
CAENDKDVKIEPCGHLMCTSLTAWQESDGQGCFFCRCEIKGTEPIIVDPFDPDEGSRCCSIIDPFGMPMLDLD
DDDDREESLMMNRLANVRKCTDRQNSPVTSPGSSPLAQRKPQPDPLQIPHLSLPPVPPRLDLIQKGIVRSPCGS
PTGSPKSSPCMVRKQDKPLPAPPPPLRDP PPPPPPERPPP IPPDNRLSRHHHVESVPSRDPMPLEAWCPRDVFG
TNQLVGCRLLGEGSPKPGITASSNVNGRHSRVGSDPVLMRKHRRHDLPLEGAKVFSNGHLGSEEDYDVPRLSPPP
PVTLLPSIKCTGPLANSLSEKTRDPVEEDDDEYKIPSSHPVSLNSQPSHCHNVKPPVRSCDNGHCMLNGTHGPS
SEKKSNIPLDSIYLKGTYRI

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FIGURE 459

CTGCCCTGACTTCTCATATCTTGCCTAGGAACTCCAGGCTTGTCTTGGCTCCAAATGGATCCCAACTGCTCCTGC
ACCACAGGTGGCTCCTGTGCCTGCGCCGGCTCCTGCAAGTGCAAAGAGTGCAAATGTACCTCCTGCAAGAAGTGC
TGCTGCTCTTGTGCCCCGTGGGCTGTGCCAAGTGTGCCAGGGCTGTGTCTGCAAAGGCTCATCAGAGAAGTGC
CGCTGCTGTGCCTGATGTTGGGAGAGCCCTGCTCCAGACATTAAATAGAGCAACCAGTACTAACCTGGATTTTTT
TTTTAACTACCCTGACCGGTTTGCTACATTCTTTTTTCTATTCAATATGTGAAAGACAATAAACACGTTTGACT
TGAAAAAAGGCATAACATTACCTGGAAGGGATTCCCAAAAATATGAAAACCTCGGGGGCGGACCCCCCTAGTCT
ATTCAGCCCACCGGATATTTACTCCGCCGATGAAAACCGGGCCAAAAAACTTTCTCAAACTAGGGCCCGGAGAG
ACCTTGCCGTCTATCTTGGCCGAATGCTTGGCATCCAGCC

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FIGURE 460

ALTSHILPRNSRLVLAPNGSQLLHHRWLLCLRRLQVQRVQMYLLQEVLVLLLPRLCQVCPGLCLQRLIREVP
LLCLMLGEPCSQT

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FIGURE 461A

GAAGGTTGCAGTGAGCCGAGATCATGCCATTGTGCTCTACCCTGGGCAACAGAGCAAGACTCCTTCTCAAAAAA
AAAAAAAATCTAATCGTTAACTTTTCAGGAATTTTGTGAGCTGATTGTAAACATAACAGTTATTACAAATTAA
AGTATATAAATGCACAAGTACATAAATGATCATATTTAATACATCATTTTCTACTTAATACATCATTTTCTACTA
TCTGTGCACTTGAGGTTATTTGCATCTATTGGTAGAAATACTATTAATACATAATAGTGTCTGCTGCAGTATTG
ATAGAACATTACCCCATTTGTAATCAGTAAAATACAACTAGAATTTGATTTATTATTTGTTGATTAACTTAAGA
AAGTGAAGGATAGAATGTTAATGCAGATTAAATTTCAAAGTGTGATGTGTCTCTGCTAGACTAAATGCAATACAA
AAAAATTGAGGAAGTTGCTTTGCAATATTCCAAAACTCGGCCAGGCATGGTGGCTCACACCTGTAATCCCAGCAC
TTTGGGAGGCCAAGGCTGGCAGATCACTTGAGGTCAGGAGTTCGAGACCAGCCTGCCAGTATAGTGAAACCTCA
TCTCTACCAAAGATACAAAACTAGCCGGGCGTGGTGGTGCATGCCTATAGTCCCACTAATTAGCCAGGTGTCG
TGGCAGTGCCTGTAATTTTCAGCTACTTGGGAGGCAGAGACATGAGAATTGCTTGAACCCGGGAGGTGGAGTTTA
CGGTGAGCTGAGATCGCGCCACTGCACTCCAGCTTGGGTGACAGAGCGAGACTCCGTCTCAAAAAAAAATTTTT
TTTTAACTCTTCATTAGTTTCGGAAAGATGTTGATGTCATTGATGAATGAGCGAAACTCTAATATATGTCTTTAT
TGTTTTCACTTTTCATCTTATTCAATTAATGTAATTGAAAATATTATCCACCCTTCATGTTGCTACTACAGTCAGCCC
TTCATATACTGTGGGTTCCACATCCGTGGATTCCACCAACTGTAGATGGAAAATATTTTTTTAAATAATAAAAAAT
ACAATAATAAACACATTAAAAAGTAATACATTATAAAAACTTTTATGGCATTGATATTATATTAGGTATTAAAAA
TAATCTAGAAATGACCTCAAGTATAGAGGAGGATATGCAAAGGTTGAGTGCAAATACTTCATTTTATACAAGGGA
CTTGAGCATGGGAGGATTTTGGTATGGGGAGGTGCAAATAGCATACTCATTTGCGAAACATATGACCAACCATT
TGCTAATTGGATGATAATTCATAGTCAAATTTGTGAACTGTTGTTGGTTGTAGAATTTTAAAACTAATAGTG
GGTTTTTCAAGAAATAGCAAGTCATATTGATATTATAGATATAAACTGAAAATCAGGTAAATATTTAAGTTTAA
AATGTATTTCCAAAATTAGATAATCACTAAGAGAATTTTTACATTGACCCTTAAAGTGTTATGAATTTTACTTA
CATATGTAAAATTATTTTTTCAGATTCTGTTTCTTAAATGCCAAAACGACAGGGTGATTTTTTGCATTTTTTAAA
TGTGAAGAAGGTGAAAACAGACACAGAAAATAATGAAGTGAGCAAAAATCACTGCAGATTGTCTAAGGCAAGGA
ACCACATTTTCGAGTATATTGAACAACCAATCATTGAAGAAAAGCCATCACTTTCATCAAAGAAAGAAATAGATAA
TCTTGTGCTTCCAGATTGTTGGAATGAAAAACAAGCATTATGTTTACAGAACAATACAAATGGCTTGAAATAAA
AGAAGGTAAATTAGGATGTAAGGATTGTTTCAGCAGTTCGGCATTGCGGATCGAAAGCAGAAAAGCATGTCCATGT
GTCCAAGGAATGGATTGCATATTTAGTAACCCCTAATGGCAGTAATAAACTACTAGGCAAGCTTCTCTACGAAA
AAAAATTAGGGAACATGATGTTTCTAAAGCCCATGGTAAATTCAGGATTTGTTAAAGGAATCACTAATGATTC
AATTTGTAATTTAGTGATAAAACAAAATAATAAAAAATATTGATGCTACTGTAAAAGTTTTCAATACTGTTTACAG
TTTAGTAAACATAACAGACCTTTATCTGATATTGAGGGGGCAAGAGAATTACAGGAAAAAATGGAGAGGTAAA
TTGTTTAAATACACGTTACAGTGCAACAAGAATAGCAGAACATATTGCAAAAGAAATGAAGATGAAGATATTTAA
GAATATTATAGAAGAGAATGCCAAAATCTGTATCATAATTGATGAGGCATCTACAGTTTCAAAGAAAACCACCCT
AGTGATTTATCTCCAGTGCACAATTCAGTCAGCTCCTGCACCTGTTATGTTATTTGTGGCTTTAAAGAATTGGT
GTCAACTATAGCAGAGTGATTGTCAATACATTATTGACTACTTTAAATGATTGTGGTTTTACAAATGAATATTT
GAAAGCAAATTTAATTGCATTTTGTCTGATGGTGCTAATACAATCCTGGGAAGAAAGTCTGGAGTAGCTACAAA
ATTGTTAGAAAATTTTCTGAAATCATCATTTTGGAACTGTTTAAATCATCGATTACAATTGTCACTTGATGATTC
TATATCCGAAATAAAACAAATTAATCATTTTAAAAATATTTATTGATAAAATTTATTCTATTTATCATCAACCTAA
TAAAAATCAAACCAAGCTTCTAGGAACCTGTAGCTAAAGAACTTGAAACTGAAATTATTAATAATTTGGTCGAGTAAT
GGGACCAAGATGGGCGGCATGTAGTTTACAAGCTGCTACTGCTGTATGGCATGCATATCCTATATTATATATGCA
TTTTTCTCATTCTTACTCTGGTTTGGCGAAGAGATTAGCTAACATTAATTTCTTACAAGACCTTGCTTTAATGAT
TGACATTTCTGAAGAATTTTCAGTACTTTCAACTGCATTACAGTCAAGATCACTAATATTAAGAAAGCACAAAA
ATTGATCAAACGTACCATAAGAGCTTTGGAAAATTTAAAAATTTGGTACTGGAAAGTATGAATCTCAAATTGAAGA
TTTGATCAAGTCAGATAAGTTTAAAGATATTCCATTTAATAAAAAACAATAAATTTAATGCTCTTCTAGGAGTAT
ATTACTAGACAAATAAATTCAGCACATGAACCTACGCCTTTTATCTGACAGAAATCATGAAGATATTTTTAATTA
CTTTGATTTGCTGGAACCTTCCACATGGCCTTATGAAGAAATAAATTCACCATGGATAGCTGGTGAAAAACATT
ATTTCAATTTGTGTAATAATTTTAAAAATATGAAGTTGATTTGAATGATTTTTCGGGAATTTGTAAATAATAATATAAA
ATCAAACAATGTTTCAATTCCTACAACCTATATACAAAGCTAAAAAGATAGTTAGCACCATTGCAATCAATAGTGC
TGAAGCTGAAAGGGGTTTCAATTTAATGAACATAATTTGTACAAGGGTGAGAAATAGTTTAAACAATAGATCATGT
ATCAGATTTAATGACAATAAATTTACTGGGGAAAGAATTAGCAGATTGGGATGCAACACCGTTTGTAATCTTG

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FIGURE 461B

GTCAAATTGCAACCACAGGTTGGCTACAGATACAAGAGTTCGGCAAAAGTCAACAAAAGTCTTCCATGAGAATCA
ATTGGCTATATGGAACCTAAAATAGAATATTGTATACGTTTTTTTGTTCATCTGTAAATTATGTACTACACATCCTT
TATATACATAAAGGTCCTTTTTTTTTTTTTGGAAAGCCAGTTAAACTTTTATCAGCATGTTGCTGTTTAAAAGGCG
TTCTTTAAGAAGATAATCTTGAAGATTGGTTTTTAGAAGCTATAGTTTTTTAGAGATTGGCCCATGTTTGCTAGAG
TGGGTCATAATACATATTCCATGAAGTTCTGTACAGAACAACACCGTTTATAATTTTGTACTGTTTTACTTTAA
GTAAGGATGCAAAAAATAGCAGGACTCAGCTAAGTTCTAAGCCCTGGAGGTTATATTAAATAAAAGAGAAATGGA
ATAAAAACTGT

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FIGURE 462

SVMNFTYICKIIFQILFPKMPKRQGDFLHFLNVKKVKTDTENNEVSKNHCRLSKAKEPHFEYIEQPIIEEKPSLS
SKKEIDNLVLPDCWNEKQAFMFTEQYKWLEIKEGKLGCKDCSAVRHLGSKAEKHVHVSKEWIAYLVTPNGSNKTT
RQASLRKKIREHDVSKAHGKIQDLLKESTNDSICNLVHKQNNKNIDATVKVFNTVYSLVKHNRPLSDIEGARELQ
EKNGEVNCLNTRYSAERIAEHIKEMKMKIFKNII EENAKICIIIDEASTVSKKTTLVIYLQCTIQSAPAPVMLF
VALKELVSTIAECIVNTLLTTLNDCGFTNEYLKANLIAFCSDGANTILGRKSGVATKLENFPEII IWNCLNHRL
QLSLDDSISEIKQINHLKIFIDKIYSIYHQPKNQTKLLGTVAKELETEI I KIGRVMGPRWAACSLQAATAVWHA
YPILYMHFSHSYGLAKRLANINFLQDLALMIDILEEF SVLSTALQSRSTNIKKAQKLIKRTIRALENLKIGTGK
YESQIEDLIKSDKFKDIPFNKNNKFNALPRSI LLDNIIQHMMNLRLLSDRNHEDIFNYFDLLEPSTWPYEEITSPW
IAGEKTLFHLCKILKYEVDLNDFRE FVNNNIKSNNVSIPTTIYKAKKIVSTIAINSAEAERGFLNMNIICTRVRN
SLTIDHVS DLM TINLLGKELADWDATPFVKWSN CNHRLATDTRVRQKSTKVFHENQLAIWNLK

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FIGURE 463

CGTACATACAATGCCTCCATCACGCTACAGCAGCAGCTAAAAGAACTGACAGCCCCGGATGAGAACATCCCAGCG
AAGATCCTTTCTTATAACCGTGCCAATCGAGCTGTTGCAATTCCTTGTAACCATCAGAGGGCACCACCAAAAACCT
TTTGAGAAGTCTATGATGAACTTGCAAACTAAGATTGATGCCAAGAAGGAACAGCTAGCAGATGCCCGGAGAGAC
CTGAAAAGTGCTAAGGCTGATGCCAAGGTTCATGAAGGATGCAAAGACGAAGAAGGTAGTAGAGTCAAAGAAGAAG
GCTGTTTCAGAGACTGGAGGAACAGTTGATGAAGCTGGAAGTTCAAGCCACAGACCGAGAGGAAAAATAAACAGATT
GCCCTGGGAACCTCCAACTCAATTATCTGGACCCTAGGATCACAGTGGCTTGGTGCAAGAAGTGGGGTGTCCCA
ATTGAGAAGATTTACAACAAAACCCAGCGGGAGAAGTTTGCCCTGGGCCATTGACATGGCTGATGAAGACTATGAG
TTTTAGCCAGTCTCAAGAGGCAGAGTTCTGTGAAGAGGAACAGTGTGGTTTGGGAAAGATGGATAAACTGAGCCT
CACTTGCCCTCGTGCCCTGGGGGAGAGAGGCAGCAAGTCTTAACAAACCAACATCTTTGCGAAAAGATAAACCTGG
AGATATTATAAGGGAGAGCTGAGCCAGTTGTCCTATGGACAACCTATTTAAAAATATTTTCAGATATCAAAATTCT
AGCTGTATGATTTGTTTTGAATTTGTTTTTATTTTCAAGAGGGCAAGTGGATGGGAATTTGTCAGCGTTCTACC
AGGCAAATTCAGTGTTCAGTGAATGTTTGGATTCTCTTAGCTACTGTATGCAAAGTCCGATTATATTGGTGCG
TTTTTACAGTTAGGGTTTTGCAATAACTTCTATATTTAATAGAAATAAATTCCTAACTCCCTTCCCTCTCTCC
CATTTTCAGGAATTTAAAATTAAGTAGAACAAAAACCCAGCGCACCTGTTAGAGTCGTCAGTCTCTATTGTCATG
GGGATCAATTTTCATTAACTTGAAGCAGTCGTGGCTTTGGCAGTGTTTTGGTTCAGACACCTGTTACAGAAAA
AGCATGATGGGAAAATATTTCTGACTTGAGTGTTCTTTTTAAATGTGAATTTTTATTTCTTTTAATTATTTT
AAAATATTTAAACCTTTTTCTTGATCTTAAAGATCGGTAGATTGGGGTTGGGGAGGGATGAAGGGCGAGTGAAT
CTAAGGATAATGAAATAATCAGTGACTGAAACCATTTCCCATCATCCTTTGTTCTGAGCATTCCGTGTACCCTT
TAAGATATCCATCTTTTTCTTTTAAACCCTAATCTTTCACTTGAAAGATTTTATTGTATAAAAAGTTTCACAGGT
CAATAAACTTAGAGGAAAATGAGTATTTGGTGCCAAAAAAGGAAAAATAATCAAGATTTTAGGGCTTTTATTTTT
TCTTTTGTAATTGTGTAAAAAATGGAAAAAACATAAAAAGCAGAATTTAATGTGAAGACATTTTGTCTATAA
TCATTAGTTTTAGAGGCATTGTAGTTTAGTGTGTGTCAGAGTCCATTTCCACATCTTTCCTCAAGTATCTTC
TATTTTTATCATGAATCCCTTTTAACTCACTGTAGGTTATTTAAATAAATTCCTACAACCTAATGGAAAAAA
AAAAAAA

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FIGURE 464

RTYNASITLQQQLKELTAPDENIPAKILSYNRANRAVAILCNHQRAPPKTFEKSMMNLQTKIDAKKEQLADARRD
LKSADAKVMKDAKTKKVESKKKAVQRLEEQLMKLEVQATDREENKQIALGTSKLNLYDPKITVAWCKKWGVP
IEKIYNKTQREKFAWAIDMADEDYEF

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FIGURE 465

ATGCCTGAGGAAGTGCACCATGGAGAGGAGGAGGTGGAGACTTTTGCCTTTCAGGCAGAAAATTGCCCAACTCATG
TCCCTCATCATCAATACCTTCTATTCCAACAAGGAGATTTTCCTTCGGGAGTTGATCTCTAATGCTTCTGATGCC
TTGGACAAGATTGCTATGAGAGCCTGACAGACCCCTCGAAGTTGGACAGTGGTAAAGAGCTGAAAATTGACATC
ATCCCCAACCTCAGGAACGTACCCTGACTTTGGTAGACACAGGCATTGGCATGACCAAAGCTGATCTCATAAAT
AATTTGGGAACCATTGCCAAGTCTGGTACTAAAGCATTTCATGGAGGCTCTTCAGGCTGGTGCAGACATCTCCATG
ATTGGGCAGTTTGGTGTGGCTTTTATTCTGCCTACTTGGTGGCAGAGAAAGTGGTTGTGATCAGAAAGCACAAC
GATGATGAACAGTATGCTTGGGAGTCTTCTGCTGGAGGTTCTTCACTGTGCGTGCTGACCATGGTGGAGCCCAT
GGCATGGGTACCAAAGTGATCCTCCATCTTAAAGAAGATCAGACAGAGTACCTAGAAGAGAGGCGGGTCAAAGAA
GTAGTGAAGAAGCATTCTCAGTTCATAGGCTATCCCATCACCCCTTTATTTGGAGAAGGAACGAGAGAAGGAAATT
AGTGATGATGAGGCAGAGGAAGAGAAAGGTGAGAAAGAAGAGGAAGATAAAGATGATGAAGAAAAGCCCAAGATC
GAAGATGTGGGTTGAGATGAGGAGGATGACAGCGGTAAGGATAAGAAGAAGAAAACCTAAGAAGATCAAAGAGAAA
TACATTGATCAGGAAGAATAAACAAGACCAAGCCTATTGGACCAGAAAACCTGATGACATCACCCAAGAGGAG
TATGGAGAATTCTACAAGAGCCTCACTAATGACTGGGAAGACCATTGGCAGTCAAGCATTCTTCTGTAGAAGGT
CAGTTGGAATTCAGGGCATTGCTATTTATTCTCGTCGGGCTCCCTTTGACCTTTTGTAGAACAAGAAGAAAAAG
AACAACATCAAATCTATGTCGCGCGTGTGTTTCATCATGGACAGCTGTGATGAGTTGATACCAGAGTATCTCAAT
TTTATCCGTGGTGTGGTTGACTCTGAGGATCTGCCCTGAACATCTCCCGAGAAATGCTCCAGCAGAGCAAAATC
TTGAAAGTCATTGCAAAAACATTGTTAAGAAGTGCCTTGAGCTCTTCTCTGAGCTGGCAGAAGACAAGGAGAAT
TACAAGAAATCTATGAGGCATTCTCTAAAAATCTCAAGCTTGAATCCACGAAGACTCCACTAACCGCCGCCGC
CTGTCTGAGCTGCTGCGCTATCATACCTCCCAGTCTGGAGATGAGATGACATCTCTGTGAGATGATGTTTCTCGC
ATGAAGGAGACACAGAAGTCCATCTATTACATCAC TGGTGAGAGCAAAGAGCAGGTGGCCAACTCAGCTTTTGTG
GAGCGAGTGCAGAAACGGGGCTTCGAGGTGGTATATATGACCGAGCCCATTGACGAGTACTGTGTGCAGCAGCTC
AAGGAATTTGATGGGAAGAGCCTGGTCTCAGTTACCAAGGAGGGTCTGGAGCTGCCTGAGGATGAGGAGGAGAAG
AAGAAGATGGAAGAGAGCAAGGCAAAGTTTGAAGACCTCTGCAAGCTCATGAAAGAAATCTTAGATAAGAAGGTT
GAGAAGGTGACAATCTCCAATAGACTTGTGTCTTCACCTTGTGTCATTGTGACCAGCACCTACGGCTGGACAGCC
AATATGGAGCGGATCATGAAAGCCCAGGCATTTCGGGACAACTCCACCATGGGCTATATGATGGCCAAAAAGCAC
CTGGAGATCAACCCTGACCACCCCATTTGTGGAGACGCTGCGGCAGAAGGCTGAGGCCGACAAGAATGATAAGGCA
GTTAAGGACCTGGTGGTGTGCTGTTTGAACCGCCCTGCTATCTTCTGGCTTTTCCCTTGAGGATCCCCAGACC
CACTCCAACCGCATCTATCGCATGATCAAGCTAGGTCTAGGTATTGATGAAGATGAAGTGGCAGCAGAGGAACCC
AATGCTGCAGTTCTGATGAGATCCCCCTCTCGAGGGCGATGAGGATGCGTCTCGCATGGAAGAAGTCGATTAG

GTTAGGAGTTCATAGTTGGAAAACCTGTGCCCTTGTATAGTGTCCCCATGGGCTCCCACTGCAGCCTCGAGTGCC
CCTGTCCACCTGGCTCCCCCTGCTGGTGTCTAGTGTTTTTTCCCTCTCCTGTCTTGTGTTGAAGGCAGTAAA
CTAAGGGTGTCAAGCCCCATTCCCTCTCTACTCTTGACAGCAGGATTGGATGTTGTGTATTGTGGTTATTTTAT
TTTCTTCATTTTGTCTGAAATTAAAGTATGCAAAATAAAGAATATGCCGTTTTTATAC

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FIGURE 466

MPPEVHHGEEEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELISNASDALDKIRYESLTDP SKLDSGKELKIDI
IPNPQERTLTTLVDTGIGMTKADLINNLGTIAKSGTKAFMEALQAGADISMIGQFGVGFYSAYLVAEKVVVIRKHN
DDEQYAWESSAGGSFTVRADHGEPIGMGTKVILHLKEDQTEYLEERRVKEVVKKHSQFIGYPITLYLEKEREKEI
SDDEAEEEEKGEKEEEDKDDEEKPKIEDVGSDEEDDSGKDKKKKTKKIKEKYIDQEELNKTPIWTRNPDDITQEE
YGEFYKSLTNDWEDHLAVKHFSVEGQLEFRALLFIPRRAPFDLFENKKKKNNIKLYVRRVFIMDSCELIPEYLN
FIRGVVDSEDLPLNISREMLQQSKILKVIRKNIVKKCLELFSELAEDKENYKKFYEAFSKNLKLGIHEDSTNRRR
LSELLRYHTSQSGDEMTSLSEYVSRMKETQKSIYYITGESKEQVANSFAVERVRKRGFEVVYMTPEID EYCVQQL
KEFDGKSLVSVTKEGLELPEDEEEKKMEESKAKFENLCKLMKEILDKKVEKVTISNRLVSSPCCIVTSTYGWTA
NMERIMKAQALRDNSTMGYMAKKHLEINPDHPIVETLRQKAEADKNDKAVKDLVVLLFETALLSSGFSLED PQT
HSNRIYRMIKLGLGIDEDEVAAEEPNAAVPDEIPPLEGDEDA SRMEEVD

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FIGURE 467A

GACCGCGGCTGCAGGAACGGAGGCGGAAGGGGCCCTGCGGCGACGACGTCGTCGACGGGGGTGGCCGTGGGAGCT
GAGCACGGAGAAGACTCCCTCTCTCGGAAGCCGGATCCCCGAGCCGGGCAGGATGGATCACCACCAGCCGGGGACT
GGGCGCTACCAGGTGCTTCTTAATGAAGAGGATAACTCAGAATCATCGGCTATAGAGCAGCCACCTACTTCAAAC
CCAGCACCAGCAGATTGTGCAGGCTGTGTCTTCAGCACCAGCACTTGAAACTGACTCTTCCCCTCCACCATATAGT
AGTATTACTGTGGAAGTACCTACAACCTTCAGATACAGAAGTTTACGGTGAGTTTTATCCCGTGCCACCTCCCTAT
AGCGTTGCTACCTCTCTTCTACATACGATGAAGCTGAGAAGGCTAAAGCTGCTGCAATGGCAGCTGCAGCAGCA
GAAACATCTCAAAGAATTCAGGAGGAAGAGTGTCCACCAAGAGATGACTTCAGTGATGCAGACCAGCTCAGAGTG
GGGAATGATGGCATTTCATGCTGGCATTTCATGGCATTATTTTCAACTGGCTTGGATTTTGTATCCTTC
TGTATACCAATACCATAGCTGGAAGGTATGGTGCTATCTGCGGATTGGCCTTTCCTTGATCAAATGGATCCTT
ATTGTGAGGTTTTCTGATTATTTTACTGGATATTTCAATGGACAGTATTGGCTTTGGTGGATATTTCTGTACTT
GGCCTGCTCCTTTTCTTCAGAGGATTTGTTAATTATCTAAAAGTCAGAAACATGTCTGAAAGTATGGCAGCTGCT
CATAGAACAAGGTATTTCTTCTTATTGTAGAGACTGCATCAACCCGACATTCCTTTCTTATACCAATGTGAAATT
TCCAGATCATCTGTAAACCTACAACCTTTAATAGAAGACTACTAATAACAGAAGACAAATTAGTGAAGAAAAGACG
GAGTTTCGAAATTGAATGGCAGGGTGGTTTTTGTCTTACAAGCCATTCTGTTCATTCTTTAAGTATCTATATTTT
ATTTGTTTTGCACATATGCATATGTGCCCCATTTAAGATATTTGCATATACTTGATAGAAACCATAAAGTTGTAGC
AGTTAAGTCCAGTCACATTTGGTTAATCAGTGTTTGATATAATTGAAAGAGTTGAGTGGATAAACAGCTCTCCAG
CTTGTAATGCCATTGACTTCTGACCTGACATTTAGTATAATAAAAAATGAAATTCTTAACCATGTCAAATGATTT
AGTTTCTGGCTCTTAGACTCATCTGGCAGTTCTACACATGAAACATCTTTGTTATATAAGGTGTATTGAAACCT
GCAGTGCTGATTATTAGAAAGGATTTGTGCGATTTTGAACATGATATTTACATTATTATTTAGGAAAACCTTC
CTGTAAATAACCATGCATAACTTACTTTCTGCAATGTTTTCTTAGAAATTGTGTCCAGATAGCTTTCCTAAATTT
TAAATTAAGTGAACATAATATATATGTGTATATGTATACACATATATATACACACACATATATATATTTAGAA
ACGTGAGTGTTAAAGATAGAATTTGTTTTAGGACAAATTTTAAAGAAAATGTGGGAATACCAAATGTCTTTATATA
GAAAAATAAATTTGTTTTAAGGGACATACCAGTTTTAGGGATTTTCAGATGGGAAGCTGCATTTTLAGGATTGC
CCATCTTAAGAGATCTTGCAGGAAGAGATTGTATTAGATATTATATTTATTTTCATTTAAGATAATTTTCAAAGTT
AATTTTCTAAATAAGATAATTTCTCATTTGTGTTTTGTCTTTTAAAGGCCAATAAAATATCTTTTCAGTATCATTGT
AATAATTTTTTAGAGTTTAAATTTGTAAGCTTAGCAATAAAATCTGTACTATGAATAGCTTCTTGCTTTATGA
CTTTAGGATTAACCTGTAAAAACATATCCTGAAC TGAGATATGCAAATACTCATTTTCAAGTTATGGAAATGT
GTTTGTGGCATATAGGACTGTGGGTCTGTGTGTGTAGTGAGAGTGTGTAGCCACTATTATAACTGGAATTTAAT
TTACATTCAAACTACTATATTTCCCATCTTGCAAATCATTTTATGTCTCATCTGTTTTCTTTCCGTTATAT
CTTTGGTTTTGAATACCAACATTTAAATGATGGTATTTTATCTTTTAACTTAAAAATTATTTAATACAGCTAT
ATGGACCTTATAAAATTGATTTCTTATTTATTATTAGACATTACTACTAAAAGGTACATCTAACTATTCAGGGAC
ATTTTTCCATTTCCAAAAATAAAATTTATTATGCTTTATAACCTCTTCTGTATTTTCTAATTTTTTCATTGTCT
TTGATAAATAAAACAGTTTTGTTTTGCTAATATAGCCTATTTTTTGTGTTGTCTCATTTCAGTTTACTTTCCTGCG
TAGAATTTTTATTGTTATATTAAATTTTTATTGTTGTATTAAAGTACCTGTGTTACACCCCTTGAAGTAAGACA
GTAGCATGGGGTAAAGAAAAAATATTAGTTTAGTTGCCTAATTTGGAAGTTAATTAATAAATAAATGTACTAAT
AACATATTCAACTCATGCTGGATCTCTTTCATATTAATTTCTTATAGACCTGTACTTTATTCTTTCAATAATTT
TTAAATGAAATTAAGCTTTGCTACATGGTAATTAATAATTACTAGGAAGCTTAGCTATCAAACATCGACTTACT
AAAATTTCAATTTAGCTTTTATGGTATATGTGCTTGTTTTCTGAATATGGATACATGTTACTTTTGATCCAGCAT
CAAACTTCATTTTGTGTTTACTTTTCCCCCAAATCTGTAAGGTTCAAGTATACATATTACTGAATCCTCTA
TAATTGGCATAATTCAATGGTAGCCTTAAATCTCATGTAAGCAGGGGAATCAGAATGTTATTTTCAAGAACT
TAATGTTCCCTTCAGATATATAAAATCCTGCATACCTTCAATTCCTGTGAGCTTGAACAGCTGCTGTTGTGTTTTG
GGGATGCTTGATCATCTTGGCACTCTGCCTTAAAGATTGAAAAATCAAACTCTTGTTAGGGTATCTAAACATTT
TTGAGTGTGAACCTGGGATTGGAAGTTAATACAAAAAATTTCAAATTTATTTCTATTGTAAATGAATAAGCTAGT
CATGGCTAGGATAATCCATTTTCATGATTTATGCAATAAACTGAATTTTAAGGCAAAAACAACACTTTTCTATA
TAGTGTATGCAGGACAGATTTTAGAACTTAGATTAAAATACAAATCCCATTACATTTGGTTAAAATGAATCTCT
GCTTAATGGAATAATACTAATCTTTAGCCTATTTTGAGTCTATAAGATATATTTCAATTTTAGACATGCCTTCTA
AGTTGTTTCACAGATTTTTACCTGCTAAAACAATATATTTCCAGTAAACCTCTCCTAACAGGAAAAGTGGAGTT
CAAAATATCCAATTGGAGAAAAATTCAGAGTTCCTTCATTAAATATAATTTTTTTCATCTAGTATGTACTATTTT

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FIGURE 467B

AAGAAGTGCAAAAAGTAATGATAGTGAATGTGATACCATACTTAACTAAGGTAATATATATCCTTAGTTTGCTCA
AAAGAGTCCTGGTTATTCCTGTTTTCTCAGCTTAATAGTGCCTCATCGTACTCTCAAAAGTGTCTAATTTGGAG
GATAAGTTATATGATCATCCTGIGTATAATTGTAGACTGTACCAAGAAGCAACTACCTTAGCTCCACTGCCCTTT
GAGGGATGGAAGTGGGGTAAGGGCAGGAGCCAGTTATTATTGCCACAGTGTTTTCTAATGAACCATTGCGCTGT
AGAAGAGGAATAGTATTTTTTTTAAATAGTTGTATTGAATGATTCCAGCTTATCGTAAATACTAACTGAATGGC
TTTTATTTTTTAACTGCTGTAAATGTTATTTTAGCATTTATTAGTTGTTTATTATTTAATTCTTCAAATAGTC
ATATGAAAACATATATTTGATAAAGGTCAATTGTTAGATGATAATGTGCCATTTCATTATCATAGGAATGTCCTTG
CCCATATATAAAACATGCTGGCATGTATTTTACTTGTTAATAAAGTTGTATAGATGTGGAAGTGTGAACCTGTGA
TGCATCCTTTTCAAATCAGTTTAAGATTGCGATATTATCATGACTGTGACCTCACTAACTGTTTATGTGACAA
ACCTTTCAAGATTGGAGATGAAAACAACACTTGTGAAATTAGGTTGGGGTTGCAACATCTTTTAACTTCTCAGTT
ATTTGTATGTCAGGAAACAGATTGTGGTTTAATTTTAATAAACAAAATATCATCTTTTGAAAAT

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FIGURE 468

DRGCRNGGGRGPAATTSSSTGVAVGAEHGEDSLSRKPDPEPGRMDHHQPGTGRYQVLLNEEDNSESSAIEQPPTSN
PAPQIVQAVSSAPALETDSPPPYSSITVEVPTTSDTEVYGEFYVPPPYSVATSLPTYDEAEKAKAAAMAAAAA
ETSQRIQEEECPPRDDFSDADQLRVGNDGIFMLAFFMAFIFNWLGFCLSFCTNTIAGRYGAICGFGLSLIKWIL
IVRFSDYFTGYFNGQYWLWWIFLVLGLLLFFRGEVNYLKVRNMSESMAAAHRTRYFFLL

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FIGURE 469

GGCTGAGGCAGTGGCTCCTTGACAGCAGCTGCACGCGCCGTGGCTCCGGATCTTCTTCGTCTTTGCAGCGTAGC
CCGAGTCGGTCAGCGCCAGAGGACCTCAGCAGCCATGTCGAAGCCCCATAGTGAAGCCGGGACTGCCTTCATTCA
GACCCAGCAGCTGCACGCAGCCATGGCTGACACATTCTTGGAGCACATGTGCCGCTGGACATTGATTCACCACC
CATCACAGCCCGGAACACTGGCATCATCTGTACCATTGGCCCAGCTTCCCGATCAGTGGAGACGTTGAAGGAGAT
GATTAAGTCTGGAATGAATGTGGCTCGTCTGAACTTCTCTCATGGAACTCATGAGTACCATGCGGAGACCATCAA
GAATGTGCGCACAGCCACGGAAAGCTTTGCTTCTGACCCCATCCTCTACCGGCCCGTGTGTGGCTCTAGACAC
TAAAGGACCTGAGATCCGAACCTGGGCTCATCAAGGGCAGCGGCACTGCAGAGGTGGAGCTGAAGAAGGGAGCCAC
TCTCAAATCAGCTGGATAACGCCCTACATGGAAAAGTGTGACGAGAACATCCTGTGGCTGGACTACAAGAATCAT
CTGCAAGGTGGTGGAAAGTGGGCAGCAAGATCTACGTGGATGATGGGCTTATTTCTCTCCAGGTGAAGCAGAAAGG
TGCCGACTTCTGGTGACGGAGGTGAAAATGGTGGCTCCTTGGGCAGCAAGAAGGTGTGAACCTTCTGGGGC
TGCTGTGGACTTGCCTGCTGTGTGCGAGAAGGACATCCAGGATCTGAAGTTTGGGGTCGAGCAGGATGTTGATAT
GGTGTTCGCTCATTATCCGCAAGGCATCTGATGTCCATGAAGTTAGGAAGGTCTGGGAGAGAAGGGAAAGAA
CATCAAGATTATCAGCAAAATCGAGAATCATGAGGGGGTTTCGGAGGTTTGTGAAATCCTGGAGGCCAGTGATGG
GATCATGGTGGCTCGTGGTGATCTAGGCATTGAGATTCTGCAGAGAAGGTCTTCTTGTCTCAGAAGATGATGAT
TGGACGGTGAACCGAGCTGGGAAGCCTGTCTGTGCTACTCAGATGCTGGAGAGCATGATCAAGAAGCCCCG
CCCCACTCGGGCTGAAGGCAGTGATGTGGCCAATGCAGTCTGGATGGAGCCGACTGCATCATGCTGTCTGGAGA
AACAGCCAAAGGGGACTATCCTCTGGAGGCTGTGCGCATGCAGAACCTGATTGCCCCGTGAGGCAGAGGCTGCCAT
CTACCACCTTGCAATTATTTGAGGAACTCCGCCGCTGGCGCCCATTACCAGCGACCCACAGAAGCCACCGCCGT
GGGTGCCGTGGAGGCCCTCCTTCAAGTGTGTCAGTGGGGCCATAATCGTCCTCACCAGTCTGGCAGGTCTGCTCA
CCAGGTGGCCAGATACCGCCACGTGCCCCATCATTTGCTGTGACCCGGAATCCCAGACAGCTCGTCAGGCCCA
CCTGTACCGTGGCATCTTCCCTGTGCTGTGCAAGGACCCAGTCCAGGAGGCCTGGGCTGAGGACGTGGACCTCCG
GGTGAACCTTTGCCATGAATGTTGGCAAGGCCCGAGGCTTCTTCAAGAAGGGAGATGTGGTCATTGTGCTGACCGG
ATGGCGCCCTGGCTCCGGCTTACCAACACCATGCGTGTGTTCTGTGCCGTGATGGACCCAGAGCCCCCTCCT
CCAGCCCCGTGTCACCCCCCTTCCCCAGCCCATCATTAGGCCAGCAACGCTTGTAGAACTCACTCTGGGCTGT
AACGTGGCACTGGTAGGTTGGGACACCAGGGAAGAAGATCAACGCCTCACTGAAACATGGCTGTGTTGCAGCCT
GCTCTAGTGGGACAGCCAGAGCCTGGCTGCCCCATCATGTGGCCCCACCCAATCAAGGGAAGAAGGAGGAATGC
TGGACTGGAGGCCCTGGAGCCAGATGGCAAGAGGGTGACAGCTTCTTTCTGTGTGTAATCTGTCCAGTTCTT
TTAGAAAAAATGGATGCCCAGAGGACTCCCAACCTGGCTTGGGGTCAAGAAACAGCCAGCAAGAGTTAGGGGCC
TTAGGGCACTGGGCTGTGTTCCATTGAAGCCGACTCTGGCCCTGGCCCTTACTTGCTTCTCTAGCTCTCTAGGC
CTCTCCAGTTTGCACCTGTCCCCACCCTCCACTCAGCTGTCTGCAGCAAACTCCACCCTCCACCTTCCATTT
TCCCCACTACTGCAGCACCTCCAGGCCTGTGCCGC

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FIGURE 470

MSKPHSEAGTAFIQTLHAAMADTFLEHMCRLDIDSPITARNTGIICTIGPASRSVETLKEMIKSGMNVARLN
FSHGTHEYHAETIKNVRTATESFASDPILYRPVAVALDTKGPEIRTGLIKSGTAEVELKKGATLKITLDNAYME
KCDENILWLDYKNICKVVEVGSKIYVDDGLISLQVKQKGADFLVTEVENGGSLGSKKGVNLPGAADVLPVSEKD
IQDLKFGVEQDVMVFASFIRKASDVHEVRKVLGEKGKNIKIISKIENHEGVRRFDEILEASDGIMVARGDLGIE
IPAENVFLAQMMIGRCNRAGKPVICATQMLESMIKKPRPTRAEKSDVANAVLDGADCIMLSGETAKGDYPLEAV
RMQNLIAREAEAAIYHLQLFEELRRLAPITSDPTEATAVGAVEASFKCCSGAIIIVLTSGRSAGQVARYRPRAP I
IAVTRNPQTARQAHLYRGIFPVLCCKDPVQEAWAEDVDLRVNFAMNVGKARGFFKKGDVVIVLTGWRPGSGFTNTM
RVVPVP

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FIGURE 471

GCAAGAGTGACACACAGGTGTTCAAAGACGCTTCTGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTGGAG
CCTCAGGGGCGGGCACTGGCACGGAACACACCCTGAGGCCAGCCCTGGCTGCCAGGCGGAGCTGCCTCTTCTCC
CGCGGGTTGGTGGACCCGCTCAGTACGGAGTTGGGGAAGCTCTTTCAC TTCGGAGGATTGCTCAACAACCACTGCT
GGGCATCTGGACCCTCCTACCTCTGGTTCCTACGTCTGTTGCTAGATTATCGTCCAAAAGTGTTAATGCCCAAGT
GACTGACATCAACTCCAAGGATTGGAATTGAGGAAGACTGTTACTACAGTTGAGACTCAGAACTTGAAGGCCT
GCATCATGATGGCCAATTCTGCCATAAGCCCTGTCCTCCAGGTGAAAGGAAAGCTAGGGACTGCACAGTCAATGG
GGATGAACCAGACTGCGTGCCCTGCCAAGAAGGGAAGGAGTACACAGACAAAGCCCATTTTTCTTCCAAATGCAG
AAGATGTAGATTGTGTGATGAAGGACATGGCTTAGAAGTGGAATAAACTGCACCCGGACCCAGAATACCAAGTG
CAGATGTAAACCAAACCTTTTTTTGTAACCTACTGTATGTGAACACTGTGACCCTTGACCCAAATGTGAACATGG
AATCATCAAGGAATGCACACTCACCAGCAACACCAAGTGCAAAGAGGAAGGATCCAGATCTAACTTGGGGTGGCT
TTGTCTTCTTCTTTTGCCAATTCCACTAATTGTTTGGGTGAAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCA
CAGAAAGGAAAACCAAGGTTCTCATGAATCTCCAACTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGT
TGACTTGAGTAAATATATCACCCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTGTTCGAAAGAA
TGGTGTCAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACAGCAGAACAGAAAGTTCAACT
GCTTCGTAATTGGCATCAACTTCATGGAAGAAAGAGCGTATGACACATTGATTAAAGATCTCAAAAAAGCCAA
TCTTTGTA CTCTTG CAGAGAAAATT CAGACTATCA TCCTCAAGGACATTACTAGTGACTCAGAAAATTCAA ACTT
CAGAAAATGAAATCCAAAGCTTGGTCTAGAGTGAAAAACAACAAATTCAGTTCTGAGTATATGCAATTAGTGTG
AAAAGATTCTTAATAGCTGGCTGTAATACTGCTTGGTTTTTTTACTGGGTACATTTTATCATTTATTAGCGCTGA
AGAGCCAACATATTTGTAGATTTTTTAATATCTCATGATTCCTGCCTCCAAGGATGTTTTAAATCTAGTTGGGAAAA
CAAACCTCATCAAGAGTAAATGCAGTGGCATGCTAAGTACCCAAATAGGAGTGTATGCAGAGGATGAAAGATTAA
GATTATGCTCTGGCATCTAACATATGATTCTGTAGTATGAATGTAATCAGTGTATGTTAGTACAAATGTCTATCC
ACAGGCTAACCCCACTCTATGAATCAATAGAAGAGCTATGACCTTTTGCTGAAATATCAGTTACTGAACAGGCA
GGCCACTTTGCCTCTAAATTACCTCTGATAATTCTAGAGATTTTACCATATTTCTAACTTTGTTTATAACTCTG
AGAAGATCATATTTATGTAAAGTATATGTATTTGAGTGCAGAAATTTAAATAAGGCTCTACCTCAAAGACCTTTGC
ACAGTTTATTGGTGTCAATTTATACAAATTTCAATTGTGAATTCACATAGAAAACATTAAATTATAATGTTTGA
CTATTATATATGTGTATGCATTTTACTGGCTCAAAACTACCTACTTCTTTCTCAGGCATCAAAAGCATTTTGAGC
AGGAGAGTATTACTAGAGCTTTGCCACCTCTCCATTTTGCCTTGGTGCTCATCTTAATGGCCTAATGCACCCCC
AAACATGGAAATATCACCAAAAAATACTTAATAGTCCACCAAAAGGCAAGACTGCCCTTAGAAATCTAGCCTGG
TTTGAGATACTAACTGCTCTCAGAGAAAGTAGCTTTGTGACATGTCATGAACCCATGTTTGCAATCAAAGATGA
TAAATAGATTCTTATTTTTTCCCCACCCCGAAAATGTTCAATAATGTCCCATGTAAACCTGCTACAAATGGC
AGCTTATACATAGCAATGGTAAATCATCATCTGGATTTAGGAATTGCTCTTGTGCATACCCCAAGTTTCTAAGA
TTTAAGATTCTCCTTACTACTATCCTACGTTTAAATATCTTTGAAAGTTTGATTAAATGTGAATTTTAAGAAAT
AATATTTATATTTCTGTAAATGTAACTGTGAAGATAGTTATAAACTGAAGCAGATACCTGGAACCACTAAAGA
ACTTCCATTTATGGAGGATTTTTTTGCCCTTGTGTTTGAATTATAAAATATAGGTAAAGTACGTAATTAAT
A

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FIGURE 472

MLGIWTLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLGLHHDGQFCHKPCPPGERKARDCTV
NGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCTRTQNTKCRCKPNFFCNSTVCEHCDPCTKCE
HGIIECTLTISNTKCKEEGSRNLGWLCLLLLPIPLIVVVKRKEVQKTCRKHRKENQGSHEPTLNPETVAINLS
DVDLSKYITTIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKK
ANLCTLAEKIQTIILKDITSSENSNFRNEIQSLV

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FIGURE 473

ATGGCTTCTCTGGACGACCCAGGGGAAGTGAGGGAGGGCTTCCTCTGCCCTCTGTGCCTGAAGGATCTGCAGTCT
TTCTATCAGCTTCACTCACATTACGAGGAAGAACA CTAGGGGAAGACCGTGATGTCAAAGGGCAAATTAAAAGT
CTTGTCAGAAAGGCTAAAAAAGCAAAGGACAGGTTGTTGAAACGAGAAGGGGATGATCGAGCAGAGTCAGGGACC
CAAGGATATGAGTCTTTCAGCTATGGAGGGGTTGATCCTTACATGTGGGAACCCAGGAGCTTGGTGCTGTGAGG
AGCCATCTTTCCGACCTCAAAAAACACCGAGCTGCTAGAATTGACCACTATGTTGTGGAAGTCAATAAACTAATA
ATCAGGTTAGAGAAGCTCACTGCATTTGACAGAACAATACTGAGTCTGCAAAGATTTCAGCAATAGAAAAGTCT
GTGGTGCCCTTGGGTCAACGACCAGGATGTCCCTTCTGTCCAGACTGTGGGAATAAGTTCAGCATCCGGAACCGC
CGCCACCACTGCCGCTCTGCGGGTCTATTATGTGCAAGAAGTGTATGGAGCTCATCAGCCTTCCCTTGGCAAAC
AAGCTCACCAGTGCCAGCAAGGAGTCCCTGAGCACCCACACCAGCCCCAGCCAGTCACCCAACAGTGTCCATGGC
TCCCGCCGAGGCAGCATCAGCAGCATGAGCAGTGTGAGTCCGGTCTGGATGAGAAGGACGATGACCGGATCCGC
TGCTGTACACACTGCAAGGACACGCTGCTCAAGAGAGAGCAGCAGATTGATGAGAAGGAGCACACACCTGACATC
GTGAAGCTCTACGAGAAATTACGACTTTGCATGGAGAAAGTTGACCAGAAAGCTCCAGAATACATCAGGATGGCA
GCATCATTAAATGCTGGGGAGACAACCTACAGTCTGGAACATGCCAGTGACCTTCGAGTGAAGTGCAGAAAGTG
TATGAGCTGATAGACGCTTTAAGTAAGAAGATCTTAACCTTGGGCTTGAACCAGGACCCTCCACCACATCCAAGC
AATTGCGGGCTGCAGAGAATGATCAGATACTCAGCTACACTTTTGTGCAGGAAAAGTTGCTTGGTTTGATGTCA
CTGCCGACCAAGAACAGTTTGAAGAACTGAAAAAGAAAGGAAGGAGGAAATGGAGAGGAAGAGGGCCGTGGAG
AGACAAGCTGCTCTGGAGTCCCAGCGAAGGCTTGAGGAAAGGCAGAGTGGCCTGGCTTCTCGAGCGGCCAACGGG
GAGGTGGCATCTCTCCGACGGGGCCCTGCCCCCTTGAGAAAGGCTGAGGGCTGGCTCCCACTGTGAGGAGTTCAG
GGGCAGAGTGAGGACTCAGACCCGCTCCTCCAGCAGATCCACAACATCACATCATTTCATCAGGCAGGCCAAGGCC
GCGGGCCGCATGGATGAAGTGCGCACTCTGCAGGAGAACCTGCGGCAGCTGCAGGACGAGTATGACCAGCAGCAG
ACAGAGAAGGCCATCGAGCTGTCCCGGAGGCAGGCTGAGGAGGAGGACCTGCAGCGGGAACAGCTGCAGATGTTG
CGTGAACGGGAGTTGGAACGAGAAAGGGAGCAGTTTCGGGTGGCATCCCTGCACACACGGACTCGGTCCCTGGAC
TTCAGAGAAATCGGCCCTTTTCAGCTGGAGCCCAGCAGAGAGCCTCGCACCCACCTTGCTTATGCTTTGGATCTA
GGCTCTTCCCCAGTTCCAAGCAGCACAGCTCCCAAGACCCCTTCACTTAGCTCAACTCAACCCACCAGAGTGTGG
TCTGGGCCCCCAGCCGTTGGCCAGGAGCGCTTACCCAGAGCAGCATGCCACAGCAACATGAGGGGCCCTCCTTA
AACCCCTTTGATGAGGAAGACCTCTCCAGCCCCATGGAAGAGGCCACTACTGGTCTCCTGCTGCAGGGGTTTCC
TTAGACCCTTCAGCCCGCATCCTGAAGGAGTACAATCCTTTTCGAGGAAGAGGACGAGGAGGAGGAAGCAGTGGCA
GGGAATCCATTTCATTCAGCCAGACAGCCAGCTCCTAACCCCTTCAGTGAGGAAGACGAACATCCCAGCAGAGG
CTCTCAAGCCCTCTGGTTCTGGTAAACCCCTTTGAGGAACCCACCTGTATCAACCCCTTGAGATGGACAGTGAC
AGTGGGCCAGAGGCTGAGGAGCCCATAGAGGAAGAGCTCCTCCTGCAGCAGATCGATAACATCAAGGCATACATC
TTTGATGCCAAGCAGTGCGGCCGCTGGATGAGGTAGAGGTGCTGACAGAGAATCTGCGGGAGCTGAAGCACACC
CTGGCCAAGCAGAAGGGGGGCACTGACTGA

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FIGURE 474

MASLDDPGEVREGFLCPLCLKDLQSFYQLHSHYEEEHSGEDRDVKGQIKSLVQKAKKAKDRLLKREGDDRAESGT
QGYESFSYGGVDPYMWEPQELGAVRSHLSDLKKHRAARIDHYVVEVNKLIIRLEKLTAFDRTNTESAKIRAIEKS
VVPWVNDQDVFPDCGKNKFSIRNRRHHCRLCGSIMCKKCMELISLPLANKLTSASKESLSTHTSPSQSPNSVHG
SRRGSISSMSSVSSVLDEKDDDRIRCCTHCKDTLLKREQQIDEKEHTPDIVKLYEKLRLCMEKVDQKAPEYIRMA
ASLNAGETTYSLEHASDLRVEVQKVYELIDALSKKIILTLGLNQDPPPHPSNRLRLQRMIRYSATLFFVQEKLLGLMS
LPTKEQFEELKKKRKEEMERKRAVERQAALLESQRRLEERQSGLASRAANGEVASLRRGPAPLRKAEGWLPLSGGQ
GQSESDPPLLQQIHNITSFIRQAKAAGRMDEVRTLQENLRQLQDEYDQQQTEKATIELSRRQAEEEDLQREQLQML
RERELEREREQFRVASLHTRTRSLDFREIGPFQLEPSREPRTHLAYALDLGSSPVPSSSTAPKTPSLSSSTQPTRVW
SGPPAVGQERLPQSSMPQQHEGPSLNPFDDEDLSSPMEEATTGPPAAGVSLDPSARILKEYNPFEEDEEEEEEAVA
GNPFIQPDSPAPNPFSEDEHPQQRLSSPLVPGNPFEEPTCINPLEMDSGPEAEFPIEEELLQQIDNIKAYI
FDAKQCGRLDEVEVLTENLRELKHTLAKQKGGTD

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FIGURE 475

GAAAGAGACAAAGCAGCAATTAAAGTCAGCCCAGCACCAACTCCGACGCCAAGCGTTACACTGGAACTACTTTT
TAAAGCAACAAAAGAGTCTAAAACAAAATACAACATTTCTTAAATACACTGTTTCCAGAAAGAGCTATTTTAAACA
GAAGCAACTCAAAGATATCCCTTCGACAGAAGTGGAAGTGCTGAAAAATGCTCATCTCTCACACAGACTTTTGAT
GGACAGGAGTTTCTAAGTATCATGCCTACCAACAAGCTGTAAAATGATCACCCCTGAACAATCAAGATCAACCTGT
CCCTTTTAAACAGCTCACATCCAGATGAATACAAAATTGCAGCCCTTGTCTTCTATAGCTGTATCTTCATAATTGG
ATTATTTGTAAACATCACTGCATTATGGGTTTTTCAGTTGTACCACCAAGAAGAGAACCACGGTAACCATCTATAT
GATGAATGTGGCATTAGTGGACTTGATATTTATAATGACTTTACCCCTTTCGAATGTTTTATTATGCAAAAAGATGA
ATGGCCATTTGGAGAGTACTTCTGCCAGATTCTTGGAGCTCTCACAGTGTTTTACCCAAGCATTGCTTTATGGCT
TCTTGCCTTTATTAGTGCTGACAGATACATGGCCATTGTACAGCCGAAGTACGCCAAAGAACTTAAAAACACGTG
CAAAGCCGTGCTGGCGTGTGTGGGAGTCTGGATAATGACCCTGACCACGACCACCCCTCTGCTACTGCTCTATAA
AGACCCAGATAAAGACTCCACTCCCGCCACCTGCCTCAAGATTTCTGACATCATCTATCTAAAAGCTGTGAACGT
GCTGAACCTCACTCGACTGACATTTTTTTTTCTTGATTCCCTTGTTCATCATGATTGGGTGCTACTTGGTCATTAT
TCATAATCTCCTTCACGGCAGGACGTCTAAGCTGAAACCCAAAGTCAAGGAGAAGTCCATAAGGATCATCATCAC
GCTGCTGGTGCAGGTGCTCGTCTGCTTTATGCCCTTCCACATCTGTTTCGCTTTCCTGATGCTGGGAACGGGGGA
GAACAGTTACAATCCCTGGGGAGCCTTTACCACCTTCCTCATGAACCTCAGCACGTGTCTGGATGTGATTCTCTA
CTACATCGTTTCAAAACAATTTCAGGCTCGAGTCATTAGTGTGATGCTATAACGTAATTACCTTCGAAGCATGCG
CAGAAAAAGTTTCCGATCTGGTAGTCTACGGTCACTAAGCAATATAAACAGTGAAATGTTATGAATAATAAGGTT
CTTTCATTTCAATCCCATCAAAATTCACCTCACTAATACTCTGGCGTCAATGGATATTCTGTATAATACTATCA
AGTCCCTTTTCTCTTGAAAAATAAATTCATTATCTTCATTTTAAAAAAAAAAAAAAAAA

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FIGURE 476

MITLNNQDQPVFPFNSSHPDEYKIAALVFYSCIFIIGLFVNITALWVFSCTTKKRTTVTIYMMNVALVDLIFIMTL
PFRMFYYAKDEWPFGEYFCQILGALTVFYPSIALWLLAFISADRYMAIVQPKYAKELKNTCKAVLACVGWIMTL
TTTTPLLLLYKDPDKDSTPATCLKISDIIYLKAVNVNLNLRLTFFFLIPLFIMIGCYLVIHNNLLHGRTSKLKPK
VKEKSIRIIITLLVQVLVCFMPFHICFAFLMLGTIGENSYNPWGAFTTFLMNLSTCLDVILYYIVSKQFQARVISV
MLYRNYLRSMRRKSFRSGSLRSLSNINSEML

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FIGURE 477

GGAATTCCAAAAAAAAAAAAATACGACTACACCTGCTCCGGAGCCCGCGGCGGTACCTGCAGCGGAGGAGCTCTGT
CTTCCCTTCATCTCACGCGAGCCCGGCGTCCCGCCGCGTGCGCCCGGCGCAGCCCGCCAGTCCGCCCGGAGCC
CGCCCAGTCGCCGCGCTGCACGCCCCGGGTGAACCCTCTGCCCTCGCTGGGACAGAGGGCCCCGCAGCCGTCATG

CTTTCCGCCATCTACACAGTCTGGCGGGACTGCTGTTCTGCCGCTCCTGGTGAACCTCTGCTGCCCATACTTC
TTCCAGGACATAGGCTACTTCTTGAAGGTGGCCGCGCTGGGCCGGAGGGTGCGCAGCTACGGGCAGCGGCGGCCG
GCGCGCACCATCCTGCGGGCGTTCTTGGAGAAAGCGCGCCAGACGCCACACAAGCCTTTTCTGCTCTTCCGCGAC
GAGACTCTCACCTACGCGCAGGTGGACCGGCGCAGCAATCAAGTGGCCCCGGCGCTGCACGACCACCTCGGCCTG
CGCCAGGGAGACTGCGTGGCGCTCCTTATGGGTAAACGAGCCGGCTACGTGTGGCTGTGGCTGGGGCTGGTGAAG
CTGGGCTGTGCCATGGCGTGCCTCAATTACAACATCCGCGCGAAGTCCCTGCTGCACTGCTTCCAGTGTGCGGG
GCGAAGGTGCTGCTGGTGTGCCAGAATAACAAGCAGCTGTGGAAGAGATACTGCCAAGCCTTAAAAAGATGAT
GTGTCCATCTATTATGTGAGCAGAACTTCTAACACAGATGGGATTGACTCTTCTGGACAAAGTGGATGAAGTA
TCAACTGAACCTATCCCAGAGTCATGGAGGTCTGAAGTCACTTTTCCACTCCTGCCTTATACATTTATACTTCT
GGAACCACAGGTCTTCCAAAAGCAGCCATGATCACTCATCAGCGCATATGGTATGGAAGTGGCCTCACTTTTGT
AGCGGATTGAAGGCAGATGATGTCTATATCACTCTGCCCTTTTACCACAGTGTGCACTACTGATTGGCATT
CACGGATGTATTGTGGCTGGTGTACTCTTGCCCTTGCGGACTAAATTTTCAGCCAGCCAGTTTTGGGATGACTGC
AGAAAATACAACGTCAGTGTCACTTCACTATATCGGTGAAGTGTCTCGGTATTTATGCAACTCACCACAGAAACCA
AATGACCGTGATCATAAAGTGAGACTGGCACTGGGAAATGGCTTACGAGGAGATGTGTGGAGACAATTTGTCAAG
AGATTTGGGGACATATGCATCTATGAGTTCTATGCTGCCACTGAAGGCAATATTGGATTTATGAATTATGCGAGA
AAAGTTGGTGCTGTTGGAAGAGTAACTACCTACAGAAAAAATCATAACTTATGACCTGATTAATATGATGTG
GAGAAAGATGAACCTGTCCGAGATGAAAATGGATATTGCGTCAGAGTTCCCAAAGGTGAAGTTGGACTTCTGGTT
TGCAAAATCACACAACTTACACCATTTAATGGCTATGCTGGAGCAAAGGCTCAGACAGAGAAGAAAAAAGTGA
GATGTCTTTAAGAAAGGAGACCTCTATTTCAACAGTGGAGATCTCTTAATGGTTGACCATGAAAATTTTCATCTAT
TTCCACGACAGAGTTGGAGATACATTCCGGTGGAAAGGGGAAAATGTGGCCACCACTGAAGTTGCTGATACAGTT
GGACTGGTTGATTTTGTCCAAGAAGTAAATGTTTATGGAGTGCATGTGCCAGATCATGAGGGTTCGCATTGGCATG
GCCTCCATCAAAATGAAAGAAAACCATGAATTTGATGGAAGAAAACCTCTTTCAGCACATTGCTGATTACCTACCT
AGTTATGCAAGGCCCGGTTTCTAAGAATACAGGACACCATTGAGATCACTGGAACCTTTTAAACACCGCAAAATG
ACCCTGGTGGAGGAGGGCTTTAACCCTGCTGTCTATCAAAGATGCCTTGTATTTCTTGGATGACACAGCAAAATG
TATGTGCCTATGACTGAGGACATCTATAATGCCATAAGTGCTAAAACCTGAAACTCTGAATATTTCCAGGAGGA
TAACTCAACATTTCCAGAAAGAACTGAATGGACAGCCACTTGATATAATCCAACTTTAATTTGATGAAGATTG
TGAGGAAATTTTGTAGGAAATTTGCATACCCGTAAAGGGAGACTTTTTTAAATAACAGTTGAGTCTTTGCAAGTA
AAAAGATTTAGAGATTATTATTTTTTCACTGTGCACCTACTGTTGTATTTGCAAACTGAGCTTGTGGAGGGAAG
GCATTATTTTTTAAATACTTAGTAAATTAATGAAC

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FIGURE 478

MLSAIYTVLAGLLFLPLLNLCCPYFFQDIGYFLKVAAGRRVRSYGQRRPARTILRAFLEKARQTPHKPFLFR
DETLTYAQVDRRSNQVARALHDHLGLRQGDCAVLLMGNEPAYVWLWLGLVKLGCMACLNYNIRAKSLLHCFQCC
GAKVLLVSPELQAAVEEILPSLKKDDVSIYYVSRTSNTDGIDSFLDKVDEVSTPIPESWRSEVTFSTPALYIYT
SGTTGLPKAAMITHQRIWYGTGLTFVSGLKADDVIYITLPPFYHSAALLIGIHGCIVAGATLALRTKFSASQFWDD
CRKYNVTVIQYIGELLRYLCNSPQKPNDRDHKVRLALGNGLRGDVWRQFVKRFGDICIYEFYAATEGNIGFMNYA
RKVGAVGRVNYLQKKIITYDLIKYDVEKDEPVRDENGVCVRVPKGEVGLLVCKITQLTPFNGYAGAKAQTEKKKL
RDVFKKGDLYFNSGDLLMVDHENFIYFHDRVGDTRWKGENVATTEVADTVGLVDFVQEVNVYGVHVPDHEGRIG
MASIKMKENHEFDGKKLFQHIADYLPYARPRFLRIQDTIEITGTFKHKRMTLVEEGFNPAVIKDALYFLDDTAK
MYVPMTEDIYNASAKTLKL

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FIGURE 479

GGTCGCGCAGCTGTGTTTCGGGACTCAGGTGGAAGGAATTTCTTCTTCGTTGACGTTGCTGGTGTTCACGTGTT
TGGAATTAGTCAAGTTTCGGGAATCACCGTCGCTGCCATCAACATGTCGGTCCCAAGCGCTCTCATGAAGCAACC
GCCCATTCACTCTACGGCTGGGGCCGTCCCAGTTCGCAATGAGAAAGGTGAGATTTCAATGGAAAAAGTGAAGGT
AAAGCGTTATGTGTCCGGAAAAAGGCCAGACTATGCCCTATGGAGTCCTCAGATGAGGAGGATGAAGAATTTCA
GTTTCATTAAGAAAGCCAAAGAACAAGAAGCAGAGCCTGAGGAACAGGAGGAGGATTTCATCCAGTGACCCCGGCT
ACGGCGTTTACAGAACCGTATTAGTGAAGATGTGGAAGAGAGATTGGCTCGACATCGAAAAATAGTGGAACCTGA
AGTGGTAGGAGAGAGTGACTCAGAAGTAGAAGGAGATGCTTGGCGCATGGAACGAGAAGACAGCAGTGAAGAAGA
GGAGGAGGAAATTGATGATGAGGAAATAGAGCGGCGGGCTGGCATGATGCGTCAGCGAGCACAGGAGAGAAAAAA
TGAAGAGATGGAAGTCATGGAAGTGAAGATGAGGGTCTGTTCTGGAGAGGAGTCAGAAATCAGAGTCTGAGTATGA
AGAGTACACAGACAGTGAAGATGAGATGGAGCCTCGCCTTAAGCCAGTCTTCATTGAAAGAAGGACCGAGTGAC
AGTTCAAGAACGTGAAGCCGAAGCATTGAAACAGAAGGAGCTGGAGCAGGAAGCCAAACGCATGGCTGAGGAAAG
GCGCCAGTACACACTCCAGATTGTCTGGAGAGGAAACCCAAAAGAGCTGGAAGAGAACAAGCGATCCCTGGCTGC
ATTGGATGCACTCAATACTGATGATGAAAATGATGAGGAGGAATATGAGGCATGGAAAGTTCGAGAGCTAAAAAG
AATCAAGAGGGACAGAGAAGATCGAGAAGCGCTTGAGAAGGAGAAAGCAGAAATTGAACGCATGCGAAACCTGAC
TGAGGAAGAGAGGAGAGCTGAACTTCGGGCAAACGGCAAAGTCATTACCAACAAAGCTGTTAAGGGCAAATACAA
GTTCTTACAGAAGTATTATCACCGGGGTGCCTTCTTCATGGATGAGGATGAAGAAGTATACAAGAGAGATTTTCAG
CGCTCCTACCCTGGAGGATCATTTCATAATAAACCAATTCTTCCTAAAGTCATGCAGGTCAAGAACTTTGGACGCTC
AGGTTCGCACCAAATACACTCACCTTGTGGATCAAGATACCACCTCCCTTTGACTCAGCTTGGGGCCAAGAGAGTGC
CCAGAACACAAAGTTCTTCAAAACAAAAGGCAGCTGGGGTACGAGATGTATTTGAGCGGCCATCTGCCAAGAAGCG
GAAAACTACCTAGGGTCCAAGTCTTATTCTTCCAAGTGTGAACACAAGGGGAGTCTCAGCATCTGGTCCTTGA
TTGGGTTTTTTTCATTGTTTCCTTGGCCCCCTGTATCCAGATATTGGACTTACTGCTATACTTGTGATACTGGGTAG
CCCAGACTTTGAAGGTGCTTTGTGAGGTTTGGACTCATGCTGAGAAACCCACAGGAAAGCACTGTCCAGGTAGGA
TTAGAGGCTTCCCACTTAAAACTATTTCTGAGAAATCTTAGGTTTTATCACTGCTATGGTTTCCCATATTTACTT
GGGACTGTTCTGACTTTCTTTTTCCAGCCCTTAGCTTGGGTTAGAAAAGTGGACATGTAAGTGAACAATGCATTA
CTTCTACCTTAGGTTTAGGAGTAATATACCCGAAATCTAAGCTCATGGAAACATGTTTTCCATTTGGGGTTGGA
GTCCGTTTTTCTAGTTGTACATACTTGXGGATCCATATATGTGTGCATGTCAWGAAATAAAAGAATCACACAACA
AAAA

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FIGURE 480

MSVPSALMKQPPIQSTAGAVPVRNEKGEISMEKVKVKRYVSGKRPDYAPMESSDEEDEEEFQFIKKAKEQEAPEE
QEEDSSSDPRLRLRLQNRISEDVEERLARHRKIVEPEVVGESDSEVEGDWRMEREDSSEEEEEIDDEEIERRG
MMRQRAQERKNEEMEVEVEDEGRSGEESESESEYEEYTDSEDEMEPRLKPVFIRKKDRVTVQEREAEALKQKEL
EQEAKRMAEERRQYTLQIVGEETPKLEENKRSALDALNTDDENDEEEYEAWKVRELKRIKRDREDREALEKE
KAEIERMRNLTEEERRAELRANGKVITNKAVKGKYKFLQKYYHRGAFFMDEDEEVYKRDFSAPTLEDHFNKTILP
KVMQVKNFGRSGRTKYTHLVDQDTTSFDSAAGQESQNTKFFKQKAAGVRDVFERPSAKKRKTT

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FIGURE 481

GCGACCCGGGGCGTTTGCAGCGGTGCCGAGGAAGAGGACGGGAACGGTGTTACGATTGCCTGCGTTTAGGAGGTG
GCTGCGTTGTGGGAAAAGCTATCAAGGAAGAAATTGCCAAACCATGTCTTTTTTCTGTTTTTCAGAGTAGTTCAC
AACAGATCTGAGTGTTTTAATTAAGCATGGAATACAGAAAACAACAAAAAAGCTTAAGCTTTAATTTTCATCTGGAA
TTCCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTATCACGTGGTGC
TCTCCGACTACTCACCCCGAGTGTAAGAACCTTCGGCTCGCGTGCTTCTGAGCTGCTGTGGATGCGCTCGGCTC
TCTGGACTGTCTTCCGAGTAGGATGTCAGTACGATCCCTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTT
TCTTTGTGATGTGGTACCTCAGCCTTCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGT
ATGAGCCGATTTACAGACAAGACTTTCAGTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAAATCCATTTT
TGGTCATTCTGGTGACCTCCACCCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAA
AGTCTTGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAGAGGCTGAAAAGGAAGACAAAATGTTGG
CATTGTCCTTAGAGGATGAACACCTTCTTTATGGTGACATAATCCGACAAGATTTTTTAGACACATATAATAACC
TGACCTTGAAAACCATTATGGCATTGAGTGGGTAACTGAGTTTTTGCCCCAATGCCAAGTACGTAATGAAGACAG
ACACTGATGTTTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTTTTCA
CAGGTTATCCTCTAATTGATAATTATCCTATAGAGGATTTTACCAAAAACCCATATTTCTTACCAGGAGTATC
CTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTGGGTATATAATGTCCAGAGATTGGTGCCAAGGATCTATG
AAATGATGGGTCACGTAAAACCCATCAAGTTTGAAGATGTTTATGTCGGGATCTGTTTGAATTTATTAAAAGTGA
ACATTATATTTCCAGAAGACACAAATCTTTCTTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTG
TGATTGCAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTGGCAGGTCATGCTAAGGAACACCACATGCC
ATTATTAA

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FIGURE 482

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQDFHFTLREHSNCSH
QNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEAEKEDKMLALSLEDEHLLYGDIIHQDFLD
TYNNLTTLKTIMAFRWVTEFCPNAKYVMKTDTDVFINTGNLVKYLNLNLNHSEKFFTGYPLIDNYSYRGFYQKTHIS
YQEYPFKVFPFYCSGLGYIMSRDLVPRIYEMMGHVKPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDVC
QLRRVIAAHGFSSKEIITFWQVMLRNTTCHY

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FIGURE 483

CGAAAGGCCGGCCTTGGCTGCGACAGCCTGGGTAAGAGGTGTAGGTCTGGCTTGGTTTTCTGCTACCCGGAGCTGG
GCAAGCGGGTTGGGAGAACAGCGAAGACAGCGTGAGCCTGGGCCGTTGCCTCGAGGCTCTCGCCCGGCTTCTCTT
GCCGACCCGCCACGTTTGTGTTGGATTTAATCTTACAGCTGGTTGCCGGCGCCCGCCCGCCCGCTGGCCTCGCGGT
GTGAGAGGGAAGCACCCGTGCCTGTGGCTGGTGGCTGGCGCCTGGAGGGTCCGCACACCCGCCCGGCCGCGCCGC
TTTGCCCGCGGCAGCCGCGTCCCTGAACCGCGGAGTCGTGTTTGTGTTTGACCCGCGGGCGCCGTTGGCGCGCGG
CCGAGGCCGCTGTCGGCGGGGCGGGCGGTTCGCGCGGAGGCAGAGGAAGAGGGAGCGGGAGCTCTGCGAGGCCG
GGCGCCGCCATGGAACTGGGCCCCGAGCCCCGCACCGCGCCGCTGCTCTTCGCCTGCAGCCCCCTCCCGCGTCG
CAGCCCGTCGTGAAGGCGCTATTTGGCGCTTCAGCCGCCGGGGACTGTGCGCTGTCACCAACCTGACCGTCACT
ATGGACCAGCTGCAGGGTCTGGGCAGTGATTATGAGCAACCACTGGAGGTGAAGAACAACAGTAATCTGCAGAGA
ATGGGCTCCTCCGAGTCAACAGATTCAAGTTTTCTGTCTAGATTCTCCTGGGCCATTGGACAGTAAAGAAAACCTT
GAAATCCTATGAGAAGAATACATTCCCTACCTCAAAGCTGTGTTGGGATGTAGTCCAGCTCTGAAGAGGAGCCAT
TCTGATTCTCTTGACCATGACATCTTTCAGCTCATCGACCCAGATGAGAACAAGGAAAATGAAGCCTTTGAGTTT
AAGAAGCCAGTAAGACCTGTATCTCGTGGCTGCCTGCACTCTCATGGACTCCAGGAGGGTAAAGATCTCTTCACA
CAGAGGCAGAACTCTGCCCAGCTCGGAATGCTTTCCTCAAATGAAAGAGATAGCAGTGAACCAGGGAATTTCAAT
CCTCTTTTACACCCAGTCACCTGTGACAGCCACTTTGTCTGATGAGGATGATGGCTTCGTGGACCTTCTCGAT
GGAGAGAATCTGAAGAATGAGGAGGAGACCCCTCGTGATGGCAAGCCTCTGGACAGCTCCTCTCGTCATGAGA
ACTACAAACCTTGACAACCGATGCAAGCTGTTTGACTCCCTTCCCTGTGTAGCTCCAGCACTCGGTCACTGTTG
AAGAGACCAGAACGTTCTCAAGAGGAGTCTCCACCTGGAAGTACAAAGAGGAGGAAGAGCATGTCTGGGGCCAGC
CCCAAAGAGTCAACTAATCCAGAGAAGGCCCATGAGACTCTTCATCAGTCTTTATCCCTGGCATCTTCCCCAAA
GGAACCATGAGAACATTTTGGACAATGACCCAAGGGACCTTATAGGAGACTTCTCCAAGGGTTATCTCTTTCAT
ACAGTTGCTGGGAAACATCAGGATTTAAATACATCTCTCCAGAAATTATGGCATCTGTTTTGAATGGCAAGTTT
GCCAACCTCATTAAAGAGTTTGTATCATCGACTGTGATACCCATATGAATACGAGGGAGGCCACATCAAGGGT
GCAGTGAACCTTGACATGGAAGAAGAGGTTGAAGACTTCTTATTGAAGAAGCCATTGTACCTACTGATGGCAAG
CGTGTCAATTGTTGTGTTTTACTGCGAGTTTTCTTCTGAGAGAGGTCCCCGCATGTGCCGGTATGTGAGAGAGAGA
GATCGCCTGGGTAATGAATACCCCAAACCTCCACTACCTGAGCTGTATGTCCTGAAGGGGGGATACAAGGAGTTC
TTTATGAAATGCCAGTCTTACTGTGAGCCCCCTAGCTACCGGCCCATGCACCACGAGGACTTTAAAGAAGACCTG
AAGAAGTTCGACCAAGAGCCGGACCTGGGCAGGGGAGAAGAGCAAGAGGGAGATGTACAGTCGTCTGAAGAAG
CTCTGAAGGGCGGCAGGACCAGCCAGCAGCCCAAGCTTCCCTCCATCCCCCTTTACCCTCTTTCCTGCAGAGA
AACTTAAGCAAAGGGGACAGCTGTGTGACATTTGGAGAGGGGGCCTGGGACTTCCATGCCTTAAACCTACCTCCC
ACACTCCCAAGGTTGGAGCCCAGGGCATCTTGCTGGCTACGCCTCTTCTGTCCCTGTTAGACGTCTCCGTCCAT
ATCAGAACTGTGCCACAATGCAGTTCTGAGCACCGTGTCAAGCTGCTCTGAGCCACAGTGGGATGAACCAGCCGG
GGCCTTATCGGGCTCCAGCATCTCATGAGGGGAGAGGAGACGGAGGGGAGTAGAGAAGTTTACACAGAAAATGCTG
CTGGCCAAATAGCAAAGAG

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FIGURE 484

MELGPSPAPRLLFACSPPPASQPVVKALFGASAAGGLSPVTNLTVTMDQLQGLGSDYEQPLEVKNNNSNLQRMGS
SESTDGFCLDSPGPLDSKENLENPMRRIHSLPQKLLGCSPALKRSHSDSLDHDIFQLIDPDENKENEAFEFKKP
VRPVSRGCLHSHGLQEGKDLFTQRQNSAQLGMLSSNERDSSEPGNFIPLFTPQSPVTATLSDEDDGFDLLDGEN
LKNEEETPSCMASLWTAPLVMRTTNLDNRCKLFDSPSLCSSSTRSVLKRPERSQEESPPGSTKRRKSMGASPKE
STNPEKAHETLHQSLSLASSPKGTTIENILDNDPRDLIGDFSKGYLFHTVAGKHQDLKYISPEIMASVLNGKFANL
IKEFVIIDCRYPYEYEGGHIKGAVNLHMEEVEDEFLKKPIVPTDGKRVIVVFHCEFSSERGPRMCRYVREDRL
GNEYPKLHYPELYVLKGGYKEFFMKCQSYCEPPSYRPMHEDFKEDLKKFRTKSRTWAGEKSKREMYSLKKL

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FIGURE 485

GGAGAAGGGGTTTGAGATAGTGAATTCCTAAGAAGAAAATAATGGATTGCATATTAGTTGTTCTCTAAGTGGACT
CAACAGTGTGCAAGCTTGTTGGAAAAGCCAAAAGAAGATGGCAACTCCTTATGTCCCAGTTTCTATGCCCATAGG
AAACTCTGCTTCCAGTTTTACAACAAACAGAAATCAAAGAAGTTCTTCTTTTGGCAGTGTCTCAACAAGCTCAAA
TTCTTCTAAGGGCCAGTTAGAAAGACTCAAATATGGGTAATTTTTAAACAGACAAGTGTTCCTGATCAAATGGATAA
TACTTCATCTGTCTGTAGCAGTCCCCTCATTAGGACTAAATTTACAGGTACAGCTTCTTCCATTGAGTATTCTAC
TAGACCAAGAGACACTGAAGAACAAAATCCGGAAACAGTGAATTGGGAAGATAGACCATCTACACCTACTATACT
GGGTTATGAAGTGTGGAAGAAAGAGCTAAATTTACTGTATATAAAATACTAGTAAAGAAAACCCCAAGAAAG
CTGGGTAGTTTTTCAGAAGATACACTGACTTCTAGGCTTAATGACAAATTTAAAGAGATGTTTCCAGGTTTTCG
ATTAGCACTTCTCCAAAACGCTGGTTTTAAAGATAATTACAATGCTGACTTTTTAGAAAGACAGACAATTAGGATT
ACAAGCGTTTTCTTCAAAATTTAGTAGCTCACAAGGACATTGCTAACTGCCTTGCAAGTGTCTGGATGAGATCTAGAGC
GGATGATCCACCGGGTCCATTTGATAGCCTAGAAGAAAGCAGGGCATTCTGTGAACTTTAGAAGAGACAAACTA
CCGCTTACAGAAAGAACTACTTGAAAAACAAAAGGAGATGGAATCACTAAAGAACTGCTCAGTGAGAAGCAACT
TCATATAGACACTTTAGAGAACAGAATCAGAACATTGTCTTTAGAACCTGAAGAATCACTGGATGTGTCAGAAAC
AGAAGGTGAACAGATCCTAAAGGTGGAGTCCCTGCACTTGAGGTTGATCAAGATGTCTGGATGAGATCTAGAGC
TGATAATAAACCATGCTTAAGTTTTAGTGAACCTGAAAATGCTGTATCAGAGATAGAAGTAGCAGAAGTGGCATA
TGATGCTGAAGAAGACTTAATGTATCACAAGCAGTTCCTCCATTTAGACTATTCAAAAATTTAGAAGAGTGGCAA
ATACTATTTTAAAGAAGAACCAAGAACTGTAAAACATATAGAAAAGAGCAAGAATGCACATGTATAAAGTTTAC
ATAAAGAGTTTTTTTAGTTATTGAGATAGGAAATAATTCAGTGTCTTTTAAATTGTATTTTATCCAATTACAT
TTAATACACTAAAAAAATCTTGTTGGAATTCGTATCAAGGCCACATTCTTAAATACTGTGCATAAATTATT
ATGGTGTTTTGCCTATATATTGCTCCAACTACTGTGTATATATGTATGTGTGTTAAATCACCAATTATATTAAT
CAAATGGAAATTAATTCGATGTTTCATATCTGGGTGATATATTCTTCTTTATATCTCTGACATGACATATTTTCAT
TAATAGTTTAAATCAGTGACCATCATAATAAAGATAAAATTTAGTTGAGTTTTTAAATGTTTACATGTTTACATCT
CTAAATAAAATTTGCTTATTTGAAATGTTAATGCTCTTTAGAAAAATGACTTTCTAGTACCAAAGGAAAACCTACT
TGAAAGAGCTGTAAATCATATAGCTAAAGTGATAAGATAGCCTTGATTTTTAAAGCTGATTCAATTAATATCAAAAT
ACTTTAATAAGTGTACAGTTATTAATATGTAACATTTGTTTAGTTTTCCACGTAATCTTTATCTCTACCTAGATT
TAGTGAGTTTGCCTCTTTCAGAATACTACCTCCTTTTGTTA

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FIGURE 486

MATPYVPVPMPIGNSASSFTTNRNQRSSSFGSVSTSSNSSKGQLEDNMGNFKQTSVPDQMDNTSSVCSSPLIRT
KFTGTASSIEYSTRPRDTEEQNPEVTNWEDRPSTPTILGYEVMEERAKFTVYKILVKKTPEESWVFRYTDFSR
LNDKLEMFPGFRLALPPKRWFKNYNADFLEDRLGLQAFLONLVAHKDIANCLAVREFLCDDPPGPFDSLEE
SRAFCETLEETNYRLQKELLEKQKEMESLKLLSEKQLHIDTLENRIRTLSLEPEESLDVSETEGEQILKVESA
LEVDDQDVMMRSRADNKPCLSFSEPENAVSEIEVAEVAYDAEED

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FIGURE 487

CCCTTTTCGCTGCGGCCTTTCCCAACCCGGACCCGGCACTTCTCGGGTTCCGCGACTGCCGATCGCCCCGGCGCG
GCACCGCTCCCTCAGGAGTCGCCTAGGCCGCGCAGTCTCCCGACTTCTCGTCAGGCTTTTCGCGCCGGCGCTCCAG
CAATCACTGGCTGGAGAAGGTGGGCGTTCCGGCTCGAGAGGACCCTGCCGCGGCTCCGGAAGAGCCTCGTCCTGG
GCGGCGGTGGTGC GGCGGTGCGCGTTATGGCCACTGGGCTGGGCGGCTGACCGCGGGCTAGGAAAGGGCCCAGGG
CCCGAATCTCGGTGGCCGCTGCTCCAGCGCGGCCTGCGCCATGGCCTCCTCCGCGCCTCCTCGGAGCATTTCGA
GAAGCTGCACGAGATCTTCCGCGGCCTCCATGAAGACCTACAAGGGGTGCCCAGCGGCTGCTGGGGACGGCGGG
GACCGAAGAAAAGAAGAAATTGATCAGGGATTTTGATGAAAAGCAACAGGAAGCAAATGAAACGCTGGCAGAGAT
GGAGGAGGAGCTACGTTATGCACCCCTGTCTTTCCGAAACCCCATGATGTCTAAGCTTCGAAACTACCGGAAGGA
CCTTGCTAACTCCATCGGGAGGTGAGAAGCACACCTTTGACAGCCACACCTGGAGGCCGAGGAGACATGAAATA
TGGCATATATGCTGTAGAGAAATGAGCATATGAATCGGCTACAGTCTCAAAGGGCAATGCTTCTGCAGGGCACTGA
AAGCCTGAACCGGGCCACCCAAAGTATTGAACGTTCTCATCGGATTGCCACAGAGACTGACCAGATTGGCTCAGA
AATCATAGAAGAGCTGGGGGAACAACGAGACCAGTTAGAACGTACCAAGAGTAGACTGGTAAACACAAGTGAAAA
CTTGAGCAAAAGTCGGAAGATTCTCCGTTCAATGTCCAGAAAAGTGACAACCAACAAGCTGCTGCTTTCCATTAT
CATCTTACTGGAGCTCGCCATCCTGGGAGGCCTGGTTTACTACAAATTCTTTTCGAGCCATTTGAACTTCTATAGG
GAAGGGTTTGTGGACCAGAACTTTGACCTTGTGAATGCATGATGTTAGGGATGTGGATAGAATAAGCATATTGCT
GCTGTGGGCTGACAGTTCAAGGATGCACTGTATAGCCAGGCTGTGGGAGGAGGGAGGAAAGATGAAAAACCACTT
AAATGTGAAGGAACAACAGCAACAAGACCAGTATGATATACCAAGGTAATAAATGCTGTTTATGACTTCTTTAAA
AAAAAAAAAAAA

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FIGURE 488

MASSAASSEHFEKLHEIFRGLHEDLQGVPERLLGTAGTEKKKLIRDFDEKQQEANETLAEMEEELRYAPLSFRN
PMMSKLRNYRKDLAKLHREVRSTPLTATPGGRGDMKYGIYAVENEHNMNRLQSQRAMLLQGTESLNRATQSIERSH
RIATETDQIGSEIIIEELGEQRDQLERTKSRLVNTSENLSKSRKILRSMSRKVTTNKLLLSIIILLELAILGGLVY
YKFFRSH

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FIGURE 489

TGCCTATCATCTGGCCACATGAGGCTGTCAAGCAAAGAATAGGAGTGTAGTTGAGTAGCTGGTTGGCCCTACAT
CTCTGAGAAGTGACGGCACACTGGGTGGCATAAGATATCCTAAAATCACGCTGGAACCTTGGGCAAGGAAGAAT
GTGAGCAAGAGTAGAGAGAGTGCCTGGATTTTCATGTCAGTGAAGCCAAGTCACCATATCATATTTTGAATGAAC
TCTGAGTCAGTTGAAATAGGGTACCATCTAGGTCAGTTTAAGAAGAGTCAGCTCAGAGAAAGCAAGCATAAGGGA
AAATGTCACGTAAACTAGATCAGGGAACAAAATCCTCTCCTTGTGGAATATCCCATGCAGTTTGTTGATAACAAC
TTAGTATCTTATTGCCTAAAAAAAAATTTCTTATCATTGTTTCAAAAAGCAAAATCATGGAAAATTTTGTGTGT
CCAGGCAAATAAAAGGTCATTTTAATTAGCTGC

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FIGURE 490

MSRKLDQGTKSSPCGNIPCSLLIQLSILLPKKKFLIIVSKKQNHGKFLLSRQIKGHFNLA

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FIGURE 491

ACAGCAGTTACACTGCGGCGGGCGTCTGTTCTAGTGTTTGAGCCGTCTGTGCTTCACCGGTCTACCTCGCTAGCAT
GTCGGGCCGCGGCAAGACTGGCGGCAAGGCCCGCGCCAAGGCCAAGTCGCGCTCGTCGCGCGCCGGCCTCCAGTT
CCCAGTGGGCGGTGTACACCGGCTGCTGCGGAAGGGCCACTACGCCGAGCGCGTTGGCGCCGGCGCGCCAGTGTA
CCTGGCGGCGAGTGCTGGAGTACCTCACCGCTGAGATCCTGGAGCTGGCGGGCAATGCGGCCCCGCGACAACAAGAA
GACGCGAATCATCCCCCGCCACCTGCAGCTGGCCATCCGCAACGACGAGGAGCTCAACAAGCTGCTGGGCGGGCGT
GACGATCGCCAGGGAGGCGTCCCTGCCAACATCCAGGCCGTGCTGCTGCCAAGAAGACCAGCGCCACCGTGGG
GCCGAAGGCGCCCTCGGGCGGCAAGAAGGCCACCCAGGCCTCCAGGAGTACTAAGAGGGCCCGCGCCGCGGGCCG
GCCGCCCCAGCTCCCCATGCCACCACAAAGGCCCTTTAAGGGCCACCACCGCCCTCATGGAAAGAGCTGAGCCG
CTTCAGACTGCGGGGCAAGCGGGCCGCGGCTCCCTTCCCCTCCCCTCCCCTCGCCCGCCTTCGCCGCCCCGGCCTC
GAGTCCCCGCCCCCCCCGCTCCCGTCCCGCACCGCCTGCCGCGTGGCCTCGGGCCTGCCCTGTCCGCCGTCCG
CCCTCCGGTAGGGTTTCGGGCCTTCCGGATGCGGCTTGGGCGCTCTTCGGGGACCTCCGTGGCGCGGAAGACCCGA
GCCTGCCGGGGGGAGGCCGGCGGCGCCGACCTGCCCGCCTCGGCGTTTCGTGACTCAGCCGCCCCATCCCGAGTC
GCTAAGGGGCTGCGGGGAGGCCGCGAGCACCTTCTGGAAGACTTGGCCTTCCGCTCTGACGCGAGGCGGAGGTGGG
CAGTCCAGGCCGAGAGCCGGCGGCCCTGAAGGTGAGTGAGGCCCTCGGCAGCTGCAGCCGGGGTGTCTGGTACCC
CCCCGGCGTGGTGCTTAGCCAGGACTTTCAGACGGCCGCTGGCCGGGAGGCTTTGGTGGGAGAGACGCGATCGC
CGATTTGCGTCTGGCGCCCCCTTCTGCGGCCGGGACCCAGGCCTTTCACATCAGCTCTCCCTCCATCTTCATTCA
AGGTCTGCGCTGGGGCCGGGACGAAGCACTTGGTAAACAGGCACATCTTCCTCCCGAGTGACTGCCTCCTAGGAGG
ACATTTAGGGGAGGGCAGAGGCCTGCAGTTTGGCTTCACGGCTGGCTATGTGGACAGCAAGAGTCGTTTTGCGGA
ACGCGACTGGCAGCCAGGCCTGTCGGGCCCCGACGCCGCCCATTTCCCTTCCAGCAAACCTCAACTCGGCAATC
CAAGCACCTAGATACCAGCACAAAGTCGGTTAATCCCTGTCTGGACTGAGCCTCCGTTGGCTTCTGAAGTGAATT
CTGCAGCTAACCCCTTCCAGACTAGAACCTTAGGCATTGGGGAGTTTTAGATGGACTAATTTTATTAAAGGATTG
TTTTTTTTTT

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FIGURE 492

MSGRGKTGGKARAKAKSRSSRAGLQFPVGRVHRLLRKGHYAERVGAGAPVYLAADVLEYLTAEILELAGNAARDNK
KTRIIPRHLQLAIRNDEELNKLGGVTIAQGGVLPNIQAVLLPKKTSATVGPKAPSGGKKATQASQY

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FIGURE 493

GATGACAATAAGGAAGTTCCTTTCCTTTGGGATTATTTCTGCCTGAAAGCTCAAGACTTTTAGCCACATCATTGT
CTGGGCTCCACGGGAAGGCAGTGCCACATGCTGAGGCATGCTGGGAAAAGACTTTGTTCCATCCTGTTTTGTTGA
CATGCTCTTCATTTTTAAGCCTGAAACCGAAGCTTCCTGCTAAGAATTCAAACCATGGAGAAAAACGCAGCCATG
ATAACGGCCACTACTTCCTGAGCCTCCAGTGTTCCCTGTGCTTGGGGATCCATATATGTCACTTAACCTTAACCT
TCACAACACCAGGGCAGCCTCCATTTTCACAAGTGAAGAAATGGAGGCCCAGAGTCACTTAGAAGATGCTCGAAG
GTGCACAGCTGCTAAGTGGTGGTGCTGGGATTTGTCTCAGGTCCTCAAGAGTCCTGACTCTTATGTGCTGGCTC
CCCACGGAGGCGTGGAGTCTTGTGTTGCTGGGCATTTGACAGAAATGTTTCTGCTCATCTTCTGCCACAGGTTGGT
CCTTCAGCGTCAAGATTCTGGGCCACTTATTAATAGAAGGCACCAGGACACAGGTGCAGGGATGCAGAGCTGGA
TGCTGCCTTCTCAATAGGAGAAGCCAAGAAACGCAGATGCCGATGCTTAATCAACTCCGTCTCTCCCTCTAGTGA
CTCGGGGATAGCTGCCCTGATGCCAAGGCGATTGTCTTCTGGAAGCAGCCACGCCGTGTGAGGTTTCTCATCACT
GCCCTGCATCTCCCTGCGAGCTCTCGGGGATAATTGCAAATCACGTTTGATTCCAGGGGAGCAGAAAGCAGCAG
GAGCCGTGAATTCTCCAACCTCTAACTGGTCCTCGACTGGAGCCACTTTCCCTGCCCACCCATCCCTGTGGCGG
ATTCAATTACAGTTATCCAAAGCCGTTTTAACTTTGCTCCCCCTGGGCTCAGAAGTCTGTGAGTGGGTCTGAGC
GGCTTCACCATTCAAGTTTATTCCTATCAGCCTGGAATACAATGCTCTATCTGGCTCCGGTTGCTTCTCCAAACC
TTCTCTC

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FIGURE 494

MLYLAPVASPNLL

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FIGURE 495

AAAAAAAAAGAAAAAAAAAGATATATATATTCCTACTCTTATTAAATGAATATAGCATTTCCTAGCAACTTCTTTT
GATTTGTGAGTATATATTTTCTTGGCCTCAAAATTAAAGTAAAAAGTATCCTCTTACTCAGAGGAGGACAGGGGC
AAGAGCCTGGGACCTTATTGCTAATTAAAATGNNNNNNNNNNNNNNNNNNNNNNNGACAGACAATTTTGAGAGC
CATTTTAATATAATTGCCTCCCTAGAAACATACCTTTTAGGGAATTTTATCACTAAACCACATGTTATTTAAAT
ACGTACATGTTTAAACATAAATACATACATAAAATTACATGCATACTTAACACTTATGTTAAATATATTCAATGT
ATATACATATGTACACAATATATGCATATATACATGTGGGTATGTGGTATGTGTGCATGTGTGTGTATGGCCAGC
TACATAATTGGGGGGGACTAGGGGCAAAATGAAACTGTACGGCCCTCGTTCAAAAATTAGGTGTGGGGTGCTTCT
AAGCACAGTCTTGTGCAACTGCACAGGTTGCATGTCCATGAAGCCATCCTGTGTGTGTGCACATATGTGTATGAA
TATGTATTTTATATAATACATATATATGCATGTATGTATCTGAGAAGAAATGTTTAAAAGGCTACATACAAGCTT
TTCCAGGTCTCTACTATCTGTAACTAACTAGAGACATAACTCACAATATGCAGTCCCCACTGAGTGTTTACCAT
AATTTGAGATTCTTGGCATGTAACTTTTCATTATGGAATATTGAATAATTTCAATATTTATCATACATTTCTTG
ATGTTCAAACATACACAAAAATAGAATAATGAAACTCTACCCATCACCCAGCCTGGGTGACAAGAGCAAACTCA
GTTTCNNNNNNNNNNNNNNNNNNNNNNNNNNNTATATATTCCTACTCTTATTAAATGAATATAGCATTTCCTTAGCA
ACTTCTTTTGATTTGTGAGTATATATTTTCTTGGCCTCAAAATTAAAGTAAAAAGTATCCTCTTACTCAGAGGAG
GACAGGGGCAAGAGCCTGGGTGACAAGAGCAAACTCAGTCTCAAAAA

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FIGURE 496

KKRKKKIYIFLLLLNEYSIS

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FIGURE 497

CCTGCCGGCAGAACTCTATGCGGTGCTTTTACAAGAGATTATCGTCACAATGTACTAAACTGTCAGGTACTTATT
ACAGTGCCGGAATGTTTTGAAATCCTGTTGCTTGCTCCTCATCGCCAAAAATGGGTGGAAAGGATCAGATATGTT
ATATTTGATGAGGCTTCCCACTGGCCAAACCCAGTAGAAGCTAGAGGGCTAAGGAGGCTGGGTGAGCCAATTCCC
AAGGTCAGACTCATTGGCCAGAGAGGAAGGTGGCGAATGGTGTAGATCTGGAAGGACATAGCTATGTTATTATCA
AAATGAATGGAAAGAACTGTAAATAGAATTCAAGCTTTGTATTTTGTGCTTCAAGGAATTTTCAACTTAAAGGA
AAACTAGGTCCATTATCTTGGCAGAGAAGTTGGAGCAAAATTTTGGGAGCTCCTCCTTGTCATTATTTCGATGTCC
CTTTTTGGTTCTTTTCAGCTACCATAAATAACCCAAATCTTCTCACCAAGTGGCTGCAATCAGTAAAACAGTACTG
GAAACAGGCAGACAAGATTATGGAAGAGAAATGTATTTCTGAAAAACAGGCTGACAAATGTCTCAACTTTCTCCA
AGACCATTATATAAAAAATCAATCATATTGAAGTTAGACTTGTGCTCTGTGGAGAGAGATACCATGATTTAGAG
AAGCATATATGTTTCAGTAAACATGATGATGTTTATTTTGATCATTTCATCCCTGTGCTGCGCTAACGACAGAT
ATTATTGAAAAGTATGGATTCCACCTGATCTTACCCTCACCCCTCAAGAAAGCATCCAGCTTTATGATACCATG
GCTCAAGTCTGGGAAACTTGGCCCAGGGCTCAGGAATTGTGTCCAGAGGAATTCATTCTTTTTAAGAATAAGATA
GTCATTAAGAAGTTGGATGCTAGAAAAATATGAAGAAAACCTTAAAGGCAGAATTGACAAATTGGATTAAAAATGGC
CAAGTGAAGAAGGTCAAAAGAGTACTGAAGAACCTTAGTCCGGATTCAATTGTCTAGTTCAAAAGATATGGTGAAA
ATGTTTCCTCTTCTTGTTTTAAAAGTTAAGACAAATGGATAAGTTGCCTGCAATATTTTTTTTGTTTAAGAATGAT
GATGTGGGAAAAAGAGCTGGAAGTGTGTGCACCTTTCTGGAGAAGACAGAGACAAAAAGCCATCCCCACACTGAA
TGTCATAGTTATGTCTTTGCAATAGATGAAGTACTTGAAAAAGTGAGGAAGACACAGAAAAGGATCACTAAAAAA
AACCCAAAGAAGGCTGAAAACTGAAAGAAAAAAAGTGTATAGGAGCTGAATATATTAATTTCTGGAGAATCT
GAAGATTCTGGA

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FIGURE 498

PAGRTL CGAFTRDYRHNVLNCQVLITVPECFEILLAPHRQKWVERIRYVIFDEASHWPNPVEARGLRRLGEP
IP
KVRLIGQRGRWRMV

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FIGURE 499

AGAGGCCACATCTGCTTCCTGTAGGCCCTCTGGGCAGAAGCATGCGCTGGTGTCTCCTCCTGATCTGGGCCCAGG
GGCTGAGGCAGGCTCCCCTCGCCTCAGGAATGATGACAGGCACAATAGAAACAACGGGGAACATTTCTGCAGAGA
AAGGTGGCTCTATCATCTTACAATGTCACCTCTCCTCCACCACGGCACAAGTGACCCAGGTCAACTGGGAGCAGC
AGGACCAGCTTCTGGCCATTTGTAATGCTGACTTGGGGTGGCACATCTCCCCATCCTTCAAGGATCGAGTGGCCC
CAGGTCCCGGCCTGGGCCTCACCCCTCCAGTCGCTGACCGTGAACGATACAGGGGAGTACTTCTGCATCTATCACA
CCTACCCTGATGGGACGTACACTGGGAGAATCTTCCTGGAGGTCCTAGAAAGCTCAGTGGCTGAGCACGGTGCCA
GGTTCAGATTCCATTGCTTGGAGCCATGGCCGCGACGCTGGTGGTCATCTGCACAGCAGTCATCGTGGTGGTGC
CGTTGACTAGAAAGAAGAAAGCCCTCAGAATCCATTCTGTGGAAGGTGACCTCAGGAGAAAAATCAGCTGGACAGG
AGGAATGGAGCCCCAGTGCTCCCTCACCCCCAGGAAGCTGTGTCCAGGCAGAAGCTGCACCTGCTGGGCTCTGTG
GAGAGCAGCGGGGAGAGGACTGTGCCGAGCTGCATGACTACTTCAATGTCCTGAGTTACAGAAGCCTGGGTAACT
GCAGCTTCTTCACAGAGACTGGTTAGCAACCAGAGGCATCTTCTGGAAGATACACTTTTGTCTTGCAATTATAG
ATGAATATATAAGCAGCTGTACTCTCCATCAGTGC

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FIGURE 500

RPHLIPVGPIGRSMRWCLLLIWAQGLRQAPLASGMMTGTTIETTGNI
SAEKGGSIILOCHLSSTTAQVTQVNWEQQ
DQLLAICNADLGWHISPSFKDRVAPGPGGLGLTLQSLTVNDTGEYFCIYHTYPDGT
YTGRIFLEVLESSVAEHGAR
FQIPLLGAMAATLVVICTAVIVVVALTRKKKALRIHSVEGDLRRKSAGQEEWSP
SAPSPPGSCVQAEAAPAGLCG
EQRGEDCAELHDYFNVLSYRSLGNCSFFTETG

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FIGURE 501

AACGGTCTAAGGTAGCCAGGCGGGTTAGGGCTCAGGCAGGGCTTGAGCGGGACGAGGGGGCGGGCTCCGAGGCGG
GCTAGATGCCCTGGGCTGGATGAAGTCCGAGTCTGGGAAGAGAACCGTGTGTGGCGGGAGGAGGCGGTGATTGGG
GTGGTGGGGCTAAGCGCGGGGGCAGGGCTCGAGCGAGGGGGCGGGGTAGCACCTCCGCCTGTCGGTGGTGGGGC
GGAGGCTGGAGGGGGTGGGCCTAGGATGCGTGAGGCGGCAGCTCGCGTGGGGCGGTGACCATGCCTGGCGGGGGC
GGGGCCGGAGGCGGGCGGTTTAGAGAGCGGGGCGGTCTGCGGGGTGGGGCGGGGCTGGTGGGGCGGGGCGCT
GTGCGGTCTGCGGCGCGGAGCCGAGTGGGCTGCGGGGATGCGGGGGACCAGCTGCGTGGGCGGCGGCGCCGAGAG
CCCCGGAGGCGCGGGGCTGAGCGAGGGCCGCGGGGGCGCTGGCTGCGCTTGGCTCCGGTATGCGCCTACTTCCT
CTGCGTCTCGCTAGCTGCCGTGCTGCTCGCCGTGTACTACGGTCTCATCTGGGTACCCACGCGGTCTCCGCGGGC
ACCCGCGGCCCCACAGCCAGCGCGCCGTCCCTCCGTGTGCTGCCCTCCCGGGCGTGCCGCCTGTCCCGGCGCC
CGCCGCTGCCTCCCTCTCCTGCCTCCTGGGAGTCCCGGCGGGCGCGACCCAGCTCCAGCTGCCGCTGAGCCG
CCGCGCGCGCTACAGCGACCCGTACCGCCGTCCGAGCCGCCAGACACCCAGAGAGACGCCAGAGGCGCGGAGGG
GCGAAGACCCGGGTAACCTCTCCCTTCCACCCCAACCCGGATCGCCAGCCCTCGAGAGCTCTGTGCTCCACGCCGA
GGATGCACCGTCTCTGGATTGGTCCGGCCTTCTTCTAATGACATCGCTCAGCGTCTCTGGAGCCGTCATCCCGC
GGAATGGGGGGCCAGGGGGTGTGAGCTCGGGGCCTTGCCCTTTGAGCTACTCTGTGGTCAGGCCGGGTCTCTCA
CCATCAGGAAGATCCCATCCTGAGCTCTGTCTCCTGCCCTCCTGCTGTGGGATGCTGAGCACAGAGCCCACAGC
CCATCTGCCTCTTACCTCCCTGAATCCGTGTCCATCTGCAATAAACGACAGCCTCGGCTGCCTCGTGCTGTGTC
AAAAAATCTATGTCGGGTGCGGAGAAAGAGGTAATGAATGGCAGGAATTCGATATCAGCTTATCGATAC

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FIGURE 502

MKWQEFDISLS

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FIGURE 503

TTTACGATATCCAAATAAACTGGACACCATCACATGGACGTGGCAAGGACCTGGAGCGCTGGAAATCCTGTGGCT
CACGCTGTGTCAAGTTTCACAACCAAGTGGAAATCGAGTTTCCTTCCCTGTGTACAGCCCTTCTGAGGAGGAGAAGAG
GAACCCCGCGCTGTATGCCAGCAACGTGCGGCGAGTCAATGGCCGAGGCCCTTGGGTGTCTCCGTGACTGACTACAC
GTTTCGAGGACTGCCAGCTGGCCCTGGCGGAAGGACAGCTCCGTCTCCCGCTGACACTTGCCTTTTAGAATTTGC
CAGGCTCGTGGGGGCCCTCGGGCTAAAACCAGAAAAGCTTGAAAAAGATCTGGACAGATACTCAGAAAGAGCCAG
GATGAAGGGAGGAGAGAAGATAGGTATTGCGGAGTTTGCCGCTCCCTGGAAGTCCCGTTCCTGACTTGCTGGA
AGACATGTTTTCACTGTTTCGACGAGAGCGGCAGCGGCGAGGTGGACCTGCGAGAGTGTGTGGTTGCCCTGTCTGT
CGTCTGCCGGCCGGCCCGGACCCTGGACACCATCCAGCTGGCTTTCAAGACGTACGGAGCGCAAGAGGACGGCAG
CGTCGGCGAAGGTGACCTGTCCTGCATCCTCAAGACGGCCCTGGGGGTGGCAGAGCTCACCGTGACCGACCTATT
CCGAGCCATTGACCAAGAGGAGAAGGGGAAGATCACATTGCTGACTTCCACAGGTTTGAGAAATGTACCCTGC
CTTCGAGAGGAATACCTGTACCCGGATCAGACACATTTGAAAGCTGTGCAGAGACCTCACCTGCGCCAATCCC
AAACGGCTTCTGTGCCGATTTCAGCCCGGAAAACCTCAGACGCTGGGCGGAAGCCTGTTTCGCAAGAAGCTGGATTA
GGACCCAGGGTTGCGGAGAGACGCGGCCCTCCCGCGTGGACATCACCGCCATGAGCCTCTTTGCGAGTGACCTC
TGGGCTCCGCTCCTCACTCCTGCTGTACAGGCACTGTCTTCAGCCCGAGTTCCAGGGGCCCTCGGGGGCTGTTTGT
ATCTTGTTTCCTTTGTGAAGTGIGTTGCAGAACCGACGCTTACTGTGCGAGAATCGGAGGGCGCGCACGCGGATCC
CCCGCTGGCCTGGACCCCGTGGGGTCAGGTTCCCTGCGGGCGGGGGCACCGGTGCGGCCCCGTGTTCTCCCA
CGGGGCCCTGGTTTCGAGTCTCTGTACAGCCTCTTCGGCGGCGAGCGTGACCGGGCGGGCCTCCGTGCACACT
CAGCACACGCTGCCACACAGCGTGCGCTTGCGTGTCACTCTGGCAGCAAACCTGTCTGCCTCTGTGGATCCACA
GCCTGGCAGAGCCGAGCGCTCACCTGATTTTTTCAGTGTCTTACCTGTGTGCTGGAGCTCATGAGTATTTTATAA
ACTCCATTTAGTACTTCAGGAAACATGCAGCATTTTTTAAAAATGAAAATTGTTTTTCTACTTCATTTTTCTCT
TTTAGAGTCAAAGGATATTTATTTATAGGCCTTTTTTTTTTAATATAGAATCTGAGGCTGTTTGGGCTTTGACTT
AAATTTCCATCAGGCCTCTCTCCAGCAGGTAATCCCTCTGCTTCCGCTGGGTCCCCTGGGGAGGTGTGAACCTCAA
GGGCTTAGCCCCAAAACACTTTTTCTGCTTTTTCTTAATCCTTTTCCAGTCCCCTCTTTTTTTATAAACGTTGGCA
GTTTGATGTTTCTGTTTCGGCATAACGTAATCCATTTCACTGTAGCCTAAACTCCAGTCCGAGGTTGGATATTGT
TCAATGAGCAGGGCCCGAGCTGGAAGCGCAAGGCAGCCGCGCCGTGCCGCTCCTCCCTTGCCCTCAGGCCAGG
TCCCTGCTGGAAGCGGCTGCATCTTCCTGTGACCCCTGGTTTCCATGGTGACTGGCGTGACGCAGCCACCTGAGT
ATGGCTGACCTTCTCTGCAGAGAGAGGAGCCGAGTCTTTTGCTGTGGAAGGAGACGCTGGGCTGTGCGGTGCGG
AGGGTGATGAGGATGTCTGGTGACAGCCGTGCGGACCACTCCTCTCTGCAGCACTGCCTCCAGCGCCAGGGT
CGCGGGCACATCCCACTGAGAGCGGGGTCTGCCCCATCTTAGAGTCAAAGGCAGAGGGGCTTCCAGGCCCTGG
ATGGGGTATTTTGGTGTCACCTGAAGTCCCTCTGACATCACCTTGTTTCATCATTTTTTATGACAGAATTAGAAA
CCCATCCTTCAAGCACAATAATCATCACAGACTTGAGTTTGCTTCCTAAAGCAAAGGCTCCGGGTTTGTTTGGAA
AATTTTTTTGATTTCTGAAATGAATTGATTTTTATATTGGGGCATCTCTATAGAAAGTGACCACCAAGGCCAGT
AAGTACGGGAAAAAATGTTTACTAACTTCTCAGAGATTCTGTGATACGCGTTTCTCCACTGACAGACATTTAAAA
ACAACCTTCAGCTCCGTTTCAATCAATCACCTCGACTTGTTTTTTAGCATGGACACTGCCAGCAGGACAGACAGG
GATGGAGTAAACCGAAGTCAATTTAGGGCTCTTGGCGTGTGGACACAGAAGAAATCCTAGTGCAGCCTTTGGT
AGCTAACAGTCACTGATTTTATAATTGGAGAATGCGTAAAGATTCAATTTTTCAAGGAGAAGAGCCTGCAATGGC
CAATGAAGGAGGTAAATAAACTAAGATATTCCGAGGGAAGGGACCCAGGCCACCTCCCTTCCGCAGGTCTGCAGA
TGAAGGGTTTTTTGAATGAAATGCCACTGCGCATTTTCAGAAAAAAAATCTCTGATAAACAGACTTTGAATGGA
TGTGTGTTCTCTGATTCTCTTTCTCTTCGTGGCGACTTAGAGTTGGCGGATATTCCGAACTGTGAATGTACA
TAGCGTTGAGTTAAACCCCTTGTGTGTGAGACAGGACGACGCGGGCCCTGGTGGCCTGGGGGCCAGACCCGTGG
GCAGGTGGGGCATGGGCCCTGGCCTGCGGGGACCTGCTGGGGTGTGAGGGCAGAGGGAGGGTTGCCATGAAGGAA
CTTGGGATTTTCAATGAATAAATAAAACATAAAGTCTATACTGGG

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FIGURE 504

MAEALGVSVTDYTFEDCQLALAEGQLRLPADTCLLEFARLVRLGLKPEKLEKDLDYRERARMKGGEKIGIAEF
AASLEVPVSDLLEDMFSLFDESGSGEVDLRECVVALSVVCRPARTLDTIQLAFKTYGAQEDGSGEGDLSCILKT
ALGVAELTVTDLFRADQEEKGITFADFHRFAEMYPAFAEEYLYPDQTHFESCAETSPAPIPNGFCADFSPENS
DAGRKEVRKKLD

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FIGURE 505

CGTCAGTATAGGGAGTGTGTGTATAGGGAGGTGGCATCCGGGAGCCCAGCCCAGCAGTGTCTCTGGGCACAGTGA
TTTCAGGGGGATGGCCAGCAGTTGTGAAAGACAGAATGATCTGGAATGTCTCATTGGGAAGACCAAACCCCTTC
TCGCTGCAGATACCAGATAAGCACCCATCTTCACTGTCCACTGTGCAGCCCAGTCCCCTCCAGACAGCCCCAGCA
CAGCATGAAGAAGGCACATGAGCACCGGCGACAGGCTTACAGGACAGGGTGCAGCGGCCAGCATCCCAGGCATCA
GGGACATGTGGGATCTTCCACACACCTGGGATGACATCGAATTAAACATGATGAGAAAATTGCATCTTACTGCTA
ATCCCAGTACAGAACCACTATGGGCAAATTTATAAACTAATCTGCAGAGAGGCAATAACTCTGTCTAAAAAGAA
AACTTGTCCCGTGTGATTACAAAACAGGAAAAGGCTCCAAGCTAGGAAATGAGATTTGAGGTATGGAGAACATT
CTCACCTGATGGAAGCATCCTGTTCTGTACAGGAGGAGGAGCTGGTGCAAGCCCTAGGCCACATATGTCACAGT
TGTTTTGGACCCCTCCGTAGCTTTTATACTCATAAAATATTAAAGTTGCCCTTTTCATATTTGGGTCATTGAAAGA
GCCCACCGTACTCTAGGTTCTGTCTACTATGCACAACATCTCAGAAGATGGCGTACAAAACATTTTTCTAACT
ATAGCACGGGTAATGTGGGGGTGGGAGGCTTGGGATATACCTAAATGTGGCAAATGATTTATCTCCACCTTGA
GGGATGAAAAGGAACTATGCACTTGAATTTTAAT TAAAATTTTAATTTAATTCATTGGATAGCTTGTGCCAGAA
AGAACAGTCAATATTCAAGAAGCAAACTGACGATTAGCTCAGTTTCGGGCCTCCCTGTCGGGGGAGTTTTCTTG
TCTGGAACACAAACACCTACAAGTAGAGTGTGAGCTGGTTCTTGACAATCAGATCTCATCAACCCTTTGAAATGT
TCTGGGCAGCACAGCTCCTTGGTCTGCATGGTTGGTGTAAGTATAATCAAGTAGTGAAATTGTATGGTATATAACC
TATATGCCAACAGTGTACACCCGTATGTGCAGAATTTGCTAATATAACCATTTCAATAAAAACCTATTGAAAAAG
CTGATTTGACCACATGGAGTATTGTTGGTGGTGACGTGTATCACTGAGGACTCTCTTGGTTACAAATGACAGAAA
ACCCAGCAAACTGGCTAACACAAAAGGGAATGTCATGGCTCCCAAAAGCCAAAATGCCAGGGGTGCCTATGTC
AGGCTTGGTGTGATTTACCCCTCAAATGCTGACACCAAGACACATGCCAACTTTG

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FIGURE 506

VSIGSVCIGRWHPGAQPSSVSGHSDFRGMASCCERQNDLECLIGKTKPPSRCRYQISTHLHCPLCSPVPSRQPQH
SMKKAHEHRRQAYRTGCSGQHPRHQGHVGSSHTPGMTSN

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FIGURE 507

CACATGCACCTGGCCTCTGCTTTTTTATTTTAAAGCACAACTAACTGGTAGATAAAGTGATTGTCTTTAGTAT
TTGATAACTAATGGGTTTTAGAGTGTTATTTATAAGATGTAGTAAATTATCCTCATCATTATTTTAAAGACAAAT
TTATAAGACAAGTGTAATAGAAATAGATCAACAGCACAAATAGAAAAAGATGGCAGAAAAACATGAATACGTAATTC
ACAGATGAAAGCAAAACAAATGGTCCTTTTATTAAGGGAATGCAAAGTTAAAAATCAACTAGACCCTTTTTTGTT
TGTTTCTTCTTGGATTGGCAAAGAGGAGCACTTAAAGCTGTATTTTGTTTGGAGGATTAGTTTGGGTTATGTC
TACTAATGACTAAATGTGTACATACATTTTGACCCATTAGTTACACTTCAAAGAATTTTTATCCAACAAAAATGT
ACTGAGACACATTGCTTAGTATAATAAGCCATTGGAAGCTTACCCAAATATTCATCAATGAGAAATAGGTTANGA
AAATTATAGTACAACCATAACATGNAACTGGATGTAGCTGTAAAAGAAATGGGATCGATTTTTTTTTNGTAATGAT
ATGGAAGGATACTCAAAGTATATCAAGTGAGAAAAGATCTAGGAACAGGANNNNNNNNNNNNNNNNNNNNNNNN
NNNGTAGGGACAGGGTCTCACCATGTTGCCAGGCTTAGGAGCAGGATATTAGCTAACTCGTGTTACTTCTGAAA
ATCTTTGAAGCTCCCCCTGCTCTTTTTTCCAGAAGTGTA AAAACAAGCATGTATTTAGTATTACACATTTTTAAA
AAATGAAAAAATGCTGCTGTGTGAATGAAAGAGTATACATCGTGTTGCTCCAGATGGTAAACTAGAGTAGAATT
TACTAAAATAAAGTTTCAGCACGTAAAGTAAAGCACTTCTCTGCTCTTGGCCATTTTAGACACTAACCATCTGGA
GCAACCATGTAACTCTTGCCACTCATAGCTAACTTAATGTAAAGCACTTCTCTGCTCTTGGCCATTTTAGACACT
AACCATCTGGAGCAACCATGTAACTCTTGCCACTCATAGCTAACTTAATGTAAAAAATCGCTTGACTT
TCTTAGCACTTCACAAATGCTTGTAAGACTGACACCAGGAGCCCTGTCAICTAAAAGGCACCTTTATAGAGTGCTT
TCAATTCTTCTGTTTTTTTCATTCAITGCTCAAATAGATCGTAGTGAGATAAGATAGTCTCTGCGCTTCTTGCTC
TTTGGCACAAGGAAGAGGGTTCCAGAGTTGAGAGTAAGGACTTTCATCCTTTGCCATAGAATTTGATTAGGGGC
CATAAAAAGGACCATTTGTGTTCTAGAATGTGAAGGACTAAGCATACCACTTTATAGTGCAAGGAATAAGTGAAGA
AGTCCTTTTATAAGAAAACTGCAGTAGAGCAATAACTTGAAATTACACTTATTTATATTTACTTTTCATTAAAT
GTAAATTATTTCTTTTACCACATTGTACTACTAGAAAGAGAATCAGGAGTTTAGGCATTCAGTCATAGATATTC
GATACCATTGATTACTTAAGCACTTCTCATGTCAACAAGACTTAAGCCTGCAGATAATTCCTATTTTATCAGTG
TTCGTTATAGCTTCCCTGTTGGTTTTACTTGTGAGTCATAAGCCTAGTATGGTGAATATCTAGGAAATTTACGG
TAACAGGGCTTGTCTTAGGTTTTGAGAACAGGTGTAACCTGACTTCTCTGCTGTTTGTCTATCCTACACTCCC
ACTACATCTGGTCCTTTTGTAGGGTGTTGAGAACACATTTTCTTTCATGCAGGGGAAAGTGGAAGTGCATGTT
TTCTAAGAAGGACAAATAGGAATAGAATAAAAGAAAAAGTATATTGG

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FIGURE 508

MKAKQMVLRLRECKVKNLDPFLFVSSWIGKEEHLKAVFCFGGLVWVMSTND

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FIGURE 509

CCAGAAACAGACCTGGGAGTGGAAACAGCAGCAGTTAGGAGAGGACCCTGCTGGGGTCCAGGAGCCCGCCTGCCTG
GCTGCCCAACCAGCTCCAACACTGCTGGAGGCCTCCATTCTCTGTTTCAGGGGAAGGCCCACTGGTTAGCTCAGAG
ATGGCTTCTGCGTGCTTTCTCCCTTCCGTCCTAGAGAACACATATTTCTGTTTCTCCCTTGCCCTTCTCCCACT
TGGACCTGCTCAGAGCCCTGTGTACTCTGGTGTGTGGCCTCTCTCCCTCTCTCTTTTCTCCTTCTGGATTCTT
TCCTATCTTATCCACAATCTCTACCCCTTTATCTTGCCGTTACTCTACCCCGAGACTGCCTTCTGCCCTGGGTCC
CACCAATAGATCCTGTCCCTTCCCTTAGTGAAAATGAGGCCACCTCTTGGGGAACAGAAGACGCCCCAGTGAAAA
CAGAGTGCAAACCTGGCCTGGCATGGGAGCCTCCTTCTGGCCAATCAGGCAGGCCAGAGAACAGCAGCGGAGGGC
CCTGTCTTTTCAGGCAGACCTCATGGCTGAGTGAGCCTCCCTTGGGCCCAGCACCCACCTCAGCATGGTCCAAGC
CCATGGGGGGCGCTCCAGAGCACAGCCGTTGACCTTGTCTTTGGGGGCAGCCATGACCCAGCCTCCGCTGAAAA
AAGCCAGCCAAGAAGCATGTGCGACTGCAGGAGAGGCGGGGCTCCAATGTGGCTCTGATGCTGGACGTTCCGGTC
CCTGGGGGCCGTAGAACCCTATCTGCTCTGTGAACACACCCCGGGAGGTACCCCTACACTTTCTGCGCACTGCTGG
ACACCCCTTACCCGCTGGGCCCTTACGCGCCAGCCACCCAGCCCCAAGCAACTGGAAGAAGAATTCTTGAAGAT
CCCTTCAAACCTTGTGAGCCCCGAAGACCTGGACATCCCTGGCCACGCTCCAAGGACCGATACAAGACCATCTT
GCCAAATCCCCAGAGCCGTGTCTGTCTAGGCCGGGCACAGAGCCAGGAGGACGGAGATTACATCAATGCCAACTA
CATCCGAGGCTATGACGGGAAGGAGAAGGTCTACATTGCCACCCAGGGCCCCATGCCCAACACTGTGTGCGACTT
CTGGGAGATGGTGTGGCAAGAGGAAGTGTCCTCATTTGTCTGCTCACTCAGCTCCGAGAGGGCAAGGAGAAATG
TGTCCTACTACTGGCCACAGAAGAGGAAACCTATGACCCCTTCCAGATCCGCATCCAGGACATGAAAGAGTGCCC
AGAATACACTGTGCGGCAGCTCACCATCCAGTACCAGGAAGAGCGCCGGTCAGTAAAGCACATCCTCTTTTCGGC
CTGGCCAGACCATCAGACACCAGAATCAGCTGGGCCCTGCTGCGCCTAGTGGCAGAGGTGGAGGAGAGCCCCGA
GACAGCCGCCACCCCGGGCCTATCGTAGTCCACTGCAGTGCCAGGATTGGCCGGACGGGCTGCTTCATCGCCAC
GCCAATTGGCTGTCAACAGCTGAAAGCCCGAGGAGAAGTGGACATTCTGGGTATTGTGTGCCAACTGCGGCTAGA
CAGAGGGGGGATGATCCAGACGGCAGAGCAGTACCAGTTCTGACCCACACTTTGGCCCTGTATGCAGGCCAGCT
GCCTGAGGAACCCAGCCCCTGACCCCTGCCACCCTCCGGTGGCCCAGGTGCCTACCTCCCTCAAGCCTGGGAAGG
TGGGTCTGGGGAAAGTGGGCCGAGTGATCTGGGGGTACCCCTTGGGTGGTGTGGGGAAGGAGTGCCCTCCTTAGT
GGTGCTTGCACTACAGGAAGCAGCAGCAGTAAGGACAAGGGGCCGGATTCCAGGTCTTCAACACTGGCCACTCC
TCTGCTTCTCTGTTGGCCCCAGATGGACAGTAAGGGGAACCTCCAATGTCTCTCTGAACCTTAAAGACAGGAGCT
GGCATTATGACAGACAAAGAAAGAGCCAGGTGTCTGGTGTCTCTGAGACACTCTTGTGAGCTTCAGTTT
CCTGTTCTATAACATGAACATAAGTGCTTAGCTGCCATGAGGGAAAAGTAATGAGAGAAGTTCTAGAAGCCACT
CCAGCCACTCCTTCTGGGGCTGACAAAAGGGTGATTCGAAGATCATCCTTACCCGAGGTCTGCCCCAAGCACA
GGCCAGATGCAAGAATGGGGAAAAGTCTGGTCTGATCTCCAAGTCTCAACATCCTATCAGTGACTCTGCTCCCT
GACCACACATCGGAAGGGCTGGATGACCCCAATCAAAGAAAGAAACAAGGACTCTGGTTACCCCTGCCTCCACCC
ATGTGTCTATAAGAGTAGGCTACAGAGGTGACCAGGCCTGGCAGTTGAAATCTCTGGAAGAGGGAAACATGTGGGGA
CTACTCAGAGGCAAAGAGGAGCTGCTCCTGCCTCCATGGTTGCTGGCCTCTCCACCAACTACTCTTAGGGAGGC
TAAGCAGTCTCTGTTTTGCTTCCATGGCTCAAATAATACCCTGGGTATGCAGGACCCACTATACTTGCATTGTC
TGAGTACACCTAGAGAGCTTGGCTGTTTCCAAAAACAATCAGGGTCATAACCATCCATGCAGACATGGAGGCTCG
GCTGAACCAGGACTCCTCACTGTCTACCTGAGAGAATGAGCACCCCTCATCCATCTCAGCATCAACACAATTTCC
AGGGGACCTCAGGTCTACCTCAGGACTGAACGCCACACCTCAGGATTCTCCTCCTTGAATCTGAGACTGGCTGC
CCATTCTGAGATGGGGATGAAGGTAAAGATGCCGCATCACCAGGCACGCCGCCCTGACAGCTGCCTTGATACCAG
CTCTCTGTGGAAACCCCGAGGAGTTGGATCTGGAGAACAGCTGGGCCTCCTCACTCAGGACTTCTCTCCTGAAG
AACACGCAGTGCTAAACTGAGGATGATTTCCCTAATGCTTCTGCTTGGCCTTATGGAGGAGCTGCTCCTTCCTT
ACAGCCTTGGGGATGACTTGCCACACCTCCACCTCCCTGAGCCCTGTGAGAGGCACGACTGTCTATGCCAAT
GAGGCTCGGTGGGGGGCTCTCAAGTGCTGATCCTGCCCTGGGCTCAGAGCCAGCCAGAGGGAAGCAACTGCAC
AGCCCCACAGGCCCTCCTTGGCACTGTCCCCCAACCCCATCTCAGAGCTCAGAGGGTACAAGCTCCAGAACAGT
AACCAAGTGGGAAAAATAAGACTTCTTGGATGACTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 510

MVQAHGGRSRAQPLTSLGAAMTQPPPEKTPAKKHVRLQERRGSNVALMLDVRS LGAVEP ICSVNTPREVTLHFL
RTAGHPLTRWALQRQPPSPKQLEEEFLKIPSNFVSPEDLDIPGHASKDRYKTI LPNPQSRVCLGRAQSQEDGDYI
NANYIRGYDGKEKVYIATQGMPNTVSDFWEMVWQEEVSLIVMLTQLREGKEKCVHYWPTEEETYGPFQIRIQDM
KECPEYTVRQLTIQYQEERRSVKHILFSAWPDHQTPE SAGPLLRLVAEVEESPETA AHGP I VVHCSAGIGRTGC
FIATRIGCQQLKARGEVDILGIVCQLRLDRGGMIQTAEQYQFLHHTLALYAGQLPEEPS P

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FIGURE 511

ATGCGCGCGGAGCTGGTGGAGGCCAAAAACATGGTGATGAGTTTTTCGAGTCTCCGACCTTCAGATGCTCCTGGGT
TTCGTGGGCCCGGAGTAAGAGTGGACTGAAGCACGAGCTCGTCACCAGGGCCCTCCAGCTGGTGCAGTTTGAAGTGT
AGCCCTGAGCTGTTCAAGAAGATCAAGGAGCTGTACGAGACCCGCTACGCCAAGAAGAACTCGGAGCCTGCCCCA
CAGCCGCACCGGGCCCTGGACCCCTGACCATGCACTCCACCTACGACCGGGCCGGCGCTGTGCCAGGACTCCG
CTGGCAGGCCCAATATTGACTACCCCGTGCTCTACGGAAAGTACTTAAACGGACTGGGACGGTTGCCCGCCAAG
ACCCTCAAGCCAGAAGTCCGCTGGTGAAGCTGCCGTTCTTTAATATGCTGGATGAGCTGCTGAAGCCCACCGAA
TTAGTCCCACAGAACAACGAGAAGCTTCAGGAGAGCCCGTGCATCTTCGCATTGACGCCAAGACAGGTGGAGTTG
ATCCGGAATTCAGGGAATGCAGCCCGGAGTTAAAGCCGTGCAGGTCTCTGAGAATCTGTTACTCAGACACC
AGCTGCCCTCAGGAGGACCAGTACCCGCCCAACATCGCTGTGAAGGTCAACCACAGCTACTGCTCCGTCCCGGGC
TACTACCCCTCCAATAAGCCCGGGGTGGAGCCCCAAGAGGCCGTGCCGCCCATCAACCTCACTCACCTCATGTAC
CTGTCTCGGCCACCAACCGCATCACTGTACCTGGGGGAACTACGGCAAGAGCTACTCGGTGGCCCTGTACCTG
GTGCGGCAGCTGACCTCATCGGAGCTGCTGCAGAGGCTGAAGACCATTGGGGTAAAGCACCCGGAGCTGTGCAAG
GCACTGGTCAAGGAGAAGCTGCGCCTTGATCCTGACAGCGAGATCGCCACCACCGGTGTGCGGGTGTCCCTCATC
TGTCCGCTGGTGAAGATGCGGCTCTCCGTGCCCTGCCGGGCAGAAACCTGCGCCACCTGCAGTGCTTCGACGCC
GTCTTCTACCTGCAGATGAACGAGAAGAAGCCACCTGGATGTGCCCCGTGTGCGACAAGCCAGCCCCCTACGAC
CAGCTCATCATCGACGGGCTCCTCTCGAAGATCCTGAGCGAGTGTGAGGACGCCGACGAGATCGAGTACCTGGTG
GACGGCTCGTGGTGCCCGATCCGCGCCGAAAAGGAGCGCAGCTGCAGCCCGCAGGGCGCCATCCTCGTGCTGGGC
CCCTCGGACGCCAATGGGCTCCTGCCCCCCCCAGCGTCAACGGGAGCGGTGCCCTGGGCAGCACGGGTGGCGGC
GGCCCGGTGGGCAGCATGGAGAATGGGAAGCCGGGCGCCGATGTGGTGGACCTCACGCTGGACAGCTCATCGTCC
TCGGAGGATGAGGAGGAGGAGGAAGAGGAGGAGGAAGACGAGGACGAAGAGGGGGCCCCGGCCCAAGCGCCGCTGC
CCCTTCAGAAGGGCCTGGTGCCGGCCTGCTGA

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FIGURE 512

MAAELVEAKNMVMSFRVSDLQMLLGFVGRSKSGLKHELVTRALQLVQFDCSPELFKKIKELYETRYAKKNSEPAP
QPHRPLDPLTMHSTYDRAGAVPRTPLAGPNIDYPVLYGKYLNLGRLPAKTLKPEVRLVKLPFFNMLDELLKPTE
LVPQNNKLQESPCIFALTPRQVELIRKFQGMQPGVKAVQVVLRICYSDTSCPQEDQYPPNIAVKVNHSYCSVPG
YYP SNKPGVEPKRPCRPI NLTHLMYLSSATNRITVTWGNYGKSYSVALYLVRQLTSSELLQRLKTIGVKHPELCK
ALVKEKLRLDPDSEIATTGVRVSLICPLVKMRLSVPCRAETCAHLQCFDAVFYLMNEKKPTWMCPVCDKPPAYD
QLIIDGLLSKILSECEDADEIEYLVDGSWCPIRAEKERSCSPOGAILVLGPSDANGLLPAPSVNGSGALGSTGGG
GPVGSMEGKPGADVVDLTLDSSSSSEDEEEEEEEEEDEDEEGPRPKRRCPFQKGLVPAC

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FIGURE 513

GATCGCGGAGTCGGTGCTTTAGTACGCCGCTGGCACCTTTACTCTCGCCGGCCGCGCGAACCCGTTTGAGCTCGG
TATCCTAGTGCACACGCCTTTGCAAGCGACGGCGCCATGAGTCTGACTTCCAGTTCCAGCGTACGAGTTGAATGG
ATCGCAGCAGTTACCATTGCTGCTGGGACAGCTGCAATTGGTTATCTAGCTTACAAAAGATTTTATGTTAAAGAT
CATCGAAATAAAGCTATGATAAACCTTCACATCCAGAAAGACAACCCCAAGATAGTACATGCTTTTGACATGGAG
GATTTGGGAGATAAAGCTGTGTACTGCCGTTGTTGGAGGTCCAAAAAGTTCCCATTTCTGTGATGGGGCTCACACA
AAACATAACGAAGAGACTGGAGACAATGTGGGCCCTCTGATCATCAAGAAAAAAGAACTTAAATGGACACTTTT
GATGCTGCAAAATCAGCTTGTCGTGAAGTTACCTGATTGTTTAATTAGAATGACTACCACCTCTGTCTGATTCACC
TTCGCTGGATTCTAAATGTGGTATATTGCAAACCTGCAGCTTTCACATTTATGGCATTGTCTTGTGAAACATCG
TGGTGCACATTGTTTAAACAAAAAAAAAAAAAAAAA

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FIGURE 514

MSLTSSSSVRVEWIAAVTIAAGTAAIGYLAYKRFYVKDHRNKAMINLHIQKDNPKIVHAFDMEDLGDKAVYCRCW
RSKKFPFCDGAHTKHNEETGDNVGPLIIKKKET

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FIGURE 515

CCACAAATGTGGGAGGGCGATAACCACTCGTAGAAAGCGTGAGAAGTTACTACAAGCGGTCTCTCCGGCCACCGT
ACTGTTCCGCTCCCAGAAGCCCCGGGCGGGCGGAAGTCGTCACTCTTAAGAAGGGACGGGGCCCCACGCTGCGCAC
CCGCGGGTTTGCTATGGCGATGAGCAGCGGGCGGAGTGGTGGCGGCGTCCCGGAGCAGGAGGATTCCGTGCTGTT
CCGGCGCGGCACAGGCCAGAGCGATGATTCTGACATTTGGGATGATACAGCACTGATAAAAGCATATGATAAAGC
TGTTGGCTTCATTTAAGCATGCTCTAAAGAATGGTGACATTTGTGAACTTCGGGTAAACCAAAAACACACCTAA
AAGAAAACCTGCTAAGAAGAATAAAAGCCAAAAGAAGAATACTGCAGCTTCCTTACAACAGTGGAAAGTTGGGGA
CAAATGTTCTGCCATTTGGTCAGAAGACGGTTGCATTTACCCAGCTACCATTTGCTTCAATTGATTTTAAGAGAGA
AACCTGTGTTGTGGTTTACTGATATGGAAATAGAGAGGAGCAAAATCTGTCCGATCTACTTTCCCAATCTG
TGAAGTAGCTAATAATATAGAACAGAATGCTCAAGAGAATGAAATGAAAGCCAAGTTTCAACAGATGAAAGTGA
GAACTCCAGGTCTCCTGGAAATAAATCAGATAACATCAAGCCCAAATCTGCTCCATGGAACCTTTTTCTCCCTCC
ACCACCCCCCATGCCAGGGCCAAGACTGGGACCAGGAAAGATAATTCCCCCACCACCTCCCATATGTCCAGATTC
TCTTGATGATGCTGATGCTTTGGGAAGTATGTAAATTTTCATGGTACATGAGTGGCTATCATACTGGCTATTATAT
GGGTTTCAGACAAAATCAAAAAGAAGGAAGGTGCTCACATTCCTTAAATTAAGGAGAAATGCTGGCATAGAGCAG
CACTAAATGACACCACTAAAGAAACGATCAGACAGATCTGGAATGTGAAGCGTTATAGAAGATAACTGGCCTCAT
TTCTTCAAAATATCAAGTGTGGGAAAGAAAAAGGAAGTGGAAATGGGTAACCTCTTCTTGATTAAAAGTTATGTA
ATAACCAAATGCAATGTGAAATATTTTACTGGACTCTTTTGAAAACCATCTGTAAAAGACTGGGGTGGGGGTGG
GAGGCCAGCACGGTGGTGAGGCAGTTGAGAAAATTTGAATGTGGATTAGATTTTGAATGATATTGGATAATTATT
GGTAATTTTATGGCCTGTGAGAAGGTGTTGTAGTTTATAAAAGACTGTCTTAATTTGCATACTTAAGCATTTAG
GAATGAAGTGTAGAGTGTCTTAAATGTTTCAAAATGGTTTAAACAAATGTATGTGAGGCGTATGTGGCAAAATG
TTACAGAATCTAACTGGTGGACATGGCTGTTTATTGTACTGTTTTTTCTATCTTCTATATGTTTAAAGTATAT
AATAAAAATATTTAATTTTTTTT

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FIGURE 516

MAMSSGGSGGGVPEQEDSVLFRRGTGQSDSDIWDDTALIKAYDKAVASFHALKNGDICETSGKPKTTPKRKPA
KKNKSQKKNTAASLQQWKVGDKCSAIWSEDGCIYPATIASIDFKRETCVVVYTG YGNREEQNLSDLLSPICEVAN
NIEQNAQENENESQVSTDESENSRSPGNKSDNIKPKSAPWNSFLPPPPMPGPRLGPGKIIPPPPICPDSLDDA
DALGSMLISWYMSGYHTGYIMGFRQNQKEGRCSHSLN

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FIGURE 517

AAGTGCAAAGCTTTTAACAATAGAAGTTTCAAGGGCTCAGGAAGGACCAGGGGGCCATCTAGGCTCTCCATGAGT
TCACGCTTAACATTATGTTTACGTCTGTCTCAGATAACAATTTTGGTTTTCCACATCAGGTGCATTGCACTGTTAGA
TGGGTCATCATAAAGGTCATCAATCTAGTGGCATTCAATTCATTTGCACATCCTAACTGTTTCAGCACTATCTGA

TTTAGCATGAAAATCTGCCAGGGCAGTCCCTTGATATTCAGGTTTCAGCTTTCCATGTATGGGCTTCAATCTTATA
AGAATTTGTTATTTATTTTTCACCTTTACTCAAGATAGCTTGGAAGTTATACCAATTTGTGATGGCAACAGGATA
GTAGCAAGTTCATCCACTTGAGTCTGTTTTTAATAGGGGCTCCACTAGAAGTGAGAAACCTCTTTGTTTCCATA
ACATGCCAAAATTGTGGACTGCAAAGGCATGTATATATACATAGCATGTCTGCTATGTATATAGCATTTTCTGAT
TTCCCTTTAGCTATATGATAAGCTCAAGTGAGAGCAAAAGTTCTGCAGTTTGAGCTGACTGAACTGGGAAGAGT
CCGCTTTTTATTAACTCATTTTGGGTTTTAATGACATATTTTGCCAAAGAATAATTCAAATGGGGGCCGGGCGT
CTGTGCT

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FIGURE 518

KCKAFNNRSFKGSGRTRGPSRLSMSSRLTLCRLSDNNFGFPHQVHCTVRWVLIKVINLVAFIQFAHPNCFSTI

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FIGURE 519

ACTAGCGGAGCCGCGAGGGAGAGGCCGCGGCCCTTCCCGTTGCCTGCGGCCACCGCCGGCATTTCAGAGCCCCT
CGCCTGGCGCTAAATTTAAAAACGTAACACGAGCAGCAGGCTGGTCTCGGAAACGAAACGAAATTCGGTCCCTGG
GCCTCCTCCCGGGCGCTGCCGGTCCCTCAGCGCGCCGCGCCACCCGGAACAGACCCTTCTCCCGCCATTTTCGGC
GGGGCTGGGAGACTGAGGCCCCGCGCGCTGAGCCTGCGGCGCCCCGGAAGAGGCGGGCGGCATGCGCGCTGGCGT
GGACTGCGGGGACGGGGTTGGCGCCCGGCAGCACGTGTTCTGGTTTCAGAATATTTAAAAGATGCTTCAAAGAA
GATGAAAAATGGGCTAATGTTTGTAAACTGGTTAACCCCTGTTTCAGGAGAAGGAGCCATTTACTTGTTCAATAT
GTGTCTACAGCAGCTGCTTGAAGTAAAAGTTTTCAAGGAAAAACACCATTCTTGGTTTATAAATCAATCAGTTCA
ATCAGGAGGTCTTCTCCATTTTGCCACACCTGTGGATCCTCTATTTCTGCTTCTCCACTACCTCATAAAGGCTGA
TAAGGAGGGGAAGTTTCAGCCCCCTTGATCAAGTTGTGGTGGATAACGTGTTTCCAAATTGCATCTTGTTGCTGAA
ACTTCTGGACTTGAGAAGTTACTTCATCATGTGACAGAGGAAAAAGGTAATCCAGAAATAGACAACAAGAAATA
TTACAAGTACAGCAAAGAGAAGACATTAAAGTGGCTGGAAAAAAGGTTAATCAAACGTGGCAGCATTAAAAAC
CAATAATGTGAATGTCAGTTCCCGGGTACAGTCAACTGCATTTTCTCTGGTGACCAAGCTTCCACTGACAAGGA
AGAGGATTATATTCGTTATGCCCATGGTCTGATATCTGACTACATCCCTAAAGAATTAAGTGATGACTTATCTAA
ATACTTAAAGCTTCCAGAACCTTCAGCCTCATTGCCAAATCCTCCATCAAAGAAAAATAAGTTATCAGATGAGCC
TGTAAGCAAAAAGAAGATTACACTAAGTTTAATACTAAAGATTTGAAGACTGAAAAGAAAAATAGCAAAATGAC
TGCAGCTCAGAAGGCTTTGGCTAAAGTTGACAAGAGTGGAATGAAAAGTATTGATACCTTTTTTGGGGTAAAAAA
TAAAAAATAATTGGAAAGGTTTGAAACTTTGAAAATAAAATCTAGCAAAATATTTGCTTTTACATGTTTCAG
TTTGTCTTCTGACTGTTAATGACTACCTTTGGTTGGGGGAAGGAAGAGGCCAATTTTCATGTTCTCTTAAACAT
TTCTTTGCATTTGGTTTTTGTGTTCTGAACAAAATATGGGAAAGTGCTAACTTCATGGCTATGGCCTTTTGGG
GTCTCATCTGACATAATGAAAAGTAATCACTTGAAGAGAATTAACATATAGCATCATGATTTTCTCAATAAACTG
ATGTGTGACAATGTT

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FIGURE 520

MAAGVDCGDGVGARQHVFVLVSEYLDASKKMKNGLMFVKLVNPCSGEGAIYLFNMCLQQLEVKVFKEKHHSWFI
NQSVQSGGLLHFATPVDPLFLLLHYLIKADKEGKFQPLDQVVVDNVFPNCILLKLPGLEKLLHHVTEEKGNPEI
DNKKYYKYSKEKTLKWLEKKVNQTVAAALKTNVNVSSRVQSTAFFSGDQASTDKEEDYIRYAHGLISDYIPKELS
DDLSKYLKLPEPSASLPNPPSKIKLSDEPVEAKEDYTKFNTKDLKTEKKNSKMTAAQKALAKVDKSGMKSIDTF
FGVKNKKKIGKV

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FIGURE 521

CGGACCTGCAGCCCTGGCCTTCCGCCACC**AT**GGAGTACCTCATCGGTATCCAAGGCCCCGACTATGTTCTTGTGCG
CCTCCGACCGGGTGGCCGCCAGCAATATTGTCCAGATGAAGGACGATCATGACAAGATGTTTAAGATGAGTGAAA
AGATATTACTCCTGTGTGTTGGAGAGGCTGGAGACACTGTACAGTTTGCAGAATATATTCAGAAAAACGTGCAAC
TTTATAAGATGCGAAATGGATATGAATTGTCTCCACGGCAGCAGCTAACTTCACACGCCGAAACCTGGCTGACT
GTCTTCGGAGTCGGACCCCATATCATGTGAACCTCCTCCTGGCTGGCTATGATGAGCATGAAGGGCCAGCGCTGT
ATTACATGGACTACCTGGCAGCCTTGGCCAAGGCCCTTTTGCAGCCCACGGCTATGGTGCCTTCCTGACTCTCA
GTATCCTCGACCGATACTACACACCGACTATCTCACGTGAGAGGGCAGTGGAACCTCCTTAGGAAATGTCTGGAGG
AGCTCCAGAAACGCTTCATCCTGAATCTGCCAACCTTCAGTGTTCGAATCATTGACAAAAATGGCATCCATGACC
TGGATAACATTTCTTCCCCAAACAGGGCTCC**TA**ACATCATGTCTCCTCCCCTCCCACTTGCCAGGGAACTTTTTTTT
GATGGGCTCCTTTATTTTTTTTCTACTCTTTTCAGGCGCACTCTTGATAAATGGTTAATTCAGAATAAAGGTGACT
ATGGATATAATT

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FIGURE 522

MEYLIIGIQGPDYVLVASDRVAASNIVQMKDDHDKMFKMSEKILLLCVGEAGDTVQFAEYIQKNVQLYKMRNGYEL
SPTAAANFTRRNLDCLRSRTPYHVNLLLAGYDEHEGPALYYMDYLAALAKAPFAAHGYGAFTLSILDRIYYTPT
ISRERAVELLRKCLEELQKRFILNLPFVSRIIDKNGIHDLDNISFPKQGS

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FIGURE 523

CCAGATCTGGAGGTGTGTCCATGGCGGCGCTTGACCTGCGAGCGGAGCTGGATTGCTGGTCCTGCAGCTGCTTG
GGGACCTGGAGGAGCTGGAGGGGAAACGAACGGTGTGAACGCCCGGGTGGAGGAGGGCTGGCTCTCGCTCGCCA
AGGCTCGCTACGCGATGGGCGCCAAGTCGGTAGGGCCCCGTCAGTATGCTTCCCACATGGAGCCCCAGGTCTGCC
TCCACGCCAGCGAGGCCCAGGAGGGACTCCAGAAGTTCAAGGTGGTGAGAGCTGGTGTCCACGCCCCAGAGGAGG
TGGGGCCTCGCGAAGCAGGTCTGCGGAGGCGCAAGGGCCCCACTAAGACCCCAGAACCGGAGTCCTCTGAGGCCC
CTCAGGACCCCCTGAACTGGTTTGGAAATCCTAGTTCCTCACAGTCTACGTCAGGCTCAAGCAAGCTTCCGGGATG
GCCTGCAGCTGGCCGCAGACATAGCCAGCCTCCAGAACCGCATTGACTGGGGTCTGAAGCCAGCTCCGGGGACTCC
AAGAGAACTCAAGCAGCTGGAGCCTGGGGCTGCCTGACATGCGCGCAAAGAGGCAGGGCAGCGAGCACAGCTGT
TCTCCGACATGGCTACGTGATCTCAGGCCTTCTTCCTTACAATTAGCTCTTGCCCCCTACCCACGCCAGCTAAT
GCCCCCTTCTGTGTCCCTGCTCTGCATGTTTCCATTTCCTTAGGIGTGAAGTTTGAAGAGGCAAACAGTAATTTT
GAAAGCCACTACTTTGAAACCATTCTAAGGCCTGAGTTCCCATAGGACACACTCACATAGGCAGGTACACGTTAG
TCAACAATTGGAAGTGCCTCTTGGATCACTCAGCTGTGCTTTCATGGCTGGATGATGGAACACTGTGCGAAGAGA
GATGGGGGCCAGGAAGTAGCGCTTCATGCTTAGTACATCCTCCAAATTGTCTTTGCTGGAGGAGAAAACCGTACT
CAGCCAAAAGATCAGGACAATATGACTTGAGTCCACAAGGACACAAACACCTGAGTAGCTGGGCAGCCCTTGGCA
GGGTCTAAGCCAGGAAGTAAAAATGATCTGGCCTAGATATTTAAGGGAACTCTAGGAAGAGGCCTAGGTTTTTAA
AATCCTGTCTCTTTGTCTTACCATAAGAGGCTGAGCCTCTCTTCATTTTTTTGAAGGGCCACTTGTGTTTTCTGT
TCTGGGAACCTTCATTCATTTTCTACTGGGTTGTTGATCTTTCAGTAATTTCTAGGAGCTGTTTATGTTTGGAG
GTAATTGGTCCTTTGTCCATATATGAGATGTAAGTCTTATTTTCCAGTTTATCTTTTTGCTTATTTTTTTTGA
CTTTTTATTGTAAATAAAACATCAAAGTGCACAGAACAGTTGAATAGCTTAATGAATAACTACAGTAAAAGCTA
TGGTAACCACTACCCAAAAAAAAAAAAAAAAAAAAA

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FIGURE 524

MGAKSVGPLQYASHMEPQVCLHASEAQEGLQKFKVVRAGVHAPEEVGPREAGLRRRKGP TKTPEPESSEAPQDPL
NWFGILVPHSLRQAQASFRDGLQLAADIASLQNRIDWGRSQLRGLQEKLKQLEPGAA

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FIGURE 525

TGGAGGTGAGAAAACAGAGCAGCGTATGGCAAAATAGTCTAAGAACAAGTAGTAAAAGCATCAGCATCAAAAAC
CCAGGCTATAAAAGACTAGGCTCAGAAAGTGCAGTTTCCACCCACAGCTGGGGTGCTTCCAATAGCATCCTTGA
GACAGACTCCGCTCTAGTACCTCCAGCGAGGAGTTCACTACTGCAACAAGCAGCCCATTCTTGGATTTTTATTTT
TTTTAACTTCCATTTTTTCTTATACATCAAGTTCTCACTCCTTTATATTTGATGACATGCACGTTCAGAACTGCT
GAATATTTCCCTTTTATCCATGCCTTCACTGCTCAATCACCTTTATACAGTTTCTTTACGGCAGCAGTGAAAGA
AGTGACTCAGAAGACCCGTCTTTGAAAAACAAACTATAAAATGTATCCACTCTGACCAAAGCAAAAAAGACAT
ATTCCTTCCCTCTCCACACAGAAAAATTCGGGATATTGAGATCTCCCTAAAGGAGGTCCTAAAAAGTCAGTATA
TGTTGGGGTAAGAAGAGAAGATGCACGCCCTAAGTAGAGATAAAAAAGAGCCAGATTTTAAACTCTTTGTTCCCT
AACTCCTTGTAATGTAATGCTCTTATTGAAAATGTTAACCGATTATTTTGAATGATTATTTTTTTGG

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FIGURE 526

MTCTFRTAEYFPFYPCLHCSITFIQFLYGSSERSDSEDPSLKKQTIKCIHSDQSKKRHIPSPLHTEKEFGILRSP

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FIGURE 527

ATGGCGTCCTATTTCGATGAACACGACTGCGAGCCGTCGGACCCTGAGCAGGAGACGCGAACCAACATGCTGCTG
GAGCTCGCAAGGTCACTTTTCAATAGGATGGACTTTGAAGACTTGGGGTTGGTAGTAGATTGGGACCACCACCTG
CCTCCACCAGCTGCCAAGACTGTGTTGAGAACCTCCCCAGGACAGTCATCAGAGGCTCTCAGGCTGAGCTCAAG
TGCCCCGTGTGTCTTTTGGAAATTTGAGGAGGAGGAGACTGCCATTGAGATGCCTTGCCATCACCTTTTCCATTCC
AGCTGCATTCTGCCCTGGCTAAGCAAGACAAATTCCTGTCCCTTGTGCCGCTATGAGCTGCCCCACTGATGACGAC
ACTTATGAGGAGCACAGACGAGATAAGGCTCGAAAACAGCAGCAGCAACACCGACTGGAGAACCTCCATGGAGCC
ATGTACACGTGA

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FIGURE 528

MASYFDEHDCEPSDPEQETRTNMLELARSLEFNRMDFEDLGLVVDWDHHLPPAAKTVVENLPRTVIRGSQAELK
CPVCLLEFEEEEETAIEMPCHHLFHSSCILPWLSKTNSCPLCRYELPTDDDTYEEHRRDKARKQQQHRLENLHGA
MYT

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FIGURE 529

GTATTCAATATGCTTATGTTTTATTATGTAGGTGGCATTATAAATACATGATGTGTTTAGGGTTACATTGTCCA
CAGAAAGCATCAAATACCACTCCTCTCCCCGCCAAAACCAAATAAACAAAGCCAACCTTTGGCAACAGTTGTGT
TAAATAAAATCCCAGGTCACACTTGTTTCTGGCTCCCAAGCCTGGGTCACTGCTACATGGATTGCGCCAAAAAT
TCCCAGCTTCAACACTGCTAGATTAAATTTGCTGGCATTTTTAAATCACAGCAAAGCTTTTCACAATGCCCTCAA
GTCCAAGAGGACAAAGGAGAAAGCAACATGAACGGCAGATCCTCATGTGAAAGGGAAGGAAAGTCACTGGGAGGG
AGCATGCAGGGAAGAAGTCAAGGCAGCCCTGGAATCTACTCCGTGCTCAATAAAAAAAAAACGTGAAGAAGCAA
TACATCATGCAAACGAAATAATGACCGGAAGTGGGCGCATCTAGTTAGAATGAAGTGACTTTCGTAAGGAGTCAA
TGTTGCGGAACTGAAACATGAGTTCAACCTCCTTGTCGGTCTCTGGGTGTTTTGCACGTGTGTAATACCGGCC
CGTTTTCCCCAGCATGGCCCTAACCCATGGACACTAGGGAGGGTGCCACTGAGCAAAAATTTTTGCTAAAAATA
ATTAGCAAAAATCCAAGAAAAAATATGGAATCTAGCAAAACCTACACCATATTTGAAGTTGAATTTGCACTACC
TGCAAAGCAAAATAATTTAAAAGAATAAACATTGTGAACATCAATTCCCATCACAGCAAGCCCTGGATGAAAACAT
GGACCTCTTGGAAGGTATAACTGGCTTTGAAGACTCTGTCCGAAAGTGTAAGTCCCTCTCTGAGGCTGGGCTCCC
CAAGGGGAAGGGGTAGGGAGTGGCAGCCAGGTCCGGGGGGACAGCTGCTCACCAGTCTCTGACCTCCACA
GTTATCTGCCATGTTGTGGGTATCACTTACCAGCACATTGACCGCTGGCTGCTGGCCGAGATGCTCGGGGATCTG
TCGGGTAAAGCCCTCTGGGTCTGGTGCACATCTGGGAGGTTGGGGGTGGCTAGGGCAGTGGACCTCAGTCAGCT
CCTCCAACAGGCCTGTCTGGGTCTCATCAGGTCAGCATGGAAGGCCAGCCCAAGGAGGAAATAAGAACTTGGTA
TAAGACAGTCTCTGCCTTGAGGGAGATCCTATGCCATTGCTCATTTATTTGCATTAATTGAGTGCCCTACCGTG
TGTCAGTGTGCTAAACTGGGCGTGCAGCAGTAAACAAAGTGGGATGGCTCCAATTCATTCTCATGGAGGTAGCAA
AGCACATGGCGACATGGAGGTGTCCAGTGGTGATTCTGTGATGAAGGAAAGCAAGACAGCTCACAGACCAGCGG
CATCTGAGCCCTTACCTCCGTAGAGAGAGGCCCGTGGCCTGAGGTAGTGCAGAGGAGGATAGTAGAGCAGGGCCC
TGACTTGTAACGTTTATGGGTAGCCAGGGTGTATGTGGCCAGAGCAGAGTAAGCATGGGCGAAAGTAGAGAGCTG
GGGGTTGGAGGGGCATTTCCAGGTCATGTGGGGCTCGGGAGGACCTTGTCCTTTCCCTGACTGAGAAGGAGCC
ACCGGAGGGCTCTGAGCAGGGTAGGGCTCTGATCAGATGGATATTTTTTAAAGATCCCCCAAGAACAAAAAAG
AAAAATAACTTATTTGCTTACTTTTGTAAGAAAGAACGTAGAAAAGGAAGTCAAGAACTAAGGAAGGCCGGGT
GCGGTGGCTCCCGCCTGTAATCCAGCACTTTGGGAGGCCGAGGTGGGCGGATCATCTGTGGTCAGGAGTTGAGA
CCAGCCTGCCAACGTGGTAAAACCCCTCTCTACTAAAAATACAAAAAATTGCTGGGTGTGGTGGCGTGACCT
GTAGTCCCGGCTACTTGGGAGGCTGAGGCAGGAGAATTGCTTCAACGCAGGAGGCGGAGGTTGCAGTGAGCTGAG
ATCGCACCATTGCACTAGTGATAAGATCGAACTCCATCTAAAAAAAAAAAAAA

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FIGURE 530

MLWVSLTSTLTAGCWPRCSGICRVTPSGSWCTSGRLGVARAVDLSQLLQQACLGLIRSAWKAQPKEEIRTWYKTV
SALREILCHLLIYFALIECLPCVSVLNWACSSKQSGMAPIHSHGGSKAHGDMEVSSGDSCHGKQDSSQTSGI

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FIGURE 531

AGTACCGGGTACGCAGGGGTGCCTCAACCACACTCCGTCCACGGACTCTCCGTTATTTTAGGAGGTCCCTGGCCA
AAGATTTATTTCTCTTGACAACCAAGGGCCTCCGTCTGGATTTCCAAGGAAGAATTTCTCTGAAGCACCGGAAC
TTGCTACTACCAGCACCATGCCCTACCAATATCCAGCACTGACCCCGGAGCAGAAGAAGGAGCTGTCTGACATCG
CTCACCGCATCGTGGCACCTGGCAAGGGCATCCTGGCTGCAGATGAGTCCACTGGGAGCATTGCCAAGCGGCTGC
AGTCCATTGGCACCGAGAACACCGAGGAGAACCGGCGCTTCTACCGCCAGCTGCTGCTGACAGCTGACGACCGCG
TGAACCCCTGCATTGGGGGTGTCATCCTCTTCCATGAGACACTCTACCAGAAGGCGGATGATGGGCGTCCCTTCC
CCCAAGTTATCAAATCCAAGGGCGGTGTTGTGGGCATCAAGGTAGACAAGGGCGTGGTCCCCCTGGCAGGGACAA
ATGGCGAGACTACCACCCAAGGGTTGGATGGGCTGTCTGAGCGCTGTGCCCAGTACAAGAAGGACGGAGCTGACT
TCGCCAAGTGGCGTTGTGTGCTGAAGATTGGGGAACACACCCCTCAGCCCTCGCCATCATGGAAAATGCCAATG
TTCTGGCCCGTTATGCCAGTATCTGCCAGCAGAATGGCATTGTGCCCATCGTGGAGCCTGAGATCCTCCCTGATG
GGGACCATGACTTGAAGCGCTGCCAGTATGTGACCGAGAAGGTGCTGGCTGCTGTCTACAAGGCTCTGAGTGACC
ACCACATCTACCTGGAAGGCACCTTGCTGAAGCCCAACATGGTCACCCCAAGGCCATGCTTGCACTCAGAAGTTTT
CTCATGAGGAGATTGCCATGGCGACCGTCACAGCGCTGCGCCGCACAGTGCCCCCGCTGTCACTGGGATCACCT
TCCTGTCTGGAGGCCAGAGTGAGGAGGAGGCGTCCATCAACCTCAATGCCATTACAAGTGCCCCCTGCTGAAGC
CCTGGGCCCTGACCTTCTCCTACGGCCGAGCCCTGCAGGCCTCTGCCCTGAAGGCCTGGGGCGGGAAGAAGGAGA
ACCTGAAGGCTGCGCAGGAGGAGTATGTCAAGCGAGCCCTGGCCAACAGCCTTGCTGTCAAGGAAAGTACACTC
CGAGCGGTCAAGCTGGGGCTGCTGCCAGCGAGTCCCTCTTCGTCTCTAACCACGCCTATTAAGCGGAGGTGTTCC
CAGGCTGCCCCCAACAACCTCAGGCCCTGCCCCCTCCCACTCTTGAAGAGGAGGCCGCTCCTCGGGGCTCCAGG
CTGGCTTGCCCGCGCTCTTCTTCCCTCGTGACAGTGGTGTGTGGTGTCTGTGAATGCTAAGTCCATCACCC
TTTCCGGCACACTGCCAAATAAACAGCTATTTAAGGGGG

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FIGURE 532

MPYQYPALTPEQKKELSDIAHRIVAPGKGILAADESTGSI AKRLQSIGTENTENRRFYRQLLLTADDRVNPCIG
GVILFHETLYQKADDGRPFQVIKSKGGVVGIVDKGVVPLAGTNGETTTQGLDGLSERCAQYKKDGADFAKWRC
VLKIGEHTPSALAIMENANVLARYASICQQNGIVP IVEPEILPDGDHDLKRCQYVTEKVLAAVYKALSDHHIYLE
GILLKPNMVTTPGHACTQKFSHEEIAMATVTALRRTVPPAVTGITFLSGGQSEEEASINLNAINKCPLLKPWALTF
SYGRALQASALKAWGGKKENLKAAQEEYVKRALANSLACQKYTPSGQAGAAASESLFVSNHAY

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FIGURE 533

ATTCAAGCCTGGGCCCTGGAAGGAGGGGTGGACAGTCCCCTCCCTTCCAGTCCAGCATGGGTCTGGGGAAGAGGA
GCAGCTTTGCCTGGAAGGGGCCCTCCTAGGAGGGGGAGCGGTGGTTTCTAGCTCAGGCTTTAGGATCAGAGAGCAG
CAGATTCAAATCCTGACGGTTTTTGGTAAAGTCAATTCAATCTCTCCAAGACTCCGTTTACTTGATCTGCGAAGTG
GGGATAATGGTATCACGTGCGAGGGTTGTCAGGCGGAGCTGGTAGGGGAGCTGCCCCCAGAGCAGC**ATGG**ATGC
CCCGCGAAGGGACATGGAGTTGCTCAGCAACAGCCTGGCTGCCTACGCGCACATCCGCGCCAACCCCGAGAGCTT
TGGCCTCTACTTCGTGCTGGGCGTCTGCTTCGGCCTGCTGCTCACCCCTCTGCCTGCTCGTCATCAGCATCTCGTG
GGCGCCCCGCCGCGGGCCCCGGGGCCGGCTCAGCGCCGGGACCCCGCAGCAGCACCCCTGGAGCCCGAGGACGA
CGACGAGGACGAGGAGGACACGGTGACTCGGCTGGGCCCCGACGACACGCTGCCGGGCCCCGAGCTGTCCGCAGA
GCCGGACGGGCCCCCTCAACGTCAACGTCTTACGTGCGCGGAGGAGCTGGAGCGGGCGCAGCGGCTGGAGGAGCG
CGAACGGATCCTGCGGGAGATCTGGCGCACCGGGCAGCCGGACCTGCTGGGCACAGGCACGCTGGGGCCCAGCCC
CACGGCCACGGGCACCCCTGGGCGCATGCACTATTACT**TGA**TGGGCCCTGGCTCCCGCCGCAAGGCGCTCGGGGTA
CCGGACCTGTACATGAGCTCAGAGCTACCCACACCTTCGGACTGCCTCGGCCCCACAGCTCCAGGTGCTACT
GGGCGTGGACCGCCACCCCTGAGAGGCTCCCTTCCCCAGTCTGCCAGAAGACCCCGGGGGCGGGGAGGGGGCA
GCATGCAGGGTCCCCACTCCCTCTCTGGGGTCGATGAAGAGGTGAAGTGACCAAATGAAAGAAAGCTGCATTCTC
AGTG

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FIGURE 534

MDAPRRDMELLSNSLAAYAHIRANPESFGLYFVLGVCFGLLLTLCLLVISISWAPRRPRGPAQRRDPRSSTLEP
EDDDEDEEDTVTRLGPDDTLPGPELSAEPDGPLNVNVFTSAEELERAQRLEERERILREIWRIGQPDLLGTGTLG
PSPTATGILGRMHYY

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FIGURE 535

GGACTGTTGAAGACAGGTCTCCACACACAGCTCCAGCAGCCACATTTGCAACCTTGGCCATCTGTCCAGAACCTG
CTCCCACCTCAGGCCCAGGCCAACCGTGCACTGCTGCAATGGGCTCTGAGCTGGAGACGGCGATGGAGACCCTCA
TCAACGTGTTCCACGCCCCACTCGGGCAAAGAGGGGGACAAGTACAAGCTGAGCAAGAAGGAGCTGAAAGAGCTGC
TGCAGACGGAGCTCTCTGGCTTCCTGGATGCCCAGAAGGATGTGGATGCTGTGGACAAGGTGATGAAGGAGCTAG
ACGAGAATGGAGACGGGGAGGTGGACTTCCAGGAGTATGTGGTGCTTGTGGCTGCTCTCACAGTGGCCTGTAACA
ATTTCTTCTGGGAGAACAGTTGAGCAGACAGCCACATTGGGCAGCGCCCTTCCTCTCCACCCTCCCAGACCTGCC
TCTTCCCCCTGCTTCCACCTCACCCCACTTATCCCTCTCCATAACCCACCCCTTGCCACCCCACCCCACCCCA
ACCAAGGGCGCAAGAGTAGCGGTCCAAGCCTGCAACTCATCTTTCATTAAAGGCTTCTCTCTCACCAGCAAAAAA
AAAAAA

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FIGURE 536

MGSELETAMETLINVFHAHSGKEGDKYKLSKKELKELLQTELSGFLDAQKDVDKVMKELDENGDEVDFOEY
VVLVAALTVACNNFFWENS

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FIGURE 537

GTCTCCGGGGATTAGAGCCGGTGGGCTCGTTGTGGGCGCCATTTCTCGGCGTCTCCCGAGGAGCCGCCCTTTTC
TCAGCCTTGCTCGGCTCTTCCCCGCTCTGGTTCGCCGGGGCTGCGCGGTCCCCAGCTCAGTGACAAAATGCTGAG
TTTCTTCCGTAGAACACTAGGGCGTGGTCTATGCGTAAACATGCAGAGAAGGAACGACTCCGAGAAGCACAAACG
CGCCGCCACACATATTCTGCAGCTGGAGATTCTAAGTCCATCATCACGTGTCGGGTGTCCCTTCTGGATGGTAC
TGATGTTAGTGTGGACTTGCCAAAAAAGCCAAAGGACAAGAGTTGTTTGATCAGATTATGTACCACCTGGACCT
GATTGAAAGCGACTATTTTGGTCTGAGATTTATGGATTGAGCACAAGTAGCACATTGGTTGGATGGTACAAAAAG
CATCAAAAAGCAAGTAAAAATTGGTTCACCCTATTGTCTGCATCTTCGAGTTAAGTTTTATTCTCAGAACCAAA
TAACCTTCGTGAGGAGCTAACCCGGTATTTATTTGTTCTTCAGTTAAAAACAAGATATTCTCAGTGGAATTAGA
CTGTCCCTTTGATACAGCAGTGCAATTGGCAGCTTATAATCTGCAAGCTGAACCTGGTGACTATGATCTTGCTGA
GCATAGTCTGAACTTGTCTCAGAGTTTCTGCTTATTTCAGACTGAAGAGATGGAACCTGGCTATTTTGA
GAAATGGAAGGAATACAGAGGTCAAACACCAGCACAGGCTGAAACCAATTATCTGAATAAAGCCAAATGGCTAGA
AATGTATGGGTTGATATGCATGTGGTCAAGGCTAGAGATGGGAATGACTATAGTTTGGGACTAACACCAACAGG
AGTCCCTTGTTTTTGAAGGAGATACCAAAATTGGCTTATTTTTTGGCCGAAGATAACCAGATTGGATTTAAGAA
GAATAAATTAACCTTGGTGGTTGTAGAAGATGATGATCAGGGCAAAGAACAGGAACATACATTTGTCTTTAGACT
GGATCATCCAAAAGCATGCAAACATTTATGGAAATGTCTGTGGAGCATCATGCTTTCTCCGCCCTTCGAGGCCC
CGTCCAAAAGAGTTCTCATCGATCAGGATTTATTCGACTAGGATCACGATTTAGATATAGTGGGAAAAACAGAGTA
TCAGACCACAAAAACCAATAAAGCAAGAAGATCAACATCCTTTGAAAGAAGGCCAGCAAACGATATTCTAGACG
AACTCTACAAATGAAAGCATGTGCTACAAAACCTGAAGAACTTAGTGTTACAATAATGTTTCGACCCAAAGTAA
TGGCTCCCAACAGGCTTGGGGGATGAGATCTGCTCTGCTGTGAGTCCTTCCATTTCTCTGCTCTGTGCCAGT
GGAGATAGAGAATCTTCCACAGAGTCCTGGAACAGACCAGCATGACAGGAAATGCATTCTCTGAATATTGATTT
GCTGAATAGCCCAGACTTATTGGAAACAACGATTGGTGATGTAATTGGGGCATCTGACACTATGGAACATCCCA
AGCACTGAATGACGTTAATGTAGCCACCAGGCTTCCGGGATTAGGGGAACCTGAAGTTGAATATGAGACATTAA
AGACACCTCAGAGAAGCTCAAACAGCTTGAGATGGAGAACAGTCCTTTGCTGTCCCTCGATCCAACATCGAIGT
TAACATAAACAGCCAGGAGGAAGTGGTGAAGTTGACTGAGAAATGCCTTAATAATGTCATTGAGAGCCCAGGATT
GAATGTCTATGAGAGTTCTCTGACTTCAAGAGTAACATTTGAAGGCTCAAGTAGAAGCAGTGCTGCTGTTAAATGA
AAAAGAAGATAGCTTATTAAGTCATAAAATGCCAATGTTTCAGGATGCTGCCACAAACAGTGCTGTGTTAAATGA
GAATAATGTGCCCCCTCCCCAAAGAGTCTCTTGAGACTCTGATGCTTATCACACCTGCCGACAGTGGTTCTGTTCT
AAAGGAAGCTACAGATGAATTGGATGCCTTGCTTGCTCTCTAACTGAGAATCTAATTGATCACACAGTTGCACC
TCAGGTGTCTTCCACATCCATGATCACACCCCGGTGGATTGTTCCGCTCTGGTCCCATTTTGGCAGAAGAAGCTG
TCCTGAAGCAGAAGTGTCTTACTGACCACAGAGCTCTGAGGGCTGTAGCTGGAATACGCATCTCTCCAGCATTCC
GTCTGGGATCCGTTTTCAGCTAGAATATGTTGGATTGAGGAGCTTGTCCATTATTTGTAGGTAAAAAAGCTGCA
CGTAGATTTGACTTCAACTCCGTAAAAAAGACAGCTGTATTTTCCGTCCAACCTGGAATTGTTGAATCACACTGCA
TAGCTGCCCCAAAAGAGAGTGTGTTGGTCTTGAACCTTCTATACTTTTATAAATGTTACAAATTCCCGAAAGAAGGG
AATTTCTTTTTCTGGGGTTTTCTTCAAACCTTGGCTCCACCTAGCGGTTCTATTTGTTTATAACAACCTTCATAA
CAAGCCTGCCTCTGGTAGTCAACAGCCTTTTGAAGCTATTTCCATCTAGTATCAGGGTGAGAGCATCCTTGATC
TGGCTGCCTGTTAGAGAAATTGCATTTTCTGACTTACCTAGAAATCAAGAATTTAGGAAATTAATGTGGACAC
TATAAAGGCAGACTTAGGGCCAACCTTTTTTTTTTTTACAATTATTACAACACTAAAGAGAAGTTTAGAATATAG
AGAGTTTTTAAATGTCTCCATTCTTTGATTCTTACTGTACTGGCTATCTTAATATTTCAAGTTTACATCAAG
ATAAACCTTGAGAAGAACTACGGAGAAATCAAATAAAATCCTGTATATTTTTTACCCTGCCTTTCCACAGGA
AGCACTCACAGGCACCACACAGTATCATGTAACCTATCAGTGGGGTGGGTTACTGTTGAAGAGACCCTGGGGCA
TTTACCTCAGGCATCTGCACTCCTCCGAGCCCGGTGGAGAATGCAGGCTGCTGTAGTCTCAGGTAATGAAGGCAC
AGCACAGCAGTACTCCACATTGTTTCTATTTGGACATAGACTTCATTTCCTTTTCAGTATAAGCTGAGTAAATTT
AGAGCTTTCAAACCTGG

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FIGURE 538

MLSFFRRTLGRSSMRKHAERLREAQRAATHIPAAGDSKSIITCRVSLLDGTDVSVDLPPKKAGQELFDQIMYH
LDLIESDYFGLRFMDSAQVAHWLDGTSIKKQVKIGSPYCLHLRVKFYSSEPNNLREELTRYLFVLQLKQDILSG
KLDCPFDTAVQLAAYNLQAEGLDYDLAEHSPELVSEFRFVPIQTEEMELAI FEKWKEYRGQTPAQAE TNYLNKAK
WLEMYGVDMHVVKARDGNDYSLGLTPTGVLVFEGD TKIGLFFWPKITRLDFKKNKLTLLVVVEDDDQGKEQEHTFV
FRLDHPKACKHLWKCAVEHHAFFRLRGFPVQKSSHRSGFIRLGSFRFYSKGTEYQTTKTNKARRSTSFERRPSKRY
SRRTLQMKACATKPEELSVHNNVSTQSNGSQQAWGMRSALPVSPSISSAPVPVEIENLPQSPGTDQHDKRCIPLN
IDLLNSPDLLETTIGDVIGASDTMETSQALNDVNVATRLPGLGEPEVEYETLKDTSEKLKQLEMENSPLLSPRSN
IDVNINSQEEVVKLTEKCLNNVIESPGLNVMRVPPDFKSNILKAQVEAVHKVTKEDSLLSHKNANVQDAATNSAV
LNENNVPLPKESLETLMLITPADSGSVLKEATDELDALLASLTENLIDHTVAPQVSSTSMITPRWIVPLWSHFGR
RSCPEAEVFTDH

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FIGURE 539

CCACCCGCCTCGCCTCCACGTCGATGGACTATAGACATGAGCCATCGTGCTTGGCCTTCTTGATTCTTGAATACG
GGGTTTTGAGGTGAAAGCATTTCATGAAAACCTAAGTTCATACACAAGAGCATCATGAATATTCTAAAAGAGGTA
TCGTGCTTTTTTTGTGACCACAAAATATTACTTCTTATGAAATGTTTACACTAGGTGAGGAAAAGTTCATTAAT
TACCTTTAAACCGTTCCTTATTTTTTTTTAAGATTTTAAATTGTATTTTGGCTTTTGCCTCCAGTATCCTTTCTGG
TTGCTCTGGTTTGAATTAAGTTCCTATTATGCTGCAGCACATATCAACCTTCCCTAAGTAACCATTTCCTGGAAT
GTGAAGCATCGGTGCCATTAGCAGACCATATGCAGAAATGTCGTGTACTTGCATTTCTTTTTTGTGCACTCTATA
AGGCTGGTTGTGACTCAGATCAGCTTAACTTTTTATATTATGTTATTTCACTAACTGCTACAGTCAAAATGATCA
AATCTTTGTACAATAGAAAATTATTTAAATTTTATTTTTCTACTGACATTTCTAATTCTAGTGAAATGTTTATC
AATAAAAAATTACTTTCAATTCTGAGTTGGAATTATTTCTTTTTGGTGGCTAATGAGTTTAAATCTTTTGTAAT
AAAATTGACTTCAGTTTTTCATTTTTTAAATAACTTAATATCTAGCATGTGTAACTTTTTTTTATGTTCTACTTCTT
ACTAATTTATGATAAAATTCTTGTTCAAAGTTGTGATTAAACCGTACTTAACATGTA

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FIGURE 540

MIKFLEKVVIKPYLTC

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FIGURE 541

GCATGTCATGGCCGCCTCCATGGCCCGGGGAGGCGTGAGTGCCAGGGTTCTGCTGCAGGCTGCCAGGGGCACCTG
GTGGAACAGACCTGGGGGCACTTCCGGGTCGGGGGAGGGGGTGGCGCTGGGGACAACCAGAAAGTTTCAAGCGAC
AGGCTCGCGCCCGGCGGGAGAGGAGGACGCGGGCGGGCCGGAGCGGCGGGGACGTGGTGAACGTGGTGTTCGT
AGACCGCTCAGGCCAGCGGATCCCAGTGAGTGGCAGAGTCGGGGACAATGTTCTTCACCTGGCCCAGCGCCACGG
GGTGGACCTGGAAGGGGCCTGTGAAGCCTCCCTGGCCTGCTCCACCTGCCATGTGTATGTGAGTGAAGACCACCT
GGATCTCCTGCCTCCTCCCGAGGAGAGGAGAACTCGCGGCTGGGCTGCCAGATTGTGCTTGACACCGGAGCTGGAA
GGAGCGGAATTACCCTGCCCAAGATCACCAGGAACCTTCTACGTGGATGGCCATGTCCCCAAGCCCCACTGACAT
GAACACCTGGACCATTCCACATTGCCATGGCCCCAGGGCCAGATTGAGGGAATAGCCAGGTGCCAGCCCTGCCC
AGAGTGCGGACAGGCCGGGAGAGACGTGGAAGCCCCTGTGAAGGACAACACCCCTGCTTGGGAGAGAGTCCCAT
GTCCAGGCTCTGGTGGGGACAGGGCCCCTAGTGGGTGGCCTTCCCCAGGCCCTGAGAATCAGGGTTTGAGTAG
GAGTGGACTCATATTGGAGCTGCAATAAATCAATAACACAG

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FIGURE 542

HVMAASMARGGV SARVLLQAARGTWWNRPGGTSGSGEGVALGTTRKFQATGSRPAGEEDAGGPERPGDVVNVV FV
DRSGQRIPVSGRVGDNVLHLAQRHGVDLEGACEASLACSTCHVYVSEDHLDLLPPPEERRTRGWAARLC

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FIGURE 543A

CGCCGGCGGGCCGTGTGTGAGGAGCAGTAGAGAACTGTGGACTATTCTGCTTGGGAAGGTCAGCTCTGAGAGAGCT
GAGTCAGATTGAGGCAGAACTGAATAAACATTGGCGGGCGATTGTTAGAGGGGCTTTCTTACTACAAACCTCCAG
TCCAAGTTCAGCTGAAAAAGTGAAAGCTAATAAAGATGTAGCTTCACCATTGAAGGAACTGGGTTTAAAGAACAG
CAAGTTTTTGGGTCTTGATGAAGAACAGAGTGTGCAGTTACTCCAGTGTACCTGCAAGAGGACTACAGGGGTAC
TCGGGACTCAGTAAAGACAGTACTGCAAGATGAGAGGCAGAGCCAGGCCCTTAATCCTGAAGATTGCAGATTATTA
TTATGAAGAAAGAACCTGTATTCTTCGTTGTGTCTTACACCTTCTCACTTACTTCCAAGATGAAAGACACCCCTA
TAGGGTTGAATATGCAGACTGTGTTGATAAATTGGAGAAGGAACTAGTTTCAAATACAGACAGCAGTTTGAAGA
GCTTTATAAACTGAAGCACCAACTTGGGAGACACATGGAAATCTCATGACAGAGCGCCAAGTGTCTCGCTGGTT
TGTTCACTGCTTCGGGAACAGTCCATGCTGCTAGAAATTATTTTCCTTTATTATGCATACTTTGAGATGGCACC
CAGTGACTTACTTGTATTAACCAAGATGTTTAAAGAGCAAGGATTGGTAGTAGGCAGACCAATAGGCACCTGGT
GGATGAGACTATGGATCCTTTTGTAGATCGGATTGGCTACTTCAGTGCCTCATCTGGTGGAGGGCATGGATAT
CGAGTCCTTGATAAGTGTGCTTTGGATGACAGAAGAGAAGTGCATCAGTTTGCAGGATGGGCTTATTTGTCA
GGATATGGACTGTTAATGTTGACCTTTGGGGACATTCCACATCATGCCCCAGTGTCTTTGGCTGGGCTCTCCT
CCGTCACACTCTGAACCCAGAAGAGACAAGCAGTGTGGTCCGGAAGATAGGTGGCACAGCCATCCAGCTGAATGT
GTTTCAGTACTTGACCGATTGCTCCAGTCCCTTGCCAGTGGGGGAAATGATTGCACCACCAGCACTGCATGCAT
GTGTGTCTATGGACTGCTCTCTTTTCGTTCTGACCTCGTTGGAGCTGCACACCCTGGGCAATCAGCAGGATATAAT
TGATACAGCATGTGAAGTATTGGCCGACCCTTCTCTCCGGAACGTGTTCTGGGGAACAGAGCCAACCTTCTGGCCT
TGGGATCATTCTGGACAGTGTGTGTGGAATGTTTCCACCTTCTCTCCCACTCCTGCAACTGCTCCGAGCCCT
GGTATCAGGGAAGTCCACAGCCAAAAGGTGTATAGCTTCTTGGATAAGATGTCTTTCTACAATGAACCTTTATAA
ACACAAGCCTCATGATGTGATCTCCCATGAAGATGGAACCTTTTGGCGGAGACAAACCCAACTCCTTTATCC
CCTTGGGGGTCAAACCAACCTTCGCATACCTCAAGGCACTGTGGGCCAAGTAATGTTGGATGATAGGGCATACCT
GGTACGCTGGGAATACTCCTATAGCAGCTGGACCCCTTTTACCTGCGAGATTGAAATGTTGCTTCATGTTGTTTC
AACTGCAGATGTGATTGAGCACTGCCAGCGAGTCAAACCCATCATTGATCTCGTCCATAAGGTCATCAGTACAGA
CCTGTGATAGCAGACTGTCTCCTGCCATCACATCTCGCATCTACATGCTGCTGCAGCGTTAACGACAGTGAT
CTCCCCACCTGTGGATGTCTGCTTCTTGTGTCAACTGCTTAACTGTTTGGCTGCCCGCAATCCAGCAAAGGT
CTGGACTGATCTTCGTACACAGGTTTTTTACCATTGTGTGGCCATCCTGTCTCCAGCCTGAGTCAGATGATTAG
TGCGGAAGGGATGAATGCTGGAGGGTACGGAACCTCTTGATGAACAGTGAACAGCCTCAGGGCGAGTATGGGGT
TACTATTGCCCTTTCTGCGCTTGATCACACCCTTGTCAGGGGCAACTTGGTAGTACCAGAGCCAAGGACTTGT
ACCCTGTGTAATGTTTGTGCTGAAGGAGATGCTTCCAGCTACCATAAGTGGCGCTACAACCTCTCATGGAGTGAG
GGAACAGATTGGTTGCCTGATCTTGGAGCTGATTATGCGATACTGAACCTGTGCCACGAGACAGACCTGCACAG
CAGTCATACTCCAGCCTGCAGTTTCTCTGCATCTGCAGCCTGGCATAACAGAAAGCAGGACAGACAGTTATCAA
TATCATGGGCATTGGCGTGGACACCATTGACATGGTGATGGCTGCTCAGCCTCGAAGTGATGGGGCAGAGGGCCA
GGGGCAGGGCCAGCTGCTGATCAAGACAGTGAAACTGGCATTCTCCGTACCAACAATGTTATTGCGCTGAAACC
TCCTTCTAATGTGGTGTCCCCCTGGAACAGGCTCTCTCACAACATGGTGCTCATGGAAACAACCTCATTGCTGT
TCTAGCCAAATACATCTACCACAAACATGACCCCTGCTTTGCCACGTCTTGCCATTGAGCTGCTGAAACGTCTGGC
CACGGTGGCCCCAATGTGAGTGTATGCTTGTCTGGGCAATGATGCGGCTGCCATTGCTGATGCCCTTCTGACCCG
ATTGCAGAGCAAAATTGAGGACATGCGCATCAAAGTCATGATTCTAGAGTTCCTCACTGTTGCAGTAGAGACCCA
GCCAGGCCTCATCGAACTGTTTCTGAACCTGGAAGTTAAGGATGGCAGTGATGGCTCAAAGGAATTCAGCCTTGG
GATGTGGAGCTGTCTCCATGCAGTGTGAGCTGATTGATTCCCAACAGCAAGATCGATACTGGTGGCCACCCCT
GCTGCATCGTGCCGCCATTGCTTTTGCATGCTCTGTGGCAGGATCGGAGGGACAGTGCCATGCTGGTCTCTCG
AACCAAACCCAAGTTTTGGGAAAATTAACCAAGTCCGCTGTTTGGAAACCCTTCTCCTCCCTCTGAAACATCAGA
GCCCAGCATCCTGGAAACCTGTGCCCTAATCATGAAGATAATTTGCTTGGAGATATACTATGTAGTAAAGGGTTC
ATTAGACCAGTCATTAAAGGATACACTGAAGAAATTTCCATCGAGAAACGCTTTGCTTACTGGTCAGGGTATGT
CAAGTCATTGGCAGTTACAGTGGCCGAAACAGAAGGCAGCAGCTGCACCTCCTTGTAGAGTACCAGATGCTGGT
GTCCGCCTGGAGGATGCTTCTCATCATTGCCACCACTCATGCAGATATAATGCACCTGACTGACTCTGTGGTGCG
TCGCCAGCTCTTTCTTGACGTGCTTGATGGAACCAAGCATTACTCCTAGTTCCAGCCTCAGTGAAGTGCCTTCG
CCTTGGCTCCATGAAGTGCATCTGCTGCTTATCCTCCTCCGGCAGTGGAAAGAGAGAGTTAGGTTCTGTGGATGA
AATCCTTGGACCTTGACGGAGATCCTGGAGGGAGTGCTGCAGGCCGACCAGCAACTCATGGAGAAGACCAAGGC

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FIGURE 543B

CAAGGTGTTCTCAGCATTTCATCACAGTGTGCAAAATGAAGGAGATGAAAGTAAGTGACATCCCCAGTACTCCCA
GCTGGTGCTGAATGTCTGTGAGACCCCTCCAAGAGGAAGTGATTGCACTCTTCGACCAGACCCGCCACAGTCTGGC
ATTAGGCAGTGCCACAGAGGACAAGGACAGCATGGAGACTGACGACTGTTCTCGGTCCCGGCACAGGGACCAGCG
TGATGGGGTGTGTGTCCTGGGCCTGCACCTGGCCAAGGAGCTGTGTGAGGTAGACGAGGATGGTGACTCCTGGCT
GCAGGTAACCCCGCAGGCTCCCCATCCTACCCACCCCTCCTCACCCTCTAGAGGTGAGCCTTCGCATGAAGCAGAA
CCTGCATTTCACTGAGGCCACATTGCATCTGCTCCTCACCCTGGCTCGCACTCAGCAGGGAGCCACAGCAGTGGC
TGGAGCTGGCATCACCCAGAGCATTGTTTGGCCCTTCTGAGTGTGTACCAGCTGAGCACCAACGGCACAGCACA
GACACCTAGTGCTCTCGGAAGTCCCTGGATGCCCCCTCTTGGCCAGGAGTCTACCGCCTGTCCATGTCCCTGAT
GGAGCAGCTGCTCAAAACTCTGCGCTACAACCTTCTGCTGAGGCCCTGGACTTCGTGGGTGTCCACCAGGAGCG
GACCTTACAGTGCTCAACGCAGTGAGGACAGTGAGAGTCTGGCCTGCCTGGAGGAGCGGACCACACCGTGGG
TTTTATTCTGCGAGCTCTCTAACTTCATGAAGGAGTGGCACTTCCACCTGCCTCAGCTCATGCGTGATATCCAGGT
CAACCTGGGTACTTGTGCCAGGCATGTACCTCTCTCCTGCACAGTCGAAAGATGCTGCAGCATTACTTACAGAA
CAAAAATGGGGATGGCCTCCCCCTCAGCTGTTGCCCAGCGAGTCCAGAGGCCACCGTCTGCTGCTTCTGCTGCCCC
CTCCTCCTCAAAGCAGCCCGCTGCTGACACAGAGGCATCAGAGCAGCAGGCCTTGACACAGTCCAGTATGGCCT
TCTCAAGATCCTCAGCAAGACGCTGGCAGCCCTGCGCCACTTCACCCAGATGTCTGCCAGATTCTGCTGGATCA
GTCCCTGGACCTTGCTGAATACAACCTTCTGTTTGGCCCTGAGCTTTACCACTCCACCTTTGACTCCGAAGTGGC
CCCCCTCCTTCGGGACCCTTCTGGCCACAGTGAATGTGGCCCTCAACATGCTTGGAGAGCTGGACAAGAAAAAGGA
GCCCCCTACCCAGGCAGTGGGGCTCAGCACACAGGCAGAAGGGACCAGGACGTTAAAGTCCCTCCTGATGTTTAC
CATGGAAAACCTGCTTCTACCTGCTCATCTCTCAGGCGATGCGGTACCTTAGGGACCCGGCTGTGCACCCCGGGA
CAAACAGCGGATGAAGCAGGAGCTCAGCTCTGAGTTGAGCACGCTGCTGTCCAGCCTCTCGCGCTACTTCCGCCG
GGGAGCCCCCAGCTCCCCCTGCCACTGGTGTCTCTCCCTCGCCGCAGGGCAAGTCCACCTCTCTCCAAAGCCAG
CCCTGAGAGTCAGGAGCCTCTGATCCAGTTGGTGCAGGCGTTTGTCCGGCATATGCAAAGATAGGGCAGTGCTGT
TCTGCCCACCTACCCCTCTCCACCAGCCTACACTGCACCCTGGCTGGCAGGGGTGCTGCTGGCTGCTAGGGCCTA
TACAATGGAGGGCACCTCCTGTCACCCCCCTCCCGGAGTAGCCACGACTCCAGCCACCACCCACTGACGTTATTT
TTATACTAGATGAAGAGGTCAACAGCAGGCATGGGGAGCCGAGTCTTCTGTGCTCAGGTCCTCAGCTGCAGACG
CCCCCTAGAGGAACTTTCCTTCTTCCAGCATTCCCACAGCACTGCCGGCCAGGGGAGAGGCGGCAGCCCAGC
AGAGGGCTCTATGCACGGGTTTCAAACCTGTTTTCCACACTCTGTCTTGCAGTTTGGTAATTCTGTGGTCTAT
TTATACAGATATTAAATCTTGTTTATAGAC

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FIGURE 544

AGGPCVRRSSRELWTILLGRSALRELSQIEAELNKHWRRLLEGLSYYKPPSPSSAEKVKANKDVASPLKELGLRIS
KFLGLDEEQSVQLLQCYLQEDYRGTRDSVKTVLQDERQSOALILKIADYEEERTCILRCVLHLLTYFQDERHPY
RVEYADCVDKLEKELVSKYRQQFEELYKTEAPTWE THGNLMTERQVSRWFVQCLREQSMLEIIFLYYAYFEMAP
SDLLVLTKMFKEQGFSGRQTNRHLVDETMDFVDRIGYFSALILVEGMDIESLHKCALDDRRELHQFAQDGLICQ
DMDCLMLTFGDIPHHAPVLLAWALLRHTLNPEETS SVVRKIGGTAIQLNVFYLTRLLQSLASGGNDCTTSTACM
CVYGLLSFVLTSLELHTLGNQQDIIDTACEVLADP SLPELFWGTEPTSGLGIILDSVCGMFPHLLSPILLQLLRAL
VSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWRRQTPKLLYPLGGQTNLRIPQGTGQVMLDDRAYL
VRWEYSYSSWTILFTCEIEMLLHVSTADVIQHCQRVKPIIDLHVHVISTDLSIADCLLPITSRIYMLLQRLTTVI
SPPVDVIASCVNCLTVLAARNPAKVWTDLRHTGFLPFVAHPVSSLSQMISAEGMNAGGYGNLLMNSEQPQGEYGV
TIAFLRLITTLVKGQLGSTQSQGLVPCVMFVLKEMLP SYHKWRYNSHGVREQIGCLILELIHAILNLCHETDLHS
SHTPSLQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQPRSDGAEGQGQGLLIKTVKLAFSVTNNVIRLKP
PSNVVSPLEQALSQHGAHGNLLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLGNDAAAIRDAFLTR
LQSKIEDMRIKVMILEFLTAVETQGLIELFLNLEVKDGDGSGKEFSLGMWSCLHAVLELIDSQQQDRYWCPPL
LHRAAIAFLHALWQDRRDSAMLVLRTPKPFWENLTSPILFGTLPSPSETSEPSILETCALIMKICLETIYYVVKGS
LDQSLKDTLKKFSIEKRFAYWSGYVKS LAVHVAETEGSSCTSLLEYQMLVSAWRMLLI IATTHADIMHLTDSVVR
RQLFLDVLDGTKALLLVPASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLEILEGVLOADQQLMEKTKA
KVFSAFITVLQMKEMKVSDIPQYSQVLNV CETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRHRDQR
DGVCVLGLHLAKELCEVDEDGDSWLQVTRRLPILP TLLTTLEVSLRMKQNLHFTEATLHLLTLARTQQGATAVA
GAGITQSICPLLSVYQLSTNGTAQTPSASRKSLDAPSWPGVYRLSMSLMEQLLKTLYNFLPEALDFVGVHQR
TLQCLNAVRTVQSLACLEEADHTVGFILQLSNFMKEWHFHPQLMRDIQVNLGYLCQACTSLLHSRKMLQHLYLQN
KNGDGLPSAVAQRVQRPPSAASAAPSSSKQPAADTEASEQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQ
SLDLAEYNFLFALSFTTPTFDSEVAPSF GTLLATVNVALNMLGELDKKKEPLTQAVGLSTQAEGRTLKSLLMFT
MENC FYLLISQAMRYLRDPAVHPRDKQRMKQELSSSELSTLLSSLSRYFRRGAPSSPATGVLPSPQ GKSTSLSKAS
PESQEPLIQLVQAFVRHMQR

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FIGURE 545

CTATTTTAGTACAAGTGAAACAGCCTCGAAAAAGGTCATCGCTTGCAAACCGCTTTTAATAAAACCGGGTTCC
AAGAAGTGTTTGATCCTCCTCATTATGAAGTGTTCCTAAGGGACAAAGAGATTCTGCAGACCTGGCAGACT
TGTCGGAAGAATTGGACAACCTACCAGAAGATGCGGCGCTCCTCCACCGCCTCCCGCTGCATCCACGACCACCT
GTGGGTGCGCAGGCCTCCAGCGTCAAACAAAGCAGGACCAACCTCAGTTCCATGGAACCTCCTTTCCGAAATGACT
TTGCACAACCACAGCCAATGAAAACATTTAATAGCACCTTCAAGAAAAGTAGTTACACTTTCAAACAGGGACATG
AGTGCCCTGAGCAGGCCCTGGAAGACCGAGTAATGGAGGAGATTCCCTGTGAAATTTATGTACAGGGGGCGAGAAG
ATTCTGCACAAGCATCCATATCCATTGACTTCTAATCTTCTGCTAATGGTGATGTGAATTCCTTAGGGTGTGTACG
TACGCAGCCTCCAGGGCACCATACTGTTTCCAGCAGCCAACCCCTTTTCTCCCATCACAACCTACGAAGACCTTGAT
TTACCGTTAACCTATTGTATGGTGATGTTTTTATTCTCTCAGGCAGTCTATATATGTTAAACCAATCAAGGAAC
TACTCTATTCAGTGGAACAATAATCATCTCTATTGCTTGGTGTCATTTATAGGAAGCACTGCCAGTTAAAGAGC
ATTAGAAGAGGTGGTTGGATGGAGCCAGGCTCAGGCTGCCTCTTCGTTTTAGCAACAAGAAGACTGCTCCTTGACT
GATAACAGCTCTGTCAATATTTTGATGCCACAATAAACTTGATTTTCTTTACATTCCTTTTATTTTCTTTCT
CTAAATTTAATTTGTTTTATAAGCCTATCGTTTTACCATTTCATTTTCTTACATAAGTACAAGTGTTAATGTAC
CACATACTTCAGTATAGGCATTTGTTCTTGAGTGTGTCAAAATACAGCTAGTTACTGTGCCAATTAAGACCCAGT
TGTATTTCACCCATCTGTTTCTTCTTGCTAATCTCTGTACTTCTGCCTTTTAATTACTGGGCCCTTATTCCTTA
TTTTCTGTGAGAAATAATAGATGATATGATTTATTACCTTTCAATTATATTTTCTCAGTTATACTAGAAAATTT
CATAATCCTGGGATATATGTACCATTTGTCAGCTATGACTAAAAATTTGAAAAGATAAAAATTTCTAGCAAGCCT
TTGAAGTTTACCAAGTATAGTCACATTCAGTGACAGCCCATTCATTCCAGTAAAGAATCATTTCATTCACCTTTGG
GAGAGGCCTATAATTACATTTATTTGCAATGTTTCTTCTCGCTAGATTGTTACATAGCTCCCATTCGTGTTGGTTT
TGCTTACAGCATATGTTAACCAAGGTTAGATGCCAGTTAAATTCCTTAGAAATTGGATGAGCCTTGAGATTGCT
TCTTAAGTGGGACATGACATTTTCTAGCTCTTATCAAGAATAACAACCTCCACTTTTTTTTAACTGCACITTT
GACTTTTTTTTATGGTATAAAAACAATAATTTATAAACATAAAAGCTCATTGTGTTTTTTAGACTTTTGATAATTAT
TTGATACTGTACAACTTTATTAATCAAGATGAAAGACCTACAGGACAGATTCCTTTTCACTGTTTACATCAGTG
GCTTTGTAIGCAAATATGCTGTGTTGGACCTGGACGCTATAACTTATTGTAAAGACCTTGGAATGTGGACATAA
GCTCTTTCTTTCTTTTGTACTGTATTTAGTTTGTGATAAAATTTTCACTGTGTGATATTTATGCTCTAAATCA
CTACACAAATCCCATATTAAATATACATTGTACCTG

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FIGURE 546

MACKTAFNKTGFQEVFDPPHYELFSLRDKEISADLADLSEELDNYQKMRRSSTASRCIHDHHCQSQASSVKQSRT
NLSSMELPFRNDFAQPQPMKTFNSTFKKSSYTFKQGHECPEQALEDRVMEEIPCEIYVRGREDQAQASISIDF

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FIGURE 547

TGGTCCATCAGCTGCTGGTTCATTATAGCCTTCTCTTAAGTACTGAATAAGACAAAATATAAATCTTGGAAGAAC
AAATTCAGACATCATCAGTAAGTCTTTAGGGACACAGGGAATATTTGAACTTGATTTAATTTGATGCCTTTTGCA
AAACCCGCTCTCCCGCATCACGTTGCTGTCCCCGCAGTCGCAGGCGCCCCCGGCCTGGCTGCGGAACATGTTGAA
GTCGTGTCCGGTGTGGTCGCCCTGGTGGAAGCACTCGGCGCACAGCGACATGCAGGGCGAGATGCCGCACGTCCG
GCAGCGGTAGGCCACGAAGTTGGCTGTCCAGACCAGGCCGCAGAGCGCCGCGGGATCGTAGGCCCGCACCGCCGC
GCAGAACTCGTCGTAGCCGCCGCCGCCGAGAGGCACTTACACCACTCCAGGGCCTCCTCCTCGGCCGCCCC
CGGACCGCCCCCGCCTCCGGCCGCCGCCGCGTCTCGCCGCCAGCAGCCGCGGCCAGCGGCCGC

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FIGURE 548

MPFAKPALPHHVAVPAVAGAPGLAAEHVEVVSGVVAVEALGAQRHAGRDAARPAAVGHEVGCPDQAAERRGIVG
PHRRAELVAAAAARQKALTPLQGILLGRPTAPASGRRRVLAASSRGQR

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FIGURE 549

CTCCTTGGGCGATCGCCTGGGTAGAGGAGAGGAGTTTCCGGGGCTCGGGTCCGGGTGCCTTCCAGGGGAACGAG
CGCGGAAGCAAGTGGGCGGCGAGAGGCGGAGCAAGAGACGCTGGAGGGCGTGGACGCAGCGGGCTTTGGAAAGGC
CCCAAGTTAATGAGGCGTGCGCCGGCTGCCGAGCGCCTCTTGGAGCTGGGCTTTCCCCCGGGTGCGGGCGCCAG
GAGCCGCCTTTTCCGCTGGGTGTCACTCGGGGGTGGGGAAGATGGCCCATTCAAAAGCGCCGCGAGGGGGCCCGG
CCAGTGCCCTTTCAGTGAGCGCTCGCAAGAGGACGGCAGAGGCCCGGCAGCTCGGAGCTCCGGGACCTTGTGGCGC
ATCAGGACGCGGCTGTCCCTCTGCCGGGACCCAGAGCCGCCCGCGCTCTGCCTCCTGCGTGTTAGCCTCCTC
TGCGCGCTCCGGGCAGGCGGCCGTGGGAGCCGCTGGGGCGAGGACGGCGCGAGGCTGCTGCTGCTGCCCCGGCC
CGCGCGGCTGGAAACGGAGAGGCCGAGCCAAGCGGCGGCCCTCTTATGCTGGGAGGATGCTGGAGAGTAGCGGC
TGCAAAGCGCTGAAGGAGGGCGTGCTGGAGAAGCGCAGCGACGGGTTGTTGCAGCTCTGGAAGAAAAAGTGTTC
ATCCTCACCGAGGAAGGGCTGCTGCTTATCCCGCCCAAGCAGCTGCAACACCAGCAGCAGCAGCAACAGCAGCAG
CAGCAGCAGCAACAACAGCCCGGGCAGGGGCCGGCCGAGCCGTCCCAACCCAGTGGCCCCGCTGTGCGCCAGCCTC
GAGCCGCCGGTCAAGCTCAAGGAAGTGCATTTCTCCAACATGAAGACCGTGGACTGTGTGGAGCGCAAGGGCAAG
TACATGTACTTCACTGTGGTGATGGCAGAGGGCAAGGAGATCGACTTTCGGTGCCCGCAAGACCAGGGCTGGAAC
GCCGAGATCACGCTGCAGATGGTGCAGTACAAGAATCGTCAGGCCATCCTGGCGGTCAAATCCACGCGGCAGAAG
CAGCAGCACCTGGTCCAGCAGCAGCCCCCTCGCAGCCGCAGCCGCAGCCGCAGCTCCAGCCCCAACCCAGCCT
CAGCCTCAGCCGCAACCCAGCCCCAATCACAACCCAGCCTCAGCCCCAACCCAAGCCTCAGCCCCAGCAGCTC
CACCCGTATCCGCATCCACATCCACATCCACACTCTCATCCTCACTCGCACCCACACCCTCACCCGCACCCGCAT
CCGCACCAAATACCGCACCCACACCCACAGCCGCACTCGCAGCCGCACGGGCACCGGCTTCTCCGCAGCACCTCC
AACTCTGCCTGAAAGGGGCAGCTCCCGGGCAAGACAAGGTTTTGAGGACTTGAGGAAGTGGG

GGAGTCCTCATGGGAATAAGGATATTACAAATGTAACAGGTACCTAAGCACTCCTTGATCACGTGACGTGTGTG
AATATTTTAGGCACACTTTCTTTTGNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTGACTTTCAACAAATTGATAGTGAGCATTAGGGTTTCCAAGTTGG
ATTTGTAACCTCCTCATCATTCCTTGATGACAACCTTTCTGAATATATGTCACTATGTAGTAAATTAACACTCC
AAACTCATCTTTCTGTTGTTAGAAGTTTTAGCGGTACTTCCATGCAACTTTAAATCTCACTGCTCTCTATGGTT
GATGTCAAATGACCTTCAGTAATGACTGAGAATTGAATACAAATAGATTACAAAGCCAAAATTTGATGTTAAATG

ACTCAGGAAATTTTAGTTGTATTTTCAATTCAAGTACTTAGTAGCCTACGTTTGCTTGGCCTCTGGTTCTTTATG
GAAAAATAGGCTTTGTAGTGGCATTGTGGAGCAAAGGAGACTGTTACACCTTAATTAACCTTTTTTTACTGATGCAA
ATAATTTGAGGATAGAGAGGAGGGAAGTAGTGAAAGCTATGACCTAAAACATTGGGACCAAATAGAGGCTCACAG
ATATTTGGATTATTTTATGTGCTTATTATTAATAAGGAAAGCATTTTGTGATATGTGGAAGACGCTATGTGAAG
TTTTACCTATCTTCTCAAAGACCTTTTCTTTTGATTTTCTTTTGGTGTTTCTTAAAGCCAAACAAAGAAATGTT
CTTAAGGAGACAGGGTGGGTTTTTCTGTGGGCCTTTGTGGTTTTTCTGTGGGCCATCGCCCTCTAATGGAATTG
ATCTCTGGCTGTTTTGATTTTTTTCATATTGTATTTTTTAAATTTGTTGTACAGTGCCCTGTGAGCACCAAGTACC
ACTAGATGAATAAAACGTATTATATCTAAAGTCTTAGTAGACCAATTTTTAATCTTAGTTGACTCTGTATTGTTA
TCACACTGCACTCTTGTGGTTGTGCCATTTTTGCAAATTGAGCTCTTTTCGGTTGTTTTTCGAAATAAGGGAACTT
AGTGTTGAAAAACCAGAGAACTTTTTCTTTAATAAGAACTAAAAAAGTTGCAGCCACATAGGTTCAAGTTTGGCT
CTTTGGTTTCCAGTGGCTCTCAAATCCCCTAAGGTATAAAGAAAACTACAGCTACCCTAGGGTTTCTCAACCT
TGGCATTATTGACATCTTGAATCAAATAATTCATTATTGTGGGGTGCTGTCTGTGCCTTGCAGAATCTTGAGC
AGTGTTCTGTACCTCTACCTATTGAGATGCCAGCAGCACACCCCCATC

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FIGURE 552

MTQEILVVFSIQVLSSLRLLGLWFFMENRLCSGIVEQRLLHLN

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FIGURE 553

AAGTTTGTGATAATTTGTTAGGACAGCAATAGAAAACAAATACAATATACAGGTTCACTCATTTAACATAATCTG
CCGTTTTACAAAACGTGATTTTGAAGTTTCTTGTTCATTGAATACACTTTTTTGAAGCTGATGTTGACACAGG
AATAAGGCAATTGAGCAAGAACAACAAGGCATGGTGTGTTAATTATGCACTAAATGACCGTGGCCATTTTGTCTA
ATAGTTTCAATAGTTTCCAATAGTTTCAAGTGTATAGGTTGAGGGCAGGGACTATATCTGGTCTTTATATCTTAC
AATGATTTTCTTATATAGTTATTAGCACAGTGCCAGAAATGTTTCCTGAATTAATAAATGCTAAACATTTCTC
ATTAAGACTGTAAGCTGTTTGGTGTAGGAAAATACTTTTTAAAATTGATCATAACAATCCAACGTTGAACAT
GGCCTGGAGCTTAACAGATGTTTATTTAAATACTAAGGAGTATGTCTGGGCTTAGGAAGGAGAGGGTGGTTACAT
TTCAGGGTGGTAGAATTCTGCCTGAAATATCTGCTTTATAATAAAAAGTAAAATGTCTCACCGATACACTGTTAAA
CTGAGAAAACAAAGATGAGGTAAGGTGGGTCAGATTATTTCTAAGGTCTGTTTACTATTTACATTTTCATATAATT
TTCATTAAATGTGGAGAATGCAAGTCTTAGGAGTCACCTGAGGTACATCCAGTTTTTTGTGACTATTTCTGATG
TTTGACAGACTGTTCTTTCAACTTGGTGTAGAGTTACAGTCTACTCTTTTAGGGAGAATGCTGTTTGTTCACATC
ATGAGGCTGTAAATATTTAAATGTTCTCACCATTGTGTTAGTTTCCAAGTACACATGGCCTGAGAGATTGGAG
TATCATTAAATCTGCAACTCTTTTAGTGCTCAGGATGTGCATGTTTATTACTTTCAGGACTAGTTCAGACATAG
TAAACTGCTAGTGACTTCATGTAATCCTTATTCTGAAGTGTATTGAAAGCAAGGGAATGAAACATGATCCCT
AATAACCTCAAACATCCAAAGATCAAGTCAATTAAGGGCAAAAAA

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FIGURE 554

MIPNNLKHPKIKSIK GK

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FIGURE 555

CTGAAAAACACTTGAAATAGCTTCTTCAACACATATATTGTATAGCTATTTAAAACCCAAATACAAATGTTATAT
GAAGACTTTCAAAGGCCGCAGGATAATTCCAATGGATCTATTTGTTTCAGTCATTGAGAAGCTATATCGGGAACC
CATCATGGATGAGCTCTGCTCTAGGCATGGGGAGAAAGGATGAGGAAGACAAATATGGCCCTAGTTCTTGTGGAT
CTTATGTTCTAGTGGTGGTGACTATTACTTTTTGAATTGTGTATTTGCCACAGGGGAGATTGGATTACTCTTCAG
AAATTTTATAAGCATCTAGAGATGACCTGCATTATTGCCTTGGGCAGGAAAATAACAGGGTTGAAAAAATCTGA
ACAAAGAAATCACCATTGATGGATATACACAGGATAATCTTTTCTGAAGTTACTAAAATGGCGAAGTTCCCAAA
AAATGTAATGCGAATTAAATTTCACTTTGCCTCTGAGAAAAAGTTAAAAGAATTTATTATTACTCTCGCTACATG
TATTATCAAAAATGAAGGTTGATATTTTTAAGGAATGAAGAGTTGGCCAGTCACTTTAGTGAAGTTTTATTTTT
TCGTAAATATAGTTTGCCTTTGCTTCCATGAAAAAATAGCTCATAAACCTTGACCCTGATGAAAGCACTGGGCCA
GTTTTCCAATTCTCTGTTATGTA AAAAGGCATAAGTCAATTGTTCAAAGT

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FIGURE 556

MDIHRIIFSEVTKMAKFPKNVMRIKFHFASEKKLKEFIITLATCI IKNEGLIFLRNEELASHFSEVLFFRKYSLP
LLP

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FIGURE 557

GGCACAAGGGGGGATAGGTGGGGGGCCCAAAGAAGGGCATGGTCAGCCTGTCTGGGAGGGAGTTGCATGTGTGCA
TCTGAGGTAGGGACAGGCAIGCATCTTACAGGATGAATATCGAGCAGAGTTACAGAGAGGGGGAAACTCCTTGAG
GTTTCAGGAATCACCTAATCCACTGTGACTCACAAATTCCTGCCTCTTGGCTTTGCCTGCAGCATATCTCCTGGA
AGTGTGCTGGGGCAAACTCATCCCAGACCACCATCTCCATCCTCCCCAATACACCCTGGCTCTCCCTGGCTAC
CCTTGAGCACGGTGCACGTGTGCATGGGTGCATGCCTGCATATATAGCTATCCCCCATGTATTTCCCAAAGCCCT
ACATAATGCTTCAGTTTGCTAAGGAAAAAATGTTAATTACTGCAAATGTGTTTAAACTGTAAAAGTACATTAAA
CAAACCTCTGTAAAGTGTGAAAAA

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FIGURE 558

GTRGDRWGAQRRAWWSACLGGSCMCASEVGTGMHLTG

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FIGURE 559

GTACTATCCTCCTTACTTTTGGGTGCGGGCCCTCCGGGAAGATGCGCGCGCTGCAGGCGGCCGAGGTGAAAAGTGGA
TGGCAGCGAGCCGAAACTGAGCAAGAATGAGCTGAAGAGACGCCTGAAAGCTGAGAAGAAAGTAGCAGAGAAGGA
GGCCAAACAGAAAGAGCTCAGTGAGAAACAGCTAAGCCAAGCCACTGCTGCTGCCACCAACCACCCACTGATAA
TGGTGTGGGTCTTGAGGAAGAGAGCGTGACCCAAATCAATACTACAAAATCCGCAGTCAAGCAATTCATCAGCT
GAAGGTCAATGGGGAAGACCCATACCCACACAAGTTCATGTAGACATCTCACTCACTGACTTCATCCAAAAATA
TAGTCACCTGCAGCCTGGGGATCACCTGACTGACATCACCTTAAAGGTGGCAGGTAGGATCCATGCCAAAAGAGC
TTCTGGGGGAAAGCTCATCTTCTATGATCTTCGAGGAGAGGGGGTGAAGTTGCAAGTCATGGCCAATTCCAGAAA
TTATAAATCAGAAGAAGAATTTATTCATATTAATAACAACTGCGTCGGGGAGACATAATTGGAGTTCAGGGGAA
TCCTGGTAAACCAAGAAGGGTGAGCTGAGCATCATTCGCTATGAGATCACACTGCTGTCTCCCTGTTTGATAT
GTTACCTCATCTTCACCTTGGGGCTCAAAGACAAGGAAACAAGGTATCGCCAGAGATACTTGGACTTGATCCTGAA
TGACTTTGTGAGGCAGAAATTTATCATCCGCTCTAAGATCATCACATATAAGAAGTTTCTTAGATGAGCTGGG
ATTCTAGAGATTGAACTCCCATGATGAACATCATCCAGGGGGAGCCGTGGCCAAGCCTTTTCATCACTTATCA
CAACGAGCTGGACATGAACCTTATATATGAGAATTGCTCCAGAACTCTATCATAAGATGCTTGTGGTTGGTGGCAT
CGACCGGGTTTATGAAATTGGACGCCAGTTCGGGAATGAGGGGATTGATTTGACGCACAATCCTGAGTTCACCAC
CTGTGAGTTCTACATGGCCTATGCAGACTATCACGATCTCATGGAATCACGGAGAAGATGGTTTCAGGGATGGT
GAAGCATATTACAGGCAGTTACAAGGTCACCTACCACCCAGATGGCCAGAGGGCCAAGCCTACGATGTTGACTT
CACCCACCCCTTCCGGCGAATCAACATGGTAGAAGAGCTTGAGAAAGCCCTGGGGATGAAGCTGCCAGAAACGAA
CCTCTTTGAAACTGAAGAACTCGCAAAATTCTTGATGATATCTGTGTGGCAAAAGCTGTTGAATGCCCTCCACC
TCGGACCACAGCCAGGCTCCTTGACAAGCTTGTGGGGAGTTCTTGGAAGTGACTTGATCAATCCTACATTCAT
CTGTGATCACCCACAGATAATGAGCCCTTTGGCTAAATGGCACCGCTCTAAAGAGGGTCTGACTGAGCGCTTTGA
GCTGTTTGTGATGAAGAAAGAGATATGCAATGCGTATACTGAGCTGAATGATCCCATGCGGCAGCGGCAGCTTTT
TGAAGAACAGGCCAAGGCCAAGGCTGCAGGTGATGATGAGGCCATGTTTCATAGATGAAAACCTTCTGTACTGCCCT
GGAATATGGGCTGCCCCCACAGCTGGCTGGGGCATGGGCATTGATCGAGTCGCCATGTTTCTCACGGACTCCAA
CAACATCAAGGAAGTACTTCTGTTTCTGCCATGAAACCCGAAGACAAGAAGGAGAATGTAGCAACCACTGATAC
ACTGGAAAGCACACAGTTGGCACTTCTGTCTAGAAAATAATAATTGCAAGTTGTATAACTCAGGCGTCTTTGCA
TTTCTGCGAAAGATCAAGGTCTGCAAGGGAATTCTGTGTGCTGCTTTCCATTTGACACCGCAGTTCTGTTTCAGC
CATCAGAAGAGAGACAAGGAATTAAAAATTTCTTTTAAATCCTGTTA

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FIGURE 560

MAAVQAAEVKVDGSEPKLSKNELEKRRRLKAEKKVAEKEAKQKELSEKQLSQATAAATNHTTDNGVGPEEESVDPNQ
YYKIRSQAIIHQKLVNGEDPYPHKFHVDISLTDIFIQKYSHLQPGDHLTDITLKVAGRIHAKRASGGKLIFYDLRGE
GVKLQVMANSRNYKSEEEFIHINNKLRRGDIIGVQGNPGKTKKGELSIIPYEITLLSPCLHMLPHLHFGGLKDKET
RYRQRYLDLILNDFVRQKFIIRSKIITYIRSFLDELGFLEIETPMNIIIPGGAVAKPFITYHNELDMNLYMRIAP
ELYHKMLVVGGIDRVYEIGRQFRNEGIDLTHNPEFTTCEFYMAYADYHDLMEITEKMOVSGMVKHITGSYKVITYHP
DGPEGQAYDVDFTPPFRRINMVEELEKALGMKLPETNLFETEETRILDDICVAKAVECPPPRTTARLLDKLVGE
FLEVTCINPTFICDHPQIMSPLAKWHRSEGLTERFELFVMKKEICNAYTELNDPMRQQLFEEQAKAKAAGDDE
AMFIDENFCTALEYGLPPTAGWGMGIDRVAMFLTDSNNIKEVLLFPAMKPEDKKENVATTDITLESTTVGTSTV

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FIGURE 561A

CCAGACATGGCGGAAGAGGAGGTGGCCAAGTTGGAGAAGCACTTGATGCTTCTGCGGCAGGAGTATGTCAAGCTG
CAGAAGAAGCTGGCGGAGACAGAGAAGCGCTGCGCTCTCTTGGCTGCGCAGGCAAACAAGGAGAGCAGCAGCAAG
TCCTTCATCAGCCGTCTGCTGGCCATCGTGGCAGACCTCTACGAGCAGGAGCAGTACAGCGATCTGAAGATAAAG
GTTGGGGACAGGCACATCAGTGCTCACAAGTTTGTCTGGCAGCCCGCAGTGACAGCTGGAGTCTGGCTAACTTG
TCTTCCACTAAAGAGTTGGACCTGTGAGATGCTAATCCTGAGGTGACGGTGACAATGCTTCGCTGGATCTATACA
GATGAGCTGGAGTTCAGAGAGGATGATGTGTTCTGACTGAACTGATGAACTAGCAAATCGGTTTCAGCTACAG
CTCCTCAGGGAGAGATGTGAGAAGGGTGTATGTCTCTAGTGAATGTCAGGAACTGTATTGCTTCTACCAGACG
GCAGAGGAGCTGAATGCCAGCACACTGATGAACTACTGTGCAGAAATTATTGCAAGTCATTGGGACGACCTGAGG
AAGGAGGATTTAGCAGCATGAGCCCTCAGTTGTTATACAAAATGATCAAATCCAAGACAGAGTACCCGCTACAT
AAAGCCATCAAAGTGGAGAGAGAAGACGTGGTCTCCCTGTATCTGATTGAAATGGATTCCCAGCTCCCTGGGAAG
CTGAATGAAGCGGACCATAACGGGGACCTGGCATTAGACCTAGCCCTCTCAGCAGCAGCTGGAGAATATTGCCACC
ACGCTGGTTAGTCACAAAGCTGATGTGGCATGGTGGCCAAGAGTGCTGGAGCTGTTACACAAAGGGATCCAAGAG
GATCTCTTTGCTGCCACTTTCTCATTAAGAATGGGGCCTTTGTCAACGCTGCTACACTAGGGTGCCAGGAGACA
CCACTGCACCTTGTTGGCCTTGACAGTTCAAGGAACCACTCAGCAGATGTGATGTCTGAGATGGCGCAGATTGCA
GAGGCCCTTCTGCAGGCTGGTGCCAACCCCAACATGCAGGACAGCAAGGGAAGGACCCCTTTACATGTGTCCATC
ATGGCCGGGGATGAATATGTGTTTCAAGTACCTGCTGCAGTGCAAACAACCTAGATTTAGAACTCAAAGACCACGAG
GGCAGCACGGCTCTGTGGCTGGCAGTGCAGCATATCACAGTGTCTTCTGACCAGTCTGTGAACCCCTTCGAAGAT
GTCCCCGTGGTAAATGGGACTTCAATTTGATGAGAACAGCTTTGCAGCCAGACTCATCCAGCGCGGCAGCCACACA
GACGCACCTGACACGGGACAGGAACTGTTTACTACAGCGGGCAGCTGGAGCAGGAAACGAGGCAGCAGCTCTT
TTCTGGCAACCAACGGTGGCCATGTCAACCACAGAAACAAGTGGGGAGAAACCCCGTTGCACACAGCGTGTCCG
CATGGCTGGCCAACCTCAGCAGAGCTCCTGCAGCAAGGCGCCAACCCAAACCTGCAGACGGAGGAAGCTCTG
CCTCTGCCAAAGGAGGCGCATCCCTGACCAGCTTGGCGGACAGCGTCCATCTGCAGACGCCACTGCACATGGCG
ATCGCCTATAACCATCCGGATGTGGTGTCTGTCTCTGAGCAGAAAGCCAATGCTCTTCATGCCACCAACAAC
TTGCAGATCATTCCGGAATTCAGCCTCAAAGATTCCCGAGACCAGACTGTGCTGGGCCTGGCATTATGGACTGGC
ATGCACACGATCGCAGCCAGCTGCTGGGCTCTGGAGCCGCCATCAATGACACCATGTGGATGGGCAGACGCTA
CTACACATGGCCATACAGCGGCAGGACAGCAAGAGCGCACTCTTCTGCTGGAGCACCGGGCAGATATAAAATGTC
AGGCCCTCAGGCCGGGAGACAGCCCTCCAGCTGGCCATCAGAAACCAGCTTCCACTCGTAGTTGATGCAATATGC
ACCCGAGGGGCTGACATGTCTGTGCCAGATGAGGAGGGGAACCCCGCTGTGGCTTGCAATTGGCAAACAATCTG
GAGGACATCGCATCCACTCTGGTTCAGACATGGCTGTGGTGCCACATGCTGGGGTCCGGGACCTGGTGGGTGCCCT
CAGACGCTCCTGCACAGAGCCATTGATGAGAACAACGAGCCCAACCGCTGCTTTCTTATTGCAAGTGGCTGTGAC
GTGAACAGTCCCAGACAACAGGCGCCAATGGAGAAGGAGAGGAAGAGGCTAGAGATGGGCAGACCCCTTTGCAT
TTGGCAGCCTCTTGGGGGCTGGAGACAGTACAGTGTCTTCTGGAGTTTGGTGCCGACGTGAACCCACAGGATGCA
GAAGGAAGAACCCCATGCCACGTGGCCATCAGCAGCCAACACGGTGTCTCATTCAGCTGTTGGTTTTCTACCCG
ATATCCAGTTTGAATGTACGGGACAAACAAGGGCTGACCCCGTTTGCCTGTGCCATGACTTTCAAGGACAACAAG
TCAGCCGAGGCCATTCTCAAACGGGGGTCCGGGGCTGCTGAGCAGGTGGATAACAAGGGCCGAATTCCCTTCAT
GTGGCAGTTCAGAATCTGATATTGAAAGTGTGCTGTCCCTGATCAGTGTCCACGCTAATGTGAATTCAAGAGCC
CAGGATGCCCCCAAGTTGACCCCTGACCTGGTGTGTCGAAGAAGGCTCAGAAATTATGTCCGCAATTGCTT
CTTGCGGGAGCCAAAGTGACCGAATTAACCAAGCATCGCAAGACTGCCCTCCATCTTGTGCCCAGGAGGACCTG
CCCACCATCTGCTCAGTCTCCTAGAGAATGCCGTGGACTTTGCTGCCGTGGATGAGAATGGAAACAATGCTCTT
CATCTTGCTGTAATGCACGGCCGGCTCAACAACATCCGGGTCTCTCTGACAGAGTGACAGTGGACGCCGAAGCC
TTTAATCTCAGAGGCCAGTCAACACTGCACATTTTGGGACAATATGGCAAGGAGAATGCAGCGGCCATCTTTGAT
CTCTTCTAGAAATGCATGCCGGGGTATCCTCTGGACAAGCCGGATGCAGACGGCAGCACGGTGCTGCTCCTGGCA
TACATGAAAGGAACGCCAACTTGTGCCGCGCCATCGTCCGGTGGGGGCTCGCCTCGGGGTGAATAACAACCAG
GGAGTCAACATCTTCAACTACCAGGTGCCACCAAGCAGCTCCTGTTCCGACTGCTGGATATGCTGTCCAAGGAG
CCCCCGTGGTGTGACGGCTCCTACTGCTATGAGTGCAGTCCAGGTTCCGAGTGCACCTCGCAACACCACTGT
CGTCACTGCCGACGTCTTCTTTGCCATAAATGCTCGACCAAGGAGATTCTATTATAAAGTTGATCTGAACAAG
CCTGTGCGGGTTTGCACAATTTGTTTTGATGTACTGACTCTGGGTGGGGTTTCTTAGTGAGCCCCCGGAGGTCCA
GGCAGCTCCTTGGTCACCTCCAGCAGCTTCTCTCTCACCAGCCTGACCCACCCAGAGCAGGAGCTGGCGGGTGT

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FIGURE 561B

CTTCCTGCGGCAATAGACTTGGACGATTAAGGACCATGGTGTGATAGATCCATGTCAAATGATCCCATATGATTG
TCAGTGTGTGTGTGTCAGACTGTGATCGATTCTACTAGATGTCTAACTCATCAGCCCAGCCATTGGCCTAAGTGGTA
AATGTGATTAGGAATTAGACCTCTCCCCATTCTGCTAGCAACATACAGGACACTTGGAAAACCATTTCCCCTTCC
AGTAGCTTGGTGTCCATCCCAGAGCATTTCATGAAGTCTTCCCGCTGGCTGACTGATGAGCAGAGCCTCTCAGCG
TAGGAAGCTGGCTGCTTAATGAGCTGGCTTTACTCTAGGGTAAGTGGCTGTGGACTTTTTCTGCACAGTGTTCAT
TAAAGATAATAGGATCCTCTTGCCCTGAAGTCTTTTCTTTTTACGCTAAGCTGTATTTTTAGTGAGCTACCCC
TTTTAAAAGGTGAAATCTTTCTTAACAGGGTTCAAAGATGAGAGCTGAAAAATCGTGGCCTTAACAACTGAAAG
CTTTACAGTGTTCATGCTACTGAGGTGTCAGGAGTGCAGCTGGGCCGCTTGACACCTCGTAGCAGCCGTCTCATT
CTCTCGTCTTGCTGCGTCCTGTCTGTGGAGTCCCTCAGTCACTCTGCTGTTGGAGAGTGTCTGGAGGAAATGCACTT
TTACTGTGCTGCACTTTTTATAGAGCTGCATTGTGCGTGATTCCAGTTTAAAATCCATATTCAAAATACCTAACA
CATCCCTGCATCAGTGATTCTAATGATCAGCTTTGACTGGACCTCAGCTCACACGATCTCCAAGGAAAACCTCTAC
AGGGCATCTTTTAGAGCAGAGATCATAAGGCCAGTGATGAGAGGGGAGTCACCAAGGCTTCAGCCCAAGGGCAT
CTCCAGCCTCAGGCCGGCAGGTCTATGTCCTTGACACAAACGTTCTTGCTGAAATCCTCCCTAGTGATGCTGCG
AGTGCTGTTGGTCCAGTTCTGTGTAGCTTGCCCTGCCCCATGAAGGGCCACCAGCCAAGGGCCCTGGCCACGTG
TGCGCCACCTTACTTTGGGAAGTCTCTGGCTTGCTGTGCTGGATGAGGCTGCCAGAACTTGTGGGCGTTTCATCGC
TGTTAGTACATATATTAACCGTGAGTGTAACTTTCTTTTGAAGGTTTGGCAGTTTCTAAAAAATGCACATTT
AAAGAGAAGCATCTACCACGGCTTTAAAACAAAACAACTCTGAGATGAACAATATGTGTTATACTCAGAGATTAA
CAATCTCAATCATACATACTGATTCTTTCAGACATTTAATAACCACTACATTTTTTGCATTAAATGAAGTTTGAC
TATATGTGTAAAGGGCCTAAATATTTTCGCACAGCCTGTTCTTTGTTTCATTCTTTCTGGATAGTGTGTCCTCTGT
ATTGCGGTAGATTATACATCTGTTGCCTAAATATGTGTGTAATGAGCTGATAAACTGGAGTACTACTTAAAAAAA
GTCTGTGATTATAAGATGTATATGCTTCTATGTGATATAAGCTTGTCACAATGTTTAAAGGAAACAATGAATTA
GAAGGGATCCCCCGTCCCAGTCTGACATATTACATACAGATGTTTAAAGAAAACCTCTGCTAGTCTTGCAAACATTG
GCCATGTGAGCATGTGGCAGTTCCATTTCTATTACCTGGAAGGCCATAAGGAAGCAGGCAGGGCTTAGGTAGCT
TGGTTACCTAAGTTAGAAAGTAAGAGAATCAIGGTTGCGATATGAATTGAAGTGGGTGGTACATGGATACCTGTT
CTTTAAAAGGAATGTGGAGATGAGTCAAGGGTGAGGCCGATTGTTCTGCCCCATGCCCTACCATACCAATTTCAAT
AACAATCTGCCTGTCAATTGCACTCAGAATCTTAAGATCATGTTTCAAATATGTTGATTCAAACCTTGCTTCTAAG
CCTGAGTCCAGGGATAGCAATGGTACTGACCAGCTATGGACTGGAGAACATTGAGTCCGTGTTTTCCATTGGCTTC
AGGGCGCATCCATGTGGATATAGGAAAAGCCTCTTTCCACAGACTTAGGAAGCCCCCGACCCACGCGGACGCTC
GCTGGGCTGCACTCAGCAGGCTGCTTGAGTGGGAGCTGACTCCAACATGCCCTGCCCTGGCTGGGACTAGGCATG
CTCCAGCCCTTCCCGTGCTCTCCCTGCTGTCAACACTTGCGTACAAACCTGCCTAGCTGTTGTAAGTTTTCATC
AGTAGCTTAAGTACTAGTAGCAAAAACCTTAAATTCATTTCAGAAAGTTGCCACTTCTGAATGAGTAGAGCAG

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FIGURE 562

MAEEEVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAQANKESSKSFISRLLAIVADLYEQEQYSDLKIKVG
DRHISAHKFVLAARSDSWSLANLSSTKELDLSDANPEVTVTMLRWIYTDELEFREDDVFLTELMKLANRFQLQLL
RERCEKGVMSLVNVRNCIRFYQTAEELNASTLMNYCAEIIASHWDDLKEDFSSMSPQLLYKMIKSKTEYPLHKA
IKVEREDVVSLLYLIEMDSQLPGKLNEADHNGDLALDLALSRRLENIATTLVSHKADVAVWPRVLELLHKGIQEDL
FAATFLIKNGAFVNAATLGCQETPLHLVALYSSRNHSADVMSAQIAEALLQAGANPNMQDSKGRTPPLHVSIMA
GDEYVFSHLLQCKQLDLELKDHEGSTALWLAVQHI TVSSDQSVNPFEDVPVVNGTSFDENSFAARLIQRGSHTDA
PDTATGNCLLQRAAGAGNEAAALFLATNGAHVNRNKNWGETPLHTACRHGLANLTAELLQOGANPNLQTEELPL
PKEAASLTSLADSVHLQTPPLHMAIAYNHPDVSVILEQKANALHATNNLQIIPDFSLKDSRDQTVLGLALWTGMH
TIAAQLLGSGAAINDTMSDGQTLHMAIQRQDSKSALFLEHRADINVRPQAGETALQLAIRNQLPLVVDICTR
GADMSVPDEEGNPPLWLALANNLEDIASTLVRHGCATCWGPGPGGCLQTLHRAIDENNEPTACFLIRSGCDVN
SPRQPGANGEGEEEEARDGQTPHLAASWGLETVQCILLEFGADVNPQDAEGRTPCHVAISSQHGVIIQLLVSHPI S
SLNVRDKQGLTPFACAMTFKDNKSAEAILKRGSGAAEQVDNKGNSLHVAVQNSDIESVLSLISVHANVNSRAQD
APKLTPLHLVVQEGSEIIVRNLLLAGAKVTELTKHRKTALHLAAQEDLPTICSVLLENADVFAAVDENGNNALHL
AVMHGRLLNNIRVLLTECTVDAEAFNLRGQSPLHLGQYGKENAAAFDLFLECMFPGYPDKPDADGSTVLLLAYM
KGNANLCRAIVRSGARLGVNNNQGVNIFNYQVATKQLLFRLLDMLSKEPPWCDGSYCYECTARFGVATRKHHCHRH
CGRLLCHKCSTKEIPIIKFDLNKPVRVCTICFDVLTGGVS

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FIGURE 563

TTCCGGCCTTGTAATCGCCGAGGGCACGTGCATGCCCCCTGGTTAAGAGTTGCAGGTAGCGGTAGCGATGGACAC
TCTGGATCGAGTAGTAAAGCCCCAAAACGAAAAGAGCCAAGAGATTCCCTTGAGAAGAGAGAACCGAAACTCAATGA
AAATATTAAAAATGCCATGCTGATTAAAGGGGGAAATGCAAAATGCAACAGTGACAAAAGTACTTAAAGATGTGTA
TGCACTGAAAAAACCATACGGGTGTACTATATAAAAAGAAAAATATTACAAGACCTTTTGAGGATCAGACATCACT
GGAATTCCTTTCAAAGAAGTCAGATTGTTCTTTATTTCATGTTTGGCTCCCATAATAAGAAGCGGCCAAATAATCT
AGTAATAGGTCGTATGTATGACTACCATGTGCTGGATATGATTGAATTAGGTATTGAGAATTTGTCTCTCTAAA
AGACATTAAGAACAGTAAATGTCTGAGGGAACAAAACCCATGCTGATATTTGCTGGCGATGATTTGATGTAAC
AGAAGATTATAGAAGACTAAAAAGTCTTCTTATTGATTTCTTCAGAGGCCCCACAGTATCAAAATATCCGCCTGGC
TGGATTAGAGTATGTTCTGCACTTCACTGCACTGAATGGGAAGATTTACTTTCGAAGCTATAAGTTGCTGTTGAA
GAAATCTGGTTGCAGAACACCACGGATTGAATTGGAAGAGATGGGACCCTCATTGGATCTGGTTCTGAGGAGGAC
ACACCTGGCATCGGATGACCTTTATAAATTATCTATGAAATGCCAAAAGCTCTCAAGCCAAAAAAAAAAAAAAAA
A

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FIGURE 564

MTLDRVVKPKTKRAKRFLEKREPKLNENIKNAMLIKGGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQ
TSLEFFSKKSDCSLFMFSGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFVSLKDIKNSKCEGTKPMLIFAGDDF
DVTEDYRRLKSLIDFFRGPTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLKKSGCRTPRIELEMGPSLDLVL
RRTHLASDDLYKLSMKMPKALKPKKKK

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FIGURE 565

GATACCATACCTGAACACCTGAACATTCTTCACAAGGTAGTAAATGCACTGCTTTATTCTGGTCTCAGTATTGTG
TGCTTAATAAGGAAATGAGAAAGGGTGGATCAGGGCATAGGATGAACAAGTTACTGCTAGACCTCTCACAATGCC
ACTAATGGATAAGATTGTATTTTCATCATTCTTGTCTCTTCGGAAGCTAACACCATGCTATAATAGGCACTAAAT
AGATGTCTAAAAACACCTTAAGTATTTGTCTAGAAATCTGGTGCATTGTTTCAGAAAGAACCAAAATTCAAAATAA
TTTCAAAGGGCCTAAAGCACTAGTTAATCAAAATTCATTAGTTTTTAATGGTACTACCACTCTCAAATTTAAAT
GTCATCTTACGTTCTCTTCCTCGCATTGGATTTATTGCTAAAACCTGGTAAACACTTTTAATCCTTTTCAATTC
CATTACCACTGCTCTTGTCCAGAATTACTTCGCAGACTAATAGTCACCTGACTTCTCCCCTGCATCCGATTTGCT
GTCTAATTCTGGTTACAAATAAGTAACTGCCAACTAATCTTTCTAAAAAGCAAGACTGATCTCGTCACTCCTTT
GCTCAACAATGTAAAAGCTCCCATTTGTCTCCCAAATAAAACCAGCTTTCCACTGTGTATACAATACATCCATGAT
CTGTATCCAGCATCATTTTGTATTAGCTCACTTTATACACCACCCCCCATGCCACATCAAATTAATTTATCCTGA
TAAATGCAACTGCATTTACCCTTTCCCTTATTTTGTCTTTATGTTGTAGGCCTCCTTTGTGCCCATTTCTTCAG
AAGACATCCCCCTACAGCCATGGTTCTCATCCAGAGGGTCTTTTGGCCCCGCAGGAGACATCTTGACAACGTTTAGA
GACAGTTACCACAACCTGGAAGATGGAATAAAAAGATGCTGCTAAACATCCTACAACAATTATCTGGCCAAAAATG
TGCTGAGGTTAAGAAACCCTGTCCTACAGATTATTTCCCTTATTCTGGGTACATAGAAGTAACTCCTTTTTTTCT
ATGAAAATTTCCACAATTTTTTTTTTTT

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FIGURE 566

MICIQHHFVLAHFIHHPPCHIKLNYPDKCNCIYPFPYFVLYVVGLLCAHFFRRHPLQPWFSSRGSFAPAGDI

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FIGURE 567

CCCGGACGTGCGGCTCCCCTCGGCCTCCTCGCC**ATGG**ACGCGGACGACTCCCGGGCCCCAAGGGCTCCTTGCGG
AAGTTCCTGGAGCACCTCTCCGGGGCCGGCAAGGCCATCGGCGTGCTGACCAGCGGCGGGGATGCTCAAGGTATG
AACGCTGCCGTCCGTGCCGTGGTGCGCATGGGTATCTACGTGGGGGCCAAGGTGTACTTCATCTACGAGGGCTAC
CAGGGCATGGTGGACGGAGGCTCAAACATCGCAGAGGCCGACTGGGAGAGTGTCTCCAGCATCCTGCAAGTGGGC
GGGACGATCATTGGCAGTGC GCGGTGCCAGGCCCTCCGCACGCGGGAAGGCCGCTGAAGGCTGCTTGCAACCTG
CTGCAGCGCGGCATCACCAACCTGTGTGTGATCGGCGGGGACGGGAGCCTCACCGGGGCCAACCTCTCCGGAAG
GAGTGGAGTGGGCTGCTGGAGGAGCTGGCCAGGAACGGCCAGATCGATAAGGAGGCCGTGCAGAAGTACGCCCTAC
CTCAACGTGGTGGGCATGGTGGGCTCCATCGACAATGATTTCTGCGGCACCGACATGACCATCGGCACGGACTCC
GCCCCTGCACAGGATCATCGAGGTCTGTCGACGCCATCATGACCACGGCCCAGAGCCACCAGAGGACCTTCGTTCTG
GAGGTGATGGGACGACACTGTGGGTACCTGGCCCTGGTGAGTGCCCTGGCCTGCGGTGCGGACTGGGTGTTCTCTT
CCAGAATCTCCACCAGAGGAAGGCTGGGAGGAGCAGATGTGTGTCAAACCTCTCGGAGAACCCTGCCCGGAAAAAA
AGGCTGAATATTATTATTGTGGCTGAAGGAGCAATTGATACCCAAAAATAAACCCATCACCTCTGAGAAAAATCAAA
GAGCTTGTCGTACGCAGCTGGGCTATGACACACGTGTGACCATCCTCGGGCACGTGCAGAGAGGAGGGACCCCT
TCGGCATTTCGACAGGATCTTGCCAGCCGCATGGGAGTGGAGGCAGTCATCGCCTTGCTAGAGGCCACCCCGGAC
ACCCAGCTTGCGTCTGTCTACTGAACGGGAACACGCCGTGCGCCTGCCGCTGATGGAGTGCCTGCAGATGACT
CAGGATGTGAGAAGGCGATGGACGAGAGGAGATTCAAGATGCGGTTGACTCCGAGGGAGGAGCTTTGCGGGC
AACCTGAACACCTACAAGCGACTTGCCATCAAGCTGCCGGATGATCAGATCCCAAAGACCAATTGCAACGTAGCT
GTATCAACGTGGGGGCACCCGCGGCTGGGATGAACGCGGCCGTACGCTCAGCTGTGCGCGTGGGCATTGCCGAC
GGCCACAGGATGCTCGCCATCTATGATGGCTTTGACGGCTTCGCCAAGGGCCAGATCAAAGAAATCGGCTGGACA
GATGTCGGGGGCTGGACCGGCCAAGGAGGCTCCATTCTTGGGACAAAACGCGTTCTCCCGGGGAAGTACTTGGA
GAGATCGCCACACAGATGCGCACGCACAGCATCAACGCGCTGCTGATCATCGGTGGATTTCGAGGCCTACCTGGGA
CTCCTGGAGCTGTGAGCCGCGGGGAGAAGCACGAGGAGTTCTGTGTCCCCATGGTCATGGTTCCCGCTACTGTG
TCCAACAATGTGCCGGGTTCCGATTTTCAGCATCGGGGCAGACACCGCCCTGAACACTATCACCGACACCTGCGAC
CGCATCAAGCAGTCCGCCAGCGGAACCAAGCGCGCGTGTTTCATCATCGAGACCATGGGCGGCTACTGTGGCTAC
CTGGCCAACATGGGGGGGCTCGCGGCCGGAGCTGATGCCGCATACATTTTCGAAGAGCCCTTCGACATCAGGGAT
CTGCAGTCCAACGTGGAGCACCTGACGGAGAAAATGAAGACCACCATCCAGAGAGGCCTTGCTGCTCAGAAATGAG
AGCTGCAGTGAAAATACACCACCGACTTCATTTACCAGCTGTATTCAGAAGAGGGCAAAGGCGTGTTTGACTGC
AGGAAGAACGTGCTGGGTCACATGCAGCAGGTGGGGCACCCCTCTCCATTTGATAGAACTTTGGAACCAAAATC
TCTGCCAGAGCTATGGAGTGGATCACTGCAAACTCAAGGAGGCCCGGGGCAGAGGAAAAAAATTTACCACCGAT
GATTCCATTTGTGTGCTGGGAATAAGCAAAAGAAACGTTATTTTCAACCTGTGGCAGAGCTGAAGAAGCAAACG
GATTTTGAGCACAGGATTCCCAAAGAACAGTGGTGGCTCAAGCTACGGCCCCCTCATGAAAATCCTGGCCAAGTAC
AAGGCCAGCTATGACGTGTGCGACTCAGGCCAGCTGGAACATGTGCAGCCCTGGAGTGTCT**TG**ACCCAGTCCCGCC
TGATGTGCTGCAGCCACCGTGGACTGTCTGTTTTGTAACTTAAGTTATTTATCAGCACTTTATGCACGT
ATTATTGACATTAATACCTAATCGGCGAGTGCCCATCTGCCCCACCAGCTCCAGTGCGTGCTGTCTGTGGAGTGT
GTCTCATGCTTTCAGATGTGCATATGAGCAGAATTAATTAA

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FIGURE 568

MDADDSRAPKGSRLRKFLHLSGAGKAIGVLTSGGDAQGMNAAVRVVRMGIYVGAKVYFIYEGYQGMVDGGSNIA
EADWESVSSILQVGGTIIGSARCQAFRTREGRLKAACNLLQRGITNLCVIGGDGSLTGANLFRKEWSGLLEELAR
NGQIDKEAVQKYAYLNVVGMVGSIDNDFCGTDMTIGTDSALHRIIEVVDAIMTTAQSHQRTFVLEVMGRHCGYLA
LVSALACGADWVFLPESPPEEGWEEQMCVKLSENRRARKRLNIIIVAEGAIDTQNKPIITSEKIKELVVTQLGYDT
RVTILGHVQRGGTPSAFDRILASRMGVEAVIALLEATPDTPACVVSLNGNHAVRLPLMECVQMTQDVQKAMDERR
FQDAVRLRGRSFAGNLNTYKRLAIKLPDDQIPKTN CNVAVINVGAPAAGMNAAVRS AVRVG IADGHRMLAIYDGF
DGFAKQIKEIGWTDVGGWTGQGSILGTRVLP GKYLEEIATQMRTHSINALLIIGGFEAYLG LLELSAAREKH
EEFCVPMVMVPATVSNNVPGSDFSIGADTALNTITDTCRIKQSASGTKRRVFI IETMGGYCGYLANMGGLAAGA
DAAYIFEFPDIRDLQSNVEHLTEKMKTTIQRGLVLRNESCSENYTTDFIYQLYSEEGKGVFDCRKNVLGHMQQG
GAPSPFDRNFGTKISARAMEWITAKLKEARGRGKKFTTDDSI CVLGISK RNVIFQPVAELKKQTD FEHRIPKEQW
WLKLRPLMKILAKYKASYDVSDSGQLEHVQPWSV

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FIGURE 569

AGCCTTAGCAAGACATTTCTACATTAAAGAGAAGGACTTTAACACAGCTCTGGACTGGGCACNTCAGGCCAAAAAT
GAAAGCACCTAAAAATTCCTATATTTTCAGATACACTAGGTCAAGTCTACAAAAGTGAAATCAAATGGTGGTTGGA
TGGGAACAAAACTGTAGGAGCATTACTGTTAATGACCTAACACATCTCCTAGAAGCTGCGGAAAAAGCCTCAAG
AGCTTTCAAAGAATCCCAAAGGCAAACCTGATAGTAAAACTATGAAACCGAGAAGTGGTCACCACAGAAGTCCCA
GAGACGATATGACATGTATAACACAGCTTGTTTCTTGGGTGAAATAGAAGTTGGTCTTTACACTATCCAGATTCT
TCAGCTCACTCCCTTTTCCACAAAGAAAATGAATTAGCCAAATTAACATTTCATTTCTGGGATCAGGAGGAATGGT
CCACTTCCTGATAAAAATTGC

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FIGURE 570

ALARHFYIKEKDFNTALDWAXQAKMKAPKNSYISDTLGQVYKSEIKWWLDGNKNCRSITVNDLTHLLEAAEKASR
AFKESQRQTDSKNYETENWSPQKSQRRYDMYNTACFLGEIEVGLYTIQILQLTPFFHKENELAK

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FIGURE 571

GGCACGAGGGTCCGCAAGCCCGGCTGAGAGCGCGC**ATG**GGGCAGGCGGGCTGCAAGGGGCTCTGCCTGTCGCTG
TTCGACTACAAGACCGAGAAGTATGTTCATCGCCAAGAACAAGAAGGTGGGCCTGCTGTACCGGCTGCTGCAGGCC
TCCATCCTGGCGTACCTGGTCGTATGGGTGTTTCTGATAAAGAAGGGTTACCAAGACGTCGACACCTCCCTGCAG
AGTGCTGTTCATCACCAGTCAAGGGCGTGGCCTTCACCAACACCTCGGATCTTGGGCAGCGGATCTGGGATGTC
GCCGACTACGTTCATTCCAGCCCAGGGAGAGAAGCTCTTTTTTGTGGTCACCAACCTGATTGTGACCCCCAACCAG
CGGCAGAACGTCTGTGCTGAGAATGAAGGCATTCTTGATGGCGCGTGCTCCAAGGACAGCGACTGCCACGCTGGG
GAAGCGGTTACAGCTGGAAACGGAGTGAAGACCGGCCGCTGCCTGCGGAGAGGGAACTTGCCAGGGGACCTGT
GAGATCTTTGCCTGGTGCCCGTTGGAGACAAGCTCCAGGCCGAGGAGCCATTCTGAAGGAGGCCGAAGACTTC
ACCATTTTTCATAAAGAACCACATCCGTTTCCCCAAATTCAACTTCTCCAAAAACAATGTGATGGACGTCAGGAC
AGATCTTTTCTGAAATCATGCCACTTTGGCCCCAAGAACCCTACTGCCCATCTTCCGACTGGGCTCCATCGTC
CGCTGGGCCGGGAGCGACTTCCAGGATATAGCCCTGCGAGGTGGCGTGATAGGAATTAATATTGAATGGAAGTGT
GATCTTGATAAAGCTGCCTCTGAGTGCCACCCTCACTATTCTTTTAGCCGTCTGGACAATAAACTTTCAAAGTCT
GTCTCCTCCGGGTACAACCTTCAGATTGCGCAGATATTACCGAGACGCAGCCGGGGTGGAGTTCCGCACCTGATG
AAAGCCTACGGGATCCGCTTTGACGTGATGGTGAACGGCAAGGGTGCTTTCTTCTGCGACCTGGTACTCATCTAC
CTCATCAAAAAGAGAGAGTTTTACCGTGACAAGAAGTACGAGGAAGTGAGGGGCCTAGAAGACAGTTCCCAGGAG
GCCGAGGACGAGGCATCGGGGCTGGGGCTATCTGAGCAGCTCACATCTGGGCCAGGGCTGCTGGGGATGCCGGAG
CAGCAGGAGCTGCAGGAGCCACCCGAGGCGAAGCGTGGAAGCAGCAGTCAGAAGGGGAACGGATCTGTGTGCCCCA
CAGCTCCTGGAGCCCCACAGGAGCACG**TGA**ATTGCCTCTGCTTACGTTACAGGCCCTGTCTAAACCCAGCCGTCT
AGCACCCAGTGATCCCATGCCTTTGGGAATCCCAGGATGCTGCCCAACGGGAAATTTGTACATTGGGTGCTATCA
ATGCCACATCACAGGGACCAGCCATCACAGAGCAAAGTGACCTCCACGTCTGATGCTGGGGTCATCAGGACGGAC
CCATCATGGCTGTCTTTTTGCCCCACCCCTGCCGTCACTTCTTCTTCTCCGTGGCTGGCTTCCCGCACTAGG
GAACGGGTTGTAAATGGGGAACATGACTTCTTCCGGAGTCTTGGAGCACCTCAGCTAAGGACCGCAGTGCCCTG
TAGAGTTTCTAGATTACCTCACTGGGAATAGCATTGTGCGTGTCGGGAAAGGGCTCCATTTGGTTCCAGCCCAC
TCCCTCTGCAAGTGCCACAGCTTCCCTCAGAGCACTCTCCAGTGGATCCAAGTACTCTCTCTCTAAAGACA
CCACCTTCTGCCAGCTGTTTGCCCTTAGGCCAGTACACAGAATTAAAGTGGGGGAGATGGCAGACGCTTCTGG
GACCTGCCCAAGATATGTATTCTCTGACACTCTTATTGGTCATAAAACAATAAATGGTGTCAATTTCAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 572

MGQAGCKGLCLSLFDYKTEKYVIAKNKKVGLLYRLLQASILAYLVVWVFLIKKGYQDVDTSLSQSAVITKVKGVAF
TNTSDLGQRIWDVADYVIPAQGENVFFVVTNLIVTPNQRONVCAENEGIPDGACSKSDCHAGEAVTAGNGVKTG
RCLRRGNLARGTCEIFAWCPLETSSRPEEPFLKEAEDFTIFIKNHIRFPKFNFSKNNVMDVKDRSFLKSCHFPGK
NHYCPIFRLGSIVRWAGSDFQDIALRGGVIGINIEWNCDLDKAASECHPHYSFSRLDNKLSKSVSSGYNFRFARY
YRDAAGVEFRTLMKAYGIRFDVMVNGKGAFCDLVLIYLIKKREFYRDKKYEEVRGLEDSSQEADEASGLGLSE
QLTSGPGLLGMPQQELQEPPEAKRGSSSQKNGSVCPQLLEPHRST

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FIGURE 573

GTGTGCCTGGTAGATCCCCGGGGCAAGCCCTGTGAGACAGTGTTCAGAGGCTAAGCTACAATGGCCAGTCCAGT
GTGGTACGGTGCCGGCCACTCACAGGCCGCACACACCAGATTCGAGTCCACCTTCAGTTCTTGGGCCATCCCATT
CTCAACGACCCCATCTACAACCTCAGTTGCCTGGGGTCCTTCTCGAGGCCGGGGCGGCTACATTCCCAAGACAAAC
GAGGAGTTGCTACGGGACCTGGTAGCAGAGCACCAGGCCAAACAGAGCCTGGATGTGCTAGATCTCTGTGAGGGT
GACCTGTCCCCAGGACTCACAGACTCTACGGCCCCCTCCTCAGAGTTGGGCAAGGACGACCTGGAAGAGTTGGCT
GCAGCTGCCCAGAAGATGGAGGAAGTAGCTGAGGCAGCCCCTCAGGAGTTGGACACAATAGCCTTGGCATCAGAG
AAGGCAGTTGAAACAGATGTCATGCATCAGAGACAGACCACTCTCTGCAGAGTGCCGGCTGGTGCGACAGGATCC
CTTGCCCCAAGACCTTGTGATGTTCTTACATGCCCTACGCTATTAAAGGGCCAGGCTTTGAGTACTTTTCACCAAT
GCCTGCCTGGGCACAGGATGACTGGCAAAAGGACTGAGGGTGTGGCCAATGGAGGGATTGCTTCTTGGGTTGTGA
CAAGGATGGGCTATAGGGCAAGGGCTGACCCCATGGGCTAGTACTTGGGGTTTCTATAGGAATGAGGACGGGCTT
CTAAAGAGACCTGCTCATACTTGCTACCTCCTTCCAGTGGGAATTTGGAGACTTTTTGGTTTGTAAATATATCCC
TTTTTCTAAC

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FIGURE 574

VCLVDPRGKPCETVFQRLSYNGQSSVVRCPILTGRTHQIRVHLQFLGHPILNDPIYNSVAWGPSRGRGGYIPKTN
EELLRDLVAEHQAKQSLDVLDLCEGDLSPGLTDSTAPSELGKDDLEELAAAQKMEEVAEAPQELDTIALASE
KAVETDVMHQRQTTLCRVPAGATGSLAPRPCDVPTCPTL

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FIGURE 575

GTCCGGGATTCCCAGCCATGGCAGATTCTCTCCGGGCAGCAGGGCAAAGGCCGGCGTGTGCAGCCCCAGTGGTCCC
CTCTGCTGGGACCCAGCCATGCAGACTCCACCTTTACAACAGCCTCACCAGGAACAAGGAAGTGTTCATACCTC
AAGATGGGAAAAAGGTGACGTGGTATTGCTGTGGGCCAACCGTCTATGACGCATCTCACATGGGGCAGCCAGGT
CCTACATCTCTTTTGATATCTTGAGAAGAGTGTGAAGGATTACTTCAAATTTGATGTCTTTTATTGCATGAACA
TTACGGATATTGATGACAAGATCATCAAGAGGGCCCGGCAGAACCACCTGTTTCGAGCAGTATCGGGAGAAGAGGC
CTGAAGCGGCACAGCTCTTGAGGATGTTTCAGGCCGCCCTGAAGCCATTTTCAGTAAAAATTAATGAGACCACGG
ATCCCGATAAAAAGCAGATGCTCGAACGGATTTCAGCACGCAGTGCAGCTTGCCACAGAGCCACTTGAGAAAGCTG
TGCAGTCCAGACTCACGGGAGAGGAAGTCAACAGCTGTGTGGAGGTGTTGCTGGAAGAAGCCAAGGATTTGCTCT
CTGACTGGCTGGATTCTACACTTGGCTGTGATGTCACTGACAATTCCATCTTCTCCAAGCTGCCAAGTTCTGGG
AGGGGGACTTCCACAGAGACATGGAAGCTCTGAATGTTCTCCCTCCAGATGTCTTAACCCGGGTAGTGAGTATG
TGCCAGAAATTGTGAACCTTTGTCCAGAAGATTGTGGACAACGGTTACGGCTATGTCTCCAATGGGTCTGTCTACT
TTGATACAGCGAAGTTTGCTTCTAGCGAGAAGCACTCCTATGGGAAGCTGGTGCCTGAGGCCGTGGAGATCAGA
AAGCCCTTCAAGAAGGGGAAGGTGACCTGAGCATCTCTGCAGACCGCCTGAGTGAGAAGCGCTCTCCCAACGACT
TTGCCTTATGGAAGGCCTCTAAGCCCGGAGAACCGTCTGCGCCGTGCCCTTGGGGAAAGGGTCGTCCGGGCTGGC
ATATCGAGTGTCTCGCCATGGCAGGCACCTCCTAGGGGCTTCGATGGACATTCACGGAGGTGGGTTCGACCTCC
GGTTCCCCCACCATGACAATGAGCTGGCAGCTCGGAGGCCTACTTTGAAAACGACTGCTGGGTTCAGGTACTTCC
TGCACACAGGCCACCTGACCATTCAGGCTGCAAAATGTCAAAGTCACTAAAAAATTTCATCACCATTAAAGATG
CCTTGAAAAAGCACTCAGCACGGCAGTTGCGGCTGGCCTTCTCATGCACTCGTGGGAAGGACACCCTGGACTACT
CCAGCAACACCATGGAGTCAGCGCTTCAATATGAGAAGTTCTTGAATGAGTTTTTCTTAAATGTGAAAGATATCC
TTCGCGCTCCTGTTGACATCACTGGTCAGTTTGAGAAGTGGGGAGAAGAAGAAGCAGAACTGAATAAGAACTTTT
ATGACAAGAAGACAGCAATTCACAAAGCCCTCTGTGACAATGTTGACACCCGCACCGTCATGGAAGAGATGCGGG
CCTTGGTCAGTCAGTGCAACCTCTATATGGCAGCCCGGAAAGCCGTGAGGAAGAGGCCCAACCAGGCTCTGCTGG
AGAACATCGCCCTGTACCTCACCCATATGCTGAAGATCTTTGGGGCCGTAGAAGAGGACAGCTCCCTGGGATTCC
CGGTGCGAGGGCCTGGAACCAGCCTCAGTCTCGAGGCCACAGTCATGCCCTACCTTCAGGTGTTATCAGAATTCC
GAGAAGGAGTGCGGAAGATTGCCCGAGAGCAAAAAGTCCCTGAGATTCTGCAGCTCAGCGATGCCCTGCGGGACA
ACATCCTGCCCCGAGCTTGGGGTTCGGTTTGAAGACCACGAAGGACTGCCACAGTGGTGAACTGGTAGACAGAA
ACACCTTATTAAAGAGAGAGAAGAAAAGAGACGGGTTGAAGAGGAGAAGAGGAAGAAGAAAGAGAGGCGGCCCC
GGAGGAAACAGGAACAAGAAGCAGCAAAGCTGGCCAAGATGAAGATTCCCCCAGTGAGATGTTCTTGTCAGAAA
CCGACAAATACTCCAAGTTTGATGAAAATGGTCTGCCACACATGACATGGAGGGCAAAGAGCTCAGCAAAGGGC
AAGCCAAGAAGCTGAAGAAGCTCTTCGAGGCTCAGGAGAAGCTCTACAAGGAATATCTGCAGATGGCCAGAATG
GAAGCTTCCAGTGAGGGGGGCACAGGACTGACTTTTTAAACCATTGTGGACTAGTGGCTGCTGTCTGCCTCAGTGA
CAATGTC

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FIGURE 576

MADSSGQQGKRRVQPOWSPPAGTQPCRLHLYNSLTRNKEVFIPODGKKVTWYCCGPTVYDASHMGHARSYISFD
ILRRVLKDYFKFDVIFYCMNITDIDDKIIKRARQNHLEQYREKRPEAAQLLEDVQAALKPFSVKLNETTIDPDKKQ
MLERIQHAVQLATEPLEKAVQSRLTGEEVNSCVELLEEAKDLLSDWLDSTLGCDVTDNSIFSKLPKFWEGDFHR
DMEALNVLPDVLTRVSEYVPEIVNFVQKIVDNGYGYVSNNGSVYFD TAKFASSEKHSYGKLVPEAVGDQKALQEG
EGDLSISADRLSEKRSPNDFALWKASKPGEPSWPCPWGKGRPGWHIECSAMAGTLLGASMDIHGGGFDLRFPHHD
NELAQSEAYFENDCWVRYFLHTGHLTIAGCKMSKSLKNFITIKDALKKHSARQLRLAFLMHSWKDTLDYSSNTME
SALQYEKFLNEFFLNVDILRAPVDITGQFEKWGEEEEELNKNFYDKKTAIHKALCDNVDTRTVMEEMRALVSQC
NLYMAARKAVRKRPNQALLENIALYLTHMLKIFGAVEEDSSIGFPVGGPGTSLSLSEATVMPYLQVLSEFREGVRK
IAREQKVPEILQLSDALRDNILPELGVRFEDEGLPTVVKLVDRNTLLKEREKRRVEEEKRKKKEEAARRKQEQ
EAAKLAKMKIPPSEMFLSETDKYSKFDENGLPTHMEGKELSKGQAKKLKLF EAQEKLYKEYLQMAQNGSFQ

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FIGURE 577

CAGCGCGGGCCAGGAGGCAGCCGGTGAGCGCCTGCGAGCAGAGTGGCGGGGGCCGCTGACAGGTCCCGCGCAGC
CCAGCCCAGCCCAGCCACGCGGCTCACAGGTGGGGTCCAAGAGCAGTTTGGAGCAACCCGGCGCTACGGAGAGGG
GTGGACGGCTCTGACGGGCCTCCTGTCTCCCGCTCGGGCAGAGGGACTCGGGGGACCTCGCTCCTTGGCCGAG
AGAACTGAACTCGGGCGGAGAGAACGCGCCCAGGCGGGCAAGGGGACCAGAGAAAGCCGGGGCTGGAAGTCACT
GTCGCTCGCCACTGTCTGGAGCGCACGGAGCGCAGAGGCCCGGCAGCCGCGCTGCCCTCCCGGGACCGAGCCA
GTGATGCAGGATCGCTGAGCGGAGATCCGCGCCGAGAAGTCTCTCGGGGCCGGGGCTGAGACGCACGCCTTCGAC
ACCGCTGCCAAGACCCCGATTCCGGCGACTCTTGCGGGGAACCGAGGGGCCAAGGCTGCCCAAGCTCAGGACTT
GGGCGAGTCTAAGACGATGGTTTCTTAAGCACGGACCCGCGTTCCCTTCCCGCCCCCTCGACTGGAGGCAGGGA
TCCTGCGCGGGGGCCCCGGGATTCCGTTTCCCGCGGAGCCCCGGCCGCTGCCTCCCGGGACAGTTCGCACGGCC
ACAGGGGCGCACGGCGATGTGGCCTCCGTCCAGCGCGCTGGCCCCGCCGGGGGATGCTCTGGCACCTGTCGGGGT
CCAGGCCTAGCATGGCCGGCGCGTTGCCCGACGTGCGCTCCGGCTAGGATGGCCCCCTCCGGGCCCGGCCAGTGCC
CTCTCCACCTCGGCCGAGCCGCTGTCCCGCAGCATCTTCCGGAAGTTCTTGCTGATGCTCTGCTCCCTGCTCACG
TCCCTTTACGTCTTCTACTGCTGGCCGAGCGCTGCCAGACCTGTCCGGCCCCGTCGTGGGGCTGTCCGGCGGC
GGCGAGGAGGCGGGGGCCCCCTGGTGGCGGCGTCTTGCCGAGGCCCGAGGGAGCTGGCGGTGTGGCCGGCGGCG
GCACAGAGAAAGCGCCTCCTGCAACTGCCGCAGTGGCGGAGGCGCCGGCCCGCGCGCCCGCGACGACGGCGAG
GAGGCGGCCTGGGAAGAAGAGTCCCTTGGCCTGTCTAGGGGTCCGGGCGGCTCCGGGGCCGGAAGCACCGTGCC
GAGCCCCCGCGGGGACCTTGGCGCTGCTCTGGACGAAGGCAGCAAGCAGCTGCCGACGGCCATCATCATCGGA
GTGAAGAAGGGGCGGCACGCGGGCGCTGCTGGAGTTCTGCGCGTGACCCCGACGTGCGCGCGTGGGCGCCGAG
CCCCACTTCTTCGACCGCAGCTACGACAAGGGCCTCGCTGGTACCGGGACCTGATGCCAGAACCCTGGACGGG
CAGATCACCATGGAGAAGACGCCAGTTACTTCGTACGCGGGAGGCCCCCGCGCGCATCTCGGCCATGTCCAAG
GACACCAAGCTCATCGTGGTGGTGCGGGACCCGGTGACCAGGGCCATCTCGGACTACACGCAGACGCTGTCCAAG
CGGCCCCGACATCCCCACCTTCGAGAGCTTGACGTTCAAAAACAGGACAGCGGGCCTCATCGACACGCTGTGGAGC
GCCATCCAGATCGGCATCTACGCCAAGCACCTGGAGCACTGGCTGCGCCACTTCCCCATCCGCCAGATGCTCTTC
GTGAGCGGCGAGCGGCTCATCAGCGACCCGGCCGGGGAGCTGGGCCGCGTGCAAGACTTCTTGGGCCCTCAAGAGG
ATCATCACGGACAAGCACTTCTACTTCAACAAGACCAAGGGCTTCCCCTGCCTGAAGAAGGCGGAGGGCAGCAGC
CGGCCCCATTGCCTGGGCAAGACCAAGGGCAGGACCCATCCTGAGATCGACCGCGAGGTGGTGCAGGCTGCGC
GAGTTCTACCGGCCTTTCAACCTCAAGTTCTACCAGATGACCGGGCACGACTTTGGCTGGGATGGATTAACCATAT
AATTTAAAAAGAAAAAATCAAAATATAATATATTTTTTTTACCAATCGGTAGAGAAGAGACAGTTTAATATT
TGTGCTGAAAATATGTTTCAGTATTTTTTTCAATGAATGTTAAGAGATTGTTCTCACTCCCGCCCCATCTTAATG
TATAACCAACACCAACACGTGGATCAACAGAAAAGGAAAAATTTCACTCGTCTAAACACTTTCAATTTTCAGTTT
TTATTTTATGTTCTATATACCCAGTCATAAAGTATAAGCATCAGTTGTCATTAAAAGTTTTTCAGAAAATCTTGAG
GTTAAACATCTCTCTCTTTTTTTTAAATACAAGGCCCTGATAAAATTGATATCTATCCTTATATTTTTCTCCC
TTTTTCCCGTGCCACTTTTTCTTAAATTATTTCCAGTTAGTATTATCATATGTTTGTACCCGTCACAGTTTCA
TAGTGCTTTCAAATACACCTTTTTTGATCATTAAAATAAAAAATAAATCTTGAAAAAATAAAAAA

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FIGURE 578

MAPPGPASALSTSAEPLSRISFRKFLMLCSLLTSLYVFYCLAERCQTLSPVVGLSGGGEEAGAPGGGVLAGGP
RELAVWPAAAQRKRLQLPQWRRRRPPAPRDDGEEAAWEEESPGLSGGPGGSGAGSTVAEAPPCTLALLLDEGSK
QLPQAIIGVKKGGTRALLEFLRVHPDVRAVGAEPHFFDRSYDKGLAWYRDLMPTLDGQITMEKTPSYFVTREA
PARISAMSKDTKLIVVVRDPVTRAI SDYTQTL SKRPDIPTFESLTFKNRTAGLIDTSWSAIQIGIYAKHLEHWLR
HFP IQMLFVSGERLISDPAGELGRVQDFLGLKRIITDKHFYFNKTKGFPCLKKAEGSSRP HCLGKTKGRTHPEI
DREVVRLREFYRPFNLKFYQMTGHDFGWDG

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FIGURE 579

GCTGTTGAGAAGCTACCCGCGGGGTTGTAGACCTCGGACCTCATGGCAGAGATAATTCAGGAACGCATAGAAGAT
CGGCTCCCGGAATTGGAACAGCTGGAGCGCATTGGACTGTTTCAGTCATGCGGAGATTAAGGCTATCATTAGAAG
GCTTCCGATCTAGAGTACAAAATCCAGAGAAGAACCCTTTTCAAGGAAGACTTTATCAATTATGTTCAATATGAA
ATTAATCTTTTGGAGCTGATCCGGAGAAGAAGAACACGCATTGGATATTCATTTAAGAAGGATGAGATTGAGAAT
TCTATTGTACACCGGTACAAGGTGTTTTCCAGCGTGCCTCAGCAAAATGGAAAAGACGATGTTCAACTTTGGCTC
TCCTATGTGGCTTTTTGTAAGAAGTGGGCTACTAAACTCGACTTAGCAAGGTATTCTCTGCCATGTTGGCGATT
CATTCCAACAAACCAGCTTTGTGGATTATGGCAGCCAAATGGGAAATGGAAGATCGATTGTCTTCAGAAAGCGCA
AGGCAACTATTTCTTCGCGCACTGCGCTTTCATCCAGAGTGCCAAAACCTTTATAAAGAATACTTTAGGATGGAG
CTGATGCATGCTGAAAACTGAGGAAGGAGAAGGAAGAATTTGAAAAAGCCAGTATGGATGTGGAGAATCCTGAT
TATTCTGAAGAAATCCTTAAGGGCGAGTTGGCATGGATCATCTACAAAAATCTGTGAAGCATAATTAAAGGTGCA
GAATTTACGTTGCTACTGCTTTTCGATTGCACAGCTATTTGACTTTGCCAAAGATCTACAAAAGAGATTTATGAT
GACCTTCAGGCTCTACACACAGATGATCCTCTCÀCTTGGGATTATGTGGCAAGGCGAGAATTAGAGATTGAGTCA
CAGACAGAAGAGCAGCCTACAACGAAACAAGCCAAAGCAGTGGAGGTCCGCCGAAGGAGGAGAGGTGCTGTGCT
GTGTATGAAGAGGCAGTGAAGACTCTGCCAACAGAGGCCATGTGGAAGTGTTACATCACCTTTTGCTTGGAAGA
TTTACTAAGAAGTCAAATAGTGGGTTCCCTTAGAGGGAAGAGGTTGGAAAGAACCATGACTGTATTAGGAAGGCA
CATGAAGTGAAGCTTCTGTCAGAATGCCAATACAGCAGTTGAGTGTTTCGTTGCTGTGTTATAACTTCCTGAGG
GAAGCTCTGGAAGTGGCAGTAGCTGGAAGTGAATTGTTTAGAGACTCTGGGACAATGTGGCAGCTGAAGCTGCAG
GTGCTGATCGAGTCAAAGAGCCCTGACATAGCCATGCTTTTTGAAGAAGCCTTTGTGCACCTGAAACCCCAGGTT
TGTCTGCCATTGTGGATTTCTGGGCAGAGTGGAGTGAAGGTGCCAAAAGCCAAGAAGACACTGAGGCAGTCTTT
AAGAAAGCTCTCTTAGCTGTCATAGGTGCCGACTCAGTAACCCTGAAGAATAAGTACCTGGATTGGGCTTATCGA
AGTGGTGGCTACAAAAGGCCAGAGCTGTGTTTAAAGTTTACAGGAGAGCCGACCATTTTCAGTTGACTTTTTTC
AGGAAAATGATTAGTTTGAAGGAGCAAGAATCCTGCAATATGGCGAACATAAGAGAATATTATGAGAGAGCT
TTGAGAGAGTTTGGATCCGCAGATTCTGATCTTTGGATGGATTATATGAAAGAAGAATTGAACCACCCCTTGGT
AGACCTGAGAAGTGTGGACAGATCTACTGGCGAGCGATGAAAATGTTGCAGGGAGAGTCAGCAGAGGCATTTGTA
GCTAAACATGCTATGCATCAGACTGGCCATTTATGAAGATGAAGAATACCGTCCGCTTTGTGAAATAGTATTGCA
AGCCAGCCCCGTGGGCAAATTTGTATTGAGTCCATCTGTAATTTGCTCAGTGATGGCAGACAAGATGGCTGTCTG
GTTTTGAGACACACACTTTAATTTTATGTTAACTTGTTAAATCTTTTTAAAAATTAAAAAATTTTTATGATTGAA
AAAAAA

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FIGURE 580

MAEIIQERIEDRLPELEQLERIGLFSHAEIKAIKKASDLEYKIQRRTLFKEDFINYVQYEINLLELIRRRRTRI
GYSFKKDEIENSIVHRVQGVFORASAKWKDDVQLWLSYVAFCKKWATKTRLSKVSAMLAHNSNKPALWIMAAKW
EMEDRLSSESARQLFLRALRFHPEC PKLYKEYFRMELMHAEKLRKEKEEF EKASMDVENPDYSEEILKGELAWII
YKNSVSIKGAEFHVSLLSIAQLFDFAKDLQKEIYDDIQLAHTDDPLTWDYVARRELEIESQTEEQPTTKQAKAV.
EVGRKEERCCAVYEEAVKTLPTTEAMWKCYITFCLERF TKKSNSGFLRGKRLERTMTVFRKAHELKLLSECQYKQL
SVSLLCYNFLREALEVAVAGTELF RD SGTMWQLKLQVLIESKSPDIAMLFEEAFVHLKPQVCLPLWISWAEWSEG
AKSQEDTEAVFKALLAVIGADSVTLKNKYLDWAYRSGGYKKARAVFKSLQESRPF SVDFFRKMIQFEKEQESCN
MANIREYYERALREFGSADSDLWMDYMKEELNHPLGRPENCGQIYWRAMKMLQGESAEAFVAKHAMHQTGHL

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FIGURE 581

GGGAGTGGCGTGGCGCAGGGATGGCACAAAAGAAATATCTTCAAGCAAAATTGACCCAGTTTTTAAGGGAAGACA
GGATTCAACTTTGGAAACCTCCATATACAGATGAAAATAAAAAAGTTGGTTTGGCATTAAAGGACCTTGCTAAGC
AGTACTCTGACAGACTAGAAATGCTGTGAAAATGAAGTAGAAAAGGTAATAGAAGAAATACGTTGCAAGGCAATTG
AGCGTGGAACAGGAAATGACAATTATAGAACAACGGGAATTGCTACAATCGAGGTGTTTTTACCACCAAGACTAA
AAAAAGATAGGAAAAACTTGTTGGAGACCCGATTGCACATCACTGGCAGAGAACTGAGGTCCAAAATAGCTGAAA
CCTTTGGACTTCAAGAAAATTATATCAAAATTGTCATAAATAAGAAGCAACTACAACCTAGGGAAAACCCTTGAAG
ACAAGGCGTGGCTCACAATGTGAAAGCGATGGTGCTGAACTAAAACAATCTGAAGAGGACGCGAGGAAAACT
TCCAGTTAGAGGAAGAGGAGCAAAATGAGGCCAACTCAAAGAAAAACAATTCAGAGGACCAAGAGAGGACTAG
AAATACTGGCAAAGAGAGCAGCAGAGACAGTGGTGGATCCAGAAATGACACCGTACTTAGACATAGCTAACCAGA
CAGGCAGATCAATCAGAATTCCTCCATCAGAAAGAAAAGCCCTTATGTTAGCTATGGGATATCATGAGAAGGGCA
GAGCTTTCTGAAAAGAAAAGAATATGGAATAGCCTTGCCATGTCTGTTGGACGCTGACAAATATTTCTGTGAGT
GTTGCAGAGAGCTGCTGGACACAGTGGATAACTATGCCGTCTCCAGCTGGATATAGTGTGGTGTACTTCCGCC
TGGAACAGCTGGAATGCCCTTGATGATGCAGAAAAAAATTAACCTTGCCCCAGAAATGCTTTAAAAATTTGTACG
GAGAAAATCATCAGAGACTGGTCCACATAAAAGGAAATGTGGGAAAGAGAAGGTACTGTTTCTAAGACTCTACT
TACTTCAAGGGATCCGAAACTATCACAGTGGAAATGATGTAGAGGCTTATGAGTATCTTAACAGGCACGTCAGCT
CTTTAAAGAGCTATATATTGATCCATCAAAAGTGGACAATTTGTTGCAGTTGGGGTTTACTGCCAGGAAGCACC
GGCTTGGCCTGAGGGCGTGTGATGGGAACGTGGATCATGCGGCCACTCATATTACCAACCGCAGAGAGGAAGTGG
CCCAAATAAGGAAGGAGGAAAAAGAGAAGAAAAGACGCCGCTCGAGAACATCAGGTTTCTGAAAGGGATGGGCT
ACTCCACGCACGCGGCCAGCAGATTCTGCTCAGCAATCCTCAGATGTGGTGGTTAAATGATTCCAATCCTGAAA
CCGACAACCGTCAAGAAAGTCCTTCCCAGGAAAACATTGACCGATTGGTGTACATGGGTTTTGATGCACTCGTGG
CCGAAGCTGCGCTGAGAGTGTTCAGAGGCAACGTCCAGCTGGCCGCCAGACCTTGCTCACAACGGAGGAAGCC
TGCTTCCCAGCTGCCGCTGTGCGCCAGAAGACTCTTGTCCCCGCCAGCCACGTCCCCTTCTGACTCCGCAGGAA
CCTCTAGTGCCTCAACAGACGAAGACATGGAGACAGAGGCCGTCAATGAGATACTGGAAGACATTCCAGAGCATG
AGGAAGACTATCTTGACTCAACTCTGGAAGATGAAGAAATATTATTGTCAGAGTACCTATCCTATGTAGAAAATA
GGAAGTCAGCAACAAAGAAAAACTAAATAATGAACAGAAATAGCGCTAATTTTCTGCTTATAAATGCTATCATT
TGAAAAGGCTAATGCAGCTCTTTCTGTTCTTACTTTTATCTGAATTACAAGTCCTCTTTGGGTGTAGGAGGGGG
TGGGCAGGGGACAAGTCCAGGAGGGGTCCCAGGGCCTTCATGCATGGTCTCGGGGAAGAAGCTTCTTTTGGCCTG
GCGCAAGCCGTTCCATCTGGCTCCCAAGTCTGCGTCCCTAACCCCTTCCCCAACTTTGGGGGTTTTACCCCGA
ACAAGGAAA

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FIGURE 582

MAQKKYLQAKLTQFLREDRIQLWKPPYTDENKKVGLALKDLAKQYSDRLECCENEVEKVIEEIRCKAIERTGND
NYRTTGIATIEVFLPPRLKKDRKNLLETRLHITGRELRSKIAETFGLQENYIKIVINKKQLQLGKTLEEQGVAHN
VKAMVLELKQSEEDARKNFQLEEEEQNEAKLKEKQIQRTKRGLEILAKRAAETVVDPEMTPYLDIANQTGRSIRI
PPSERKALMLAMGYHEKGRAFLKRKEYGIALPCLLDADKYFCECCRELLDTVDNYAVLQLDIVWCYFRLEQLECL
DDAEKKLNLAQCFKNCYGENHQRLVHIKGNCGKEKVLFLRLYLLQGIRNYHSGNDVEAYEYLNHRHVSSLKSYIL
IHQKWTICCSWGLLPKHLRGLRACDGNVDHAATHITNRREELAQIRKEEKEKKRRRLENIRFLKGMGYSTHAAQ
QILLSNPQMWWLNDSPETDNRQESPSQENIDRLVYMGFDALVAEALRVFRGNVQLAAQTLAHNGGSLPPELPL
SPEDSLSPPATSPSDSAGTSSASTDEDMETEAVNEILEDIPEHEEDYLDSTLEDEEIIIAEYLSYVENRKSATKK
N

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FIGURE 583

GATCAGAGGGCGATCAGCTGGACAGCAACTCAGGATGGCATCAGGCAGGGCACGCTGCACCCGAAAACTCCGGAA
CTGGGTGGTGGAGCAAGTGGAGAGTGGGCAGTTTCCCGAGTGTGCTGGGATGATACAGCTAAGACCATGTTCCG
GATTCCCTGGAAACATGCAGGCAAGCAGGACTTCCGGGAGGACCAGGATGCTGCCTTCTTCAAGGCCCTGGGCAAT
ATTTAAGGAAAGTATAAGGAGGGGGACACAGGAGGTCCAGCTGTCTGGAAGACTCGCCTGCGCTGTGCACTCAA
CAAGAGTTCTGAATTTAAGGAGGTTTCTGAGAGGGGCCGCATGGATGTTGCTGAGCCCTACAAGGTGTATCAGTT
GCTGCCACCAGGAATCGTCTCTGGCCAGCCAGGGACTCAGAAAGTACCATCAAAGCGACAGCACAGTTCTGTGTC
CTCTGAGAGGAAGGAGGAAGAGGATGCCATGCAGAACTGCACACTCAGTCCCTCTGTGCTCCAGGACTCCCTCAA
TAATGAGGAGGAGGGGGCCAGTGGGGGAGCAGTCCATTAGACATTGGGAGCAGCAGCAGCAGCAGCAGCCCTGA
GCCACAGGAAGTTACAGACACAAGTGGAGCCCCCTTTCAAGGGGATCAGAGGTCCCTGGAGTTTCTGCTTCCTCC
AGAGCCAGACTACTCACTGCTGCTCACCTTCATCTACAACGGGCGCGTGGTGGGCGAGGCCCAGGTGCAAAGCCT
GGATTGCCGCCTTGTGGCTGAGCCCTCAGGCTCTGAGAGCAGCATGGAGCAGGTGCTGTTCCCCAAGCCTGGCCC
ACTGGAGCCCACGCAGCGCCTGCTGAGCCAGCTTGAGAGGGGCATCCTAGTGGCCAGCAACCCCCGAGGCCTCTT
CGTGCAGCGCCTTTGCCCCATCCCCATCTCCTGGAATGCACCCAGGCTCCACCTGGGCCAGGCCCCGATCTGCT
GCCCAGCAACGAGTGGTGGAGCTCTTCAGAACCGCCTACTTCTGCAGAGACTTGGTCAGGTACTTTAGGGCCT
GGGCCCCCACCAGTTCAGGTAACACTGAATTTCTGGGAAGAGAGCCATGGCTCCAGCCATACTCCACAGAA
TCTTATCACAGTGAAGATGGAGCAGGCCTTTGCCCCGATACTTGCTGGAGCAGACTCCAGAGCAGCAGGCAGCCAT
TCTGTCCCTGGTGTAGAGCCTGGGGGACCCATCTTCCACCTCACCTCTTTGTTCTTCCTGTCTCCTTTGAAGTAG
ACTCATTCTTCACACGATTGACCTGTCCTCTTTGTGATAATTCTCAGTAGTTGTCCGTGATAATCGTGTCCCTGAA
AATCCTCGCACACACTGGCTGGTGGAGAACTCAAGGCTAATTTTTATCCTTTTTTTTTTTTTTTTTTTGAGATA
TACGCCCTCTTTTATCTGTAAAGGACTAGGAAATCCAAATGGTGTGAACCCAGGGGGCCTTTCCCTCTTCCCTG
ACCTCCCAACTCTAAAGCCAAGCACTTTATATTTTCTCTTAGATATTTACTAAGGACTTAAAATAAAATTTTTT
TGAAAGAGG

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FIGURE 584

MASGRARCTRKLNRWVVEQVESGQFPGVCWDDTAKTMFRIPWKHAGKQDFREDQDAAFFKAWAIFKGKYKEGDTG
GPAVWKTRRLRCALNKSSEFKEVPERGRMDVAEPYKVYQLLPPGIVSGQPGTQKVPSKRQHSSVSSERKEEEDAMQ
NCTLSPSVLQDSLNNEEEGASGGAVHSDIGSSSSSSSPEPQEVTDTEAPFQGDQRSLEFLLPPEPDYSLLLTFI
YNGRVVGEAQVQSLDCRLVAEPGSESSMEQVLFFKPGPLEPTQRLLSQLERGILVASNPRGLFVQRLCPIPISW
NAPQAPPGPGLLP SNECVELFRTAYFCRDLVRYFQGLGPPPKFQVTLNFWEEESHGSSHTPQNLI TVKMEQAF
RYLLEQTPEQQAAILSLV

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FIGURE 585

ATAAAAAATAAAAAAGAAAATTAACCTTTGGTACCAGGTACAAACCAGTCTGGGAGCAGATCAGCAAAGAACT
CTTGAAATAAACGGTTAAGATAAAAGGAGTAACAAAGGTGTAATACCAACGCATCGGCAGTGGCGCTGACCTTAG
AAGGCTTCCGACAGTCAATCACAATACTTCAGGACCTATCAGAGGTAGGATCTAAGCCTCCAGAGTCCCCGCAC
GCCCTTGTGAGCTCCCTGCTCCTCTCCTGATGCTTCCTGGGATCACTTCCGAAATAAATTACTTGCACTT

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FIGURE 586

IKNKKKKINFGTRYKPVWEQISKETLEING

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FIGURE 587

ATTGAANTTAGGTGACCCNATNGAAGNGCTATNACGTNGCATGCACNGCGTACGTAAGCTCGGAATTCGGCTCGA
GAAAAAAAAAAGTGCCAGCGTATGAGGTAATTAGATTGGTTCTCTCCAGAGGTAACCTGCCAAGAAGAGATGCTA
TAGATGTTACTCCTATACTGTAAAACATTGTGAAATCAGATTACTTTAAAATGATGTATTACAAAGTTATGCAAA
AAAGCAGTTGTGACTATGGAAGCCCAAGGCTTATATCCAGCTCTGTCTTACACTAAATATGGGTACAGTGTTTC
CACTCTGTCCATAAAATGGGAGCTAATATTCTCCAACCTGTGTGCCTGACATGATGGTTAAAGGGATTAAACAAA
ACAATAGTTTGTAATTTATTCTGTGAGAGCAAACCTGCTGGTAAATAAAAGGGACTAAGTTGACGAAAAATAAATT
TTAAAAACCTAATAAAACAAGTTTGTAATTTATAATTGTATACAAATAAAAGATGTTACAAAAATTGCGCACTT
ATATGTATGTACCATGACATAACTAATTCGTTGAACAAGTTGTGAGACAATCCTTTCTGAGAAAAGGTAGACCTG
TTACATCGTCTGTGGGTTAGGGTCATGTCAGCACGTACCAGGTACATTCTAGCTTTTGTAGAGAAAGTAAAAATCT
AGTGTTGAGTATGTAGGCACTGAGCCAGGTGGCCTGCTTAACATAAAAGGACTGATTTACAGGGTGGCTGTGGGAG
CCTTTCTAATGCTCTAATTCCTAGCCCCTTGCCCTGATCCAGCTGATTCCAAGAGCCAAGATTTTAGTCTTTCTT
GGTTGGCTTTTTTAAATGCTTTGGGCTTTCTTTAATGTATCTTCAAAATCATTTC

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FIGURE 588

LXLGDPXEXLXRXMHXVRKLGIRLEKKKSASV

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FIGURE 589

GCGCTGCAGCTCACTTTCTCCCTGTTTGCTGGCCAGCAGGGTTTGTGGCCGCCCTCTGCTGTGACGCCACAGCCTG
GTGAGGAGGGGGCTGCAGTTCCTCAGGAACTGCCAGTGGACAAAGTCATAAACAAGAGTTCCAGTTCCTTGGAA
CCTGAGTCGGGAGGCCTGCAACTCACTTTCTCCCTGTTTGCTGGCCCAGACAGGCCTGTGCTAGAGGGCTGGATA
GTGTGGTAGTGTGGTGGATAGAGTGTGCTGCCTCTATCCACAACGCAGCCATATGCTGACTGAAGATAACTTTGTGT
CTGGAAGAGCCCTCTGATTTCTTACACTAATGCGCCTTACACGAGATGGAGGATTTTACATTTGATGGAACAAAGC
GCTTAAGTGTCAACTACGTGAAGGGAATTTCAACCGACAGACACCTGTGACATCTGGGATAAGATCTGGAAC
TCCAAGCCAAGCCTGATGACCTGCTTATTTCTACCTATCCTAAAGCAGGAACAACATGGACTCAGGAGATAGTGG
AATTAATACAAAATGAAGGTGATGTGGAGAAAAGTAAACGGGCACCGACTCATCAACGATTTCTTTCTCGAAA
TGAAAATCCCATCCTTAGGATCTGGTTTGGAAACAAGCTCATGCAATGCCCTCACCACGGATCCTGAAAACACATC
TTCCCTTTCACTTGCTGCCACCATCCTTGCTAGAGAAAACTGTAAGATAATCTATGTAGCAAGAAATCCCAAGG
ACAACATGGTGTCTATTACCATTTCCAAAGAATGAATAAGCTCTTCTGCTCCAGGAACATGGGAAGAGTATT
TTGAGACTTTTCTGGCTGGGAAAGTGTGCTGGGGCTCCTGGCATGAACATGTGAAAGGATGGTGGGAAGCCAAAG
ACAAACACCGTATTCTCTATCTCTTCTATGAGGACATGAAGAAGAACCCAAAGCATGAAATTCAGAAGCTGGCAG
AATTTATTGGGAAGAAATTAGATGACAAAGTTCTAGATAAAATGTCCATTACACTTCGTTTGATGTCATGAAAC
AGAATCCAATGGCAAATATTTCATCGATTCTGCTGAAATCATGGACCACTCCATTTCTCCATTTCATGAGAAAAG
GGCAGTGGGAGACTGGAAGAAACACTTCACCGTGGCTCAGAATGAGAGATTGATGAAGATTACAAGAAGAAAA
TGACTGATACCAGACTAACTTTCCACTTCCAGTTCAGTAAGGAAGAAAACTGAAAATGTTTTAGTTTATTACC
CAGTATATTTGGGTAATAATGAAAGTTTAAATTCATAACAAATGATATCAGATTCCAGTTATCAGAATAGTTTA
CTGTGTTTGCTCTTATTCACTCTACTAAAAAATTATTTTAAAGGCTGGAGGCAAGGTGGTGACAGGCAGCAGGG
TGGCGACATGGAGAGAGGGAAGCTCAATAAATCAC TAGGTACAATCCTGGTATCATTGCCAATTATCATCATATT
TACATTTTCTACAATCATGTGCTTATTAACATATTGGAAATGCTTCAGTCCTCACATGATAATACACTAACATTT
TCAGATTAAGTTTTGGTTCAAGTTAATTTTTTTTTTTTTTTTTTTGAGACGGAGTCTCGCTCTGTGCGCCAGGCT
GGAGTGCAGTGGCACGATCTCGGCTCACTGCAAGCTCTGCTTCCTGGGTTACAGCCATTCCCTGCCTCAGCCTC
CCGAGTAGCTGGGACTATGGGCGCCACCACCACTCCCGGCTAATTTTTTTTTTTTGTATTCTTAGTAGAGACGAG
GTTTACCGTGTTAGCCAGGATGTTCTCGATCTCTGACCCCATGATCCACCCGCCTCAGCCTAGACCTGCTGAT
CCAGGGTGTGTGAGTTGAGGGTGGGTGGAGGGGTTGCAGTGTGGGAATGTGGCCCTGCAGTTGACCTGAGCT
GCTTCACATGGTTGTCCATTCTGGGGCTTAAAGAACTGGGACCAGACCAAGTAGAGGCCTTGGTGCTGGTTGGGG
TGGGGCCTGCAGAGTCTTAGTTACTGATTTCAATTAATGTAGGTTTGTACATGAGTTTCCCAATTAA
AAAAAATGACTTCTTGTCCAGTGCAAAAAAAAAAAAAAAAAA

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FIGURE 590

MALHEMEDFTFDGTRKLSVNYVKGILQPTDTCDIWDKIWNFQAKPDDLLISTYPKAGTTWTQEIVELIQNEGDVE
KSKRAPHQRFPFLEMKIPSLGSGLEQAHAMPSPRILKTHLPFHLLPPSLLEKNCKIIYVARNPKDNMVSYYHFQ
RMNKALPAPGTWEEYFETFLAGKVCWGSWHEHVKGWWEAKDKHRILYLFYEDMKKNPKHEIQKLAFIGKKLDDK
VLDKIVHYTSFDVMKQNPMANYSSIPAEIMDHSISPFRKGAVGDWKKHFTVAQNERFDEDYKKKMTDTRLTFHF
QF

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FIGURE 591

TGGAGTCTTTTGAAAAATTAAAGTCCAGGATTAAATTATATGTTGTCACCATTACACCACCTACCACCCTCCCC
ACCAATCTCTCCCACCGGTAAACTCGTCTTCTAATCCTGTAGAATCACATGAACATAAATGAAGAAGTAAGAAGT
TGAAGGCTCAGACTGACACTGTTACAACTAGCATCTTCAGATGCATGGTATTTACTTTAAATGTGCTTATATAC
AGTGTAGAGAAGCTCTTGTATAAGAAGACATCTATGCTAGCTAACTTAGTAGTAGTAGAGGGAACATATTCAGTG
AGCTGCCTTTATATCTGTAGTGTCTGGAGACTTGTTACTGGTTCATTTGTGGTTATCAGTTGAAGGTTCTGTTCTT
GAGATGTGCAATAGTAGTGTGAAAGGTATTGTTTAATAGTGATGGGGAACAGACATATTGGACTTTTTTTTCCA
TATTAAATTATTTAGTTTGCATGCCTGTTTGAAATTGGACCTCTCAGCAGCACTTTGAAATAGTTTAAATTAGGT
TAACATTTGCGTACACTTTAAATAAGCTAGCATATCGATGGCTTGATTTACCTAGATGCTGTTCAAATTTCTGA
AAGCACAAAGGTATTTTCATC

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FIGURE 592

MVFTLNVLIIYSVEKLLYKKTSM LANLVVVEGTYSVSCLYICSVGDLLLVHLWLSVEGSPPEMCNSSVERYCLIVM
GNRHIGLFFPY

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FIGURE 593

GCAGGCTGCTGTCTCACAGAGCGAGAAGGTGTGAGGAGCAGCCAGTTGTGTCTCTCTCTCTACCTCTGTGAAGG
GCGCGAATGGGCAGAGCAGAACTTCTAGAAGGGAAGATGAGCACCCAGGATCCCTCAGATCTGTGGAGCAGATCC
GATGGAGAGGCTGAGCTGCTCCAGGACTTGGGGTGGTATCACGGCAACCTCACACGCCATGCTGCTGAAGCTCTT
CTCCTCTCAAATGGATGTGACGGCAGCTACCTTCTGAGGGACAGCAATGAGACCACCGGGCTGTACTCTCTCTCT
GTGAGGGCCAAAGATTCTGTAAACACTTTTCATGTTGAATATACTGGATATTCATTTAAATTTGGCTTTAATGAA
TTCTCATCTTTGAAGGATTTTGTCAAGCATTTTGCAAATCAGCCTTTGATTGGAAGCGAGACAGGCACCTCTGATG
GTTCTAAACATCCCTACCCAAGAAAAGTGGGAAGAACCCTCCATTATGAATCTGTCCGGGTTACACAGCAATG
CAGACAGGAAGAACAGAAGATGACCTTGTGCCACAGCACCTTCTCTGGGCACCAAAGAAGGTTACCTACCCAAA
CAGGGAGGCCTGGTCAAGACCTGGAAAACAAGATGGTTTACTCTGCACAGGAATGAACTGAAATACTTCAAAGAC
CAGATGTCACCAGAACCAATTCGGATCCTAGACCTAACAGAATGTTTCAGCTGTACAATTCGATTATTACAAAGAA
AGGGTAAACTGTTTTTGTGGTATTTCATTTCAGGACATTTTATCTCTGTGCAAAGACCGGAGTAGAAGCTGAT
GAGTGGATCAAGATATTACGCTGGAAATTGGTCAAGGACAAAAGCTGATTTTGTCTGCTCTCTGTATATCTCCC
GAGGAGAAGACTGATCACAAATAGAAAACAGCTCAACCAAGGGGAAGGCACGATCCGATCTCGGTCGTTTCATCT
TTAAATAGATCTTTCTTGCCAAGGAATGCTCTGGCCCAGGAGCAAGGTGGAATGTTTCCCTGACGCTGTGATCTG
CAGCAGGCTTCAAATGAAAACCGACTAAGGATTTTCTTCAAAAACAAATCAGAAGCAGATGCTGATTGGGACCC
ATATACCACGTTGCTGACTCACGTTGCTGCCCTTCCATGATGTTGCCATCTCCTTGAGAACACTGAAGCAATCAC
CATTCTGATAGAAAGTGCTTAAACCACCACTCTTAGGTCGCTCACTCTTAGAACACACAATGGAAGAGGAAGGG
TTTTTGTTTTCACTCATTGTGGTCCCCAAGCCTATTGACACTAGTTGCCCTAGAGTCCCACTGTGAGTCATGGTCA
GCCTGTCTGACATCCAGGTTGTGCTATTAACCAAGAAGGAAACAGATACTTGGAGGCTTAGATGACTTCTGCAGG
ATTTATATTTCAGATAGAAAACATCAAATATTTTCAGGGGAGAGGTTTTTTTTTTTAAATTTTCCCCCTTTATACA
AAAAAAAAGAACATTTCCAAAACATAAAATAGAAAATGCTTGTGGCATTATTTTTCTCTTTTTTAAAGGTTTCAGAA
ATTTGGCAGGTCCTTTGCTTCTAATGACAAAACCTGTGAGAGCTAGATGTCTATGGGCAATTAGGTAGTATAATA
AAGGTAAATGAAGGTACAATTTTAAACCAATTATTTTACCCTGTTGGGGTAAATGTTTTTAAAGAGTGAGAAAAC
ATAAATTGAGAAAGGGTGATAAAGTAATAGATAACTTTTAGTTTAATAATAATTATTGTTATTATACTACTAATA
ATAGAGCACTTGTAAGCACTAAGTTATCTTTATCCAACATTTCTCCAATGGACTGAAAGAACTTTTCAAGGAC
AGTGTATTATAACAATCCCTTCCCGAATTAGTTGTATAGGGTTGGCCCAAGAGATGTAAGAAAAATCTCGCAT
TGCTCCCTAAGCACCTGGGCCCTATTAAAGAGCAACTTCTATTTCAGTCGGGGGAGTAACACTAAAGCTACAA
GAAATATGTAATAATGATAGGTAATAATGTGTTCCAAAGCTTTTTCAAAGCTAGAAATAGGAGGCAAAATAGAAGAA
TGAGATACTGATGTCCACAGTTCATTGGCAGAATCTAACCCCTTCTGTTATCTTTTTTAAATACTATTTTTGTGTTA
GATAGAAGTTTCAAAGAAGATAAAAATGCTTGAAGAGCCTGAGAGTAAAAAGATTATGCTGCAAAGCTATGATAT
AACTGCTCTTGCAGTCCAAAGGGATACCTGATTAAAGAAGTTTCTTATTTAAACATCTCAGACGCAAAAATTAC
ATTAAATTTTTGTATATTTCAACAACATTTTAAATGTATTTTGTATGTTTGTATTATATAGGATAAAGCAAATG
TCAAGTTAAATGTATTGTGTTGTTTGTAAAGTAAGAAGTTACTGGCCAGGAGCGGCGGCTCATGCCTGTAATCC
CAGGACTTTGGTAGGCCAAGACAAGCAGATCACTTGAAGTCAGGAGTTCAACATCAGCCTGGCCAACATGATGAA
ACCTTGCTCTTTACTAAAAATACAAAATTAGCTGGGCATGGTGGCAGGCGCCTGTAATCCAGCTACTCAGGAGG
CTGAGGCAGGAGAATTGCTTGAACCCGGGAGGTGGAGGTTGCAGTGAACCAAGATCGCGGCGCTGCACTCTAGCC
TGGGTGACAGAGTCAGACTCCGTCCCCAAAAAACAACAAACAAAAACAAAAAACAAGATTACAAATG
AATACTCACGGATATGTATAGTTTTATGTTTGTCTTCTAGAAAACAAATGTGTTTCTTTGGGTGGGTAATATTGT
GTTTTACTATGTTTACCTTTTATAAAACATAACCTGTTATTTATATTCTTTGGCTTTGTTTATAAAAAGCATG
ATTTTGCTGIGCATGTACCAATTTTG

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FIGURE 594

MGRAELLEKGMSTQDPSDLWSRSDGEAELLQDLGWYHG NLTRHAAEALLSNGCDGSYLLRDSNETTGLYSLSVR
AKDSVKHFHVEYTGYSFKFGFNEFSSLKDFVKHFANQPLIGSETGTLMLKHPYPRKVEEPSIYESVRVHTAMQT
GRTEDDLVP TAPSLGTKEGYLTKQGGLVKTWKTRWFTLHRNELKYFKDQMSPEPIRILDLTECSAVQFDYSQERV
NCFCLVFPFRTFYLCAKTGVEADEWIKILRWKLVKDKSCILSALCISPEEKTDHK

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FIGURE 595

GGTGTGGTAGCCGGCGCCGCGCCCATAGCCGGACGGGGATCTGAGCTGGCAGGATGAATGTGGGGGTGGCACACA
GCGAAGTAAACCCCAACACCCGAGTGATGAATAGCCGAGGCATCTGGCTGGCCTACATCATCTTGGTAGGATTGC
TGCATATGGTTCTACTCAGCATCCCCCTTCTTCAGCATTCCGTGTGTCTGGACCCTGACCAACGTCATCCATAACC
TGGCTACGTATGTCTTCCTTCATACGGTGAAAGGGACACCCTTTGAGACTCCTGACCAAGGAAAGGCTCGGCTAC
TGACACACTGGGAGCAAATGGACTATGGGCTCCAGTTTACCTCTTCCCGCAAGTTCCTCAGCATCTCTCCTATTG
TGCTCTATCTCCTGGCCAGCTTCTATACCAAGTATGATGCTGCGCACTTCCTCATCAACACAGCCTCATTGCTAA
GTGTACTGCTGCCGAAGTTGCCCCAGTTCCATGGGGTTCGTGTCTTTGGCATCAACAAATACTGAGGGATGGGTT
TTGGGACAGCTCCATGGGCATGGGGAAGGCACTGAAACAGAGGACTATAAAACACCAAAAAAAAAAAAAAAAAAA
AAAAAAAAA

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FIGURE 596

MNVGV AHSEVNP NTRVMNSRGIW LAYI I LVGLLHMVLLSIPFFSIPV VWTLTNVIHNLATYVFLHTVKGTPFETP
DQ GKARLLTHWEQMDYGLQFTSSRKFLSISP I VLYLLASFYTKYDAAHFLINTASLLSVLLPKLPQFHGVRVFGI
NKY

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FIGURE 597

CGCTCATTCTGACCCCGCAGTGGGCGCGATGGCGGAGGCTGTACTGAGGGTCGCCCCGGCGGCAGCTGAGCCAGC
GCGGCGGGTCTGGAGCCCCCATCCTCCTGCGGCAGATGTTTCGAGCCTGTGAGCTGCACCTTCACGTACCTGCTGG
GTGACAGAGAGTCCCGGGAGGCCGTTCTGATCGACCCAGTCCTGGAAACAGCGCCTCGGGATGCCAGCTGATCA
AGGAGCTGGGGCTGCGGCTGCTCTATGCTGTGAATACCCACTGCCACGCGGACCACATTACAGGCTCGGGGCTGC
TCCGTTCCCTCCTCCCTGGCTGCCAGTCTGTATCTCCCGCCTTAGTGGGGCCCAGGCTGACTTACACATTGAGG
ATGGAGACTCCATCCGCTTCGGGCGCTTCGCGTTGGAGACCAGGGCCAGCCCTGGCCACACCCAGGCTGTGTCA
CCTTCGTCCTGAATGACCACAGCATGGCCTTCACTGGAGATGCCCTGTTGATCCGTGGGTGTGGGCGGACAGACT
TCCAGCAAGGCTGTGCCAAGACCTTGTACCACTCGGTCCATGAAAAGATCTTCACACTTCCAGGAGACTGTCTGA
TCTACCTGCTCACGATTACCATGGGTTACAGTGTCCACCGTGGAGGAGGAGAGGACTCTGAACCTCGGCTCA
CCCTCAGCTGTGAGGAGTTTGTCAAATCATGGGCAACCTGAACTTGCCTAAACCTCAGCAGATAGACTTTGCTG
TTCCAGCCAACATGCGCTGTGGGTGCAGACACCCACTGCCATCTCACTTCTGTGATGCTCCCATCCACTA
TTAATGCACTAGGTGGGAGGAGAGGGCGGCAATGACACTGCACCTCTCCTTTCCCACCGCATTCCCTGGAGCTCC
CTAAATAAACTTTTTTTAACGTGAAAAAAAAAAAAAAAAA

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FIGURE 598

MAEAVLRVARRQLSQRGSGAPILLROMFEPVSCFTTYLLGDRESREAVLIDPVLETAPRDAQLIKELGLRLLYA
VNTHCHADHITGSGLLRSLPGCQSVISRLSGAQADLHIEDGDSIRFGRFALETRASPGHTPGCVTFVLNDHSMA
FTGDALLIRGCGRTDFQQGCAKTYHSVHEKIFTLPGDCLIYPADYHGFTVSTVEEERTLNPRLTLSCEEVVKI
MGNLNLKPKPQQIDFAVPANMRCGVQTPTA

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FIGURE 599

GGCTGTTGAGCTTGGTGATGAACTACAAATAGATGCCATAGATGATCAAAAATGTGATATTTTGGTTCAGGAAGA
ACTTCTAGCTTCACCTAAGAACTCTTAGAAGATACTTTATTTCCCTCCTCAAAGAAGCTCAAGAAAGACAACCA
AGAGAGCTCAGACGCTGAGCTTAGTAGTAGTGAGTACATAAAAACAGATTTGGATGCGATGGATATTAAGGGCCA
GGAATCAAGCAGTGATCAAGAGCAGGTTGATGTGGAATCCATTGATTTTAGCAAAGAGAACAAAATGGACATGAC
TAGTCCAGAGCAGTCTAGAAATGTGCTACAGTTTACTGAAGAAAAAGAAGCTTTTATCTCTGAAGAGGAGATTGC
AAAATACATGAAGCGTGAAAAGGAAAGTATTATTGCAAAATTTGTTGCTGTCGTGCTATGAAAAAGGTGCTGT
TTTGCATCATTGGTTAATAAGCATAATGTTTCATAGCCCTTACAAATGCACAATCTGTGGAAAGGCTTTTCTTTT
GGAATCTCTCCTTAAAAATCATGTAGCAGCCCATGGGCAAAGTTTACTTAAATGTCCACGTTGTAATTTTGAATC
AAATTTCCCAAGAGGTTTTAAGAAACATTTAACTCATTGTCAAAGCCGGCATAATGAAGAGGCAAATAAAAAGCT
AATGGAAGCTCTTGAACCGCCACTGGAGGAGCAGCAAATTTGATAACACAGTGTGAATATTTGTTCTACAAAGGT
GTTTGTGGAACCATTCCTTTGTAAGTATAGCTTATCAGATAGCATAGTTGGATCAGTAGATGACATGTATGGTGT
ACCGTGTTCACGTCTCAGTTGTGTTACTAAGAATGAGCATTGATCATTTTTTTCTGGTCTCTGTCTATGTGA
CTATCTTGTAAGTCAATAAAATTTCTGTATAGTCCAGATGGATTAACTTCTCATTTCCTTTTAAATATGTATGAAT
AATAATACAAGGAAGTAGGCATTCCATTTAATAATCAAGAGCAAGTTGTACTCAAAGCATTTCAGTTAAAGTGTAT
CTGTGTGTGGAACCTAATTTAGACAATAGAAAATATTAGTTGAAATGTTTAAGAATTAGGCATGAAAAATAAAT
TGAGAAATTTGTTTCCTTACATGTATTTTTTAAATCATAAGAGTTATTTTCTATCTGATGTAAATTAGTTTATA
AATCTTAATCAGCTTCTAGATGTTTATTAGCTTTTATGTCATGAAATGTTGGAGTCTCAGGGTTGCTGATTTTCT
GCTAATGGGAAAAATTGACTAAGTCTTTAAATAGTTTGCAGCCTTCTCCACAGGAGACAAGTGAAAGATAAGT
GTGATTTTAGATCTTTCTGTCCATAGTTGTTTTCAGTGGAGTCTTCCATTCTGTATCTTACCCTAAGATCTGGT
TCTTCCCTCCCATCCCCACCCCCACCCACCGCTGCCAGCTCACACTAATAGATGATTCTTAATTGCCAAATG
TGTTAGAGTTTGATATCCTACTCCTGGGCCTTACATGTCGCTGTTGGGGCTTAAGACCAGGTTGATAAGTAGG
AACTGAAAGTCTTCCAGATTCACAGTAGAAAATTTTATAGACATTTCTGTAAAGAAATATATCGATTTTATGTT
TTTCAATTATGTTACTGTAAATACCTTGACCTGTTTCATGGATTATTTTATTCTAAAATATTTTGTCAAATGTGT
ATCAACCAAAATAAAAAGAAAGGTTTTTCATGTCAAAAAAAAAAAAAAAAAAAAA

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FIGURE 600

AVELGDELQIDAIDDQKCDILVQEELLASPKKLEDTLFPSSKKLKKDNQESSDAELSSSEYIKTDLDAMDIKGQ
ESSSDQEQVDVESIDFSKENKMDMTSPEQSRNVLQFTTEEKEAFISEEEIAKYMKRGKGKYYCKICCCRAMKKGAV
LHHLVNKHNVHSPYKCTICGKAFLLLESLLKNHVAAHGQSLLKPCRCNFESNFPRGFKKHLTHCQSRHNEEANKKL
MEALEPPLEEQQI

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FIGURE 601

GGCCCTCGGGCCAAGATTCCGGCACGAGGCGAACGGAGCAGCTGCTGCAGCAGGGCCCCATGGCGGACACCCAGTAC
ATCCTGCCCCAATGACATCGGCGTGTCTAGCCTGGACTGCCGTGAGGCCTTCCGCGCTGCTGTACCCACAGAGCGC
CTCTATGCCTACCACCTGTCCCGTGCCGCGCTGGTACGGAGGCCTGGCTGTGCTGCTTTCAGACCTCCCCCTGAGGCC
CCCTACATCTATGCTCTGCTCAGCCGCGCTCTTCCGCGCCCAGGACCCCGACCAGCTGCGCCAACATGCCCTGGCT
GAAGGCCCTTACCGAGGAGGAGTATCAGGCGTTCTGGTCTATGCCGCGGGTGTCTTACTCCAACATGGGCAACTAC
AAGTCCTTTGGTGACACCAAGTTTGTTCCTCAACTTGCCCAAGGAAAAGCTGGAACGGGTGATCCTAGGGAGTGAG
GCTGCTCAGCAGCACCCAGAAGAAGTCAGGGGCGCTGGCATACTGCGGGGAGCTTATGTTCTCTCTGGAGCCA
AGGCTTCGACACCTCGGACTGGGGAAGGAGGGAATCACCACCTATTTCTCTGGGAATTGTACCATGGAAGATGCC
AAATTGGCCCAGGACTTTCTGGACTCACAGAACCTCAGTGCCCTACAACACCCGCGCTCTTCAAAGAGGTCGATGGA
GAAGGGAAGCCCTACTACGAGGTGCGGCTGGCTTCTGTGCTTGGCTCAGAGCCTTCCCTGGACTCTGAGGTGACT
TCCAAGCTGAAGAGCTATGAATTCCGGGGAAGCCCTTCCAGGTGACCCGGGGGGGACTACGCGCCCATCTCCAG
AAGGTGGTGGAGCAGCTGGAGAAAGCCAAGGCCTATGCAGCCAACAGCCACCAGGGGCGAGATGCTGGCCAGTAT
ATAGAGAGCTTACCCAGGGCTCCATCGAGGCCACAAAGAGGGGCTCCCGCTTCTGGATCCAGGACAAAGGCCCC
ATCGTGGAGAGTTACATCGGGTTTCATCGAGAGCTACCGCGACCCCTTTGGTTCCCGAGGAGAATTTGAAGTTTC
GTAGCTGTGGTGAACAAGGCCATGAGTGCCAAGTTTGAGCGGCTGGTGGCGAGCGCAGAGCAGCTGCTGAAGGAG
CTGCCCTGGCCCCAACCTTTGAGAAGGACAAGTTCTCACCCTGACTTCACCTCCCTGGATGTTCTCACCTTC
GCTGGCTCCGGCATCCCTGCCGGCATCAACATCCCCAACTACGATGATCTGAGGCAGACGGAAGGCTTTAAGAAC
GTGTCGCTGGGGAATGTGCTGGCTGTGGCCTACGCCACGCAGCGGGAGAAGCTTACCTTTCTGGAGGAGGATGAC
AAGGACCTGTACATCTCTGGAAGGGGCCCTCCTTCGATGTGCAGGTGGGCCTGCACGAGCTGCTGGGCCATGGC
AGTGGCAAGCTCTTCGTACAGGACGAAAAAGGAGCATTCAACTTTGACCAGGAAACAGTGATCAACCCAGAGACG
GGCGAGCAGATTACAGCTGGTATCGGAGCGGGGAGACCTGGGATAGCAAGTTCAGCACCATCGCCTCCAGCTAC
GAAGAGTGCCGGGCTGAGAGCGTGGGTCTCTACCTCTGTCTCCACCCGCAAGTGCTGGAGATCTTTGGCTTTGAG
GGGGCTGATGCGGAGGACGTGATCTACGTGAACCTGGCTCAACATGGTTTCGGGCGGGGCTGCTCGCTCTGGAGTTC
TACACACCTGAGGCCCTTCAACTGGCGACAGGCCCATATGCAGGCCCCGTTTTGTGATCCTGAGAGTCTTGCTGGAG
GCTGGCGAGGGACTCGTTACCATCACTCCCACCACAGGCTCCGATGGGCGCCAGATGCCCGGGTCCGCCTCGAC
CGCAGCAAGATCCGGTCTGTGGGCAAGCCTGCTCTAGAGCGCTTCTGCGGAGACTTCAGGTGCTGAAGTCCACA
GGGGATGTGGCCGAGGGCGGGCCCTGTACGAGGGGTATGCAACGGTCACTGATGCGCCCCCGAGTGCTTCCTC
ACCCTCAGGGACACGGTGCTGCTGCGTAAGGAATCTCGAAGCTCATTGTTAGCCCAACACTCACCTGAAGGC
TCAGACGTGCAGCTTCTGGAATACGAGGCGTCAGCTGCTGGCCTCATCCGATCCTTCTCTGAGCGTTTCCAGAG
GATGGACCCGAGTTGGAGGAGATCCTCACACAGCTGGCCACAGCCGATGCCCGATTCTGGAAGGGCCCCAGTGAG
GCCCCATCTGGCCAAGCTTGAAGGAAGATGTGTGGCCTTGCCCCCAATTCCATCAGACCAAGGCTGCAAGTGGCCC
TCCATTCTGTGTGTATTTAGGGGCTGGGGAGGGGAGGGGCGAGGAGCTTGACCTTGGTACTACCTCAGCTGAG
GGTGGTGACACAACCCCTTCCATTGTGTCAGCACTTCCAGCCTGCCAATTGCTTCCCTCTGTGATCTCATTTC
TCTGCACTGCCATACGTGGAGTGAGCAAGACAGGGCTTACCATCCTGTCTACCAGATGAGGAAATGGCAGTTCTG
AGAAGTCACTGGTCTAGATCCCGCAGGTGGCACGTGACAGCTAGGGTTCAAACGTTCTACCAAAATCCAATGCT
CCTCACATATTAATTTTATAACCAGACAAATAAATATTAGAGACAACCACCAAAAAAAAAAAAAA

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FIGURE 602

MADTQYILPNDIGVSSLDCEAFRLLSPTERLYAYHLSRAAWYGGLAVLLQTSPEAPYIYALLSRLFRAQDPDQL
RQHALAEGLTEEYQAFLVYAAGVYSNMGNYSFGDTKFVFNLPKEKLERVILGSEAAQQHPPEVRGLWHTCGEL
MFSLEPRLRHLGLGKEGITYFSGNCTMEDAKLAQDFLDSQNL SAYNTRLFKEVDGEGKPYEVRLASVLGSEPS
LDSEVTSKLSYEFGRSFFQVTRGDYAPILQKVVEQLEKAKAYAANSHQGQMLAQYIESFTQGSIEAHKRGRSRFW
IQDKGPIVESYIGFIESYRDPFGSRGEFEGFVAVVNKAMSAKFERLVASAEQLLKELPWPPTFEKDKFLTPDFTS
LDVLT FAGSGIPAGINIPNYDDL RQTEGFKNVSLGNVLAVAYATQREKLT FLEEDDKDLYILWKGPSFDVQVGLH
ELLGHGSGKLFVQDEKGAFNFDQETVINPETGEQIQSWYRSGETWDSKFSTIASSYEECRAESVGLYLCLHPQVL
EIFGFEGADAEDVIYVNWLNMV RAGLLALEFYTP EAFNWRQAHMQARFVILRVLLEAGEGLVTITPTTGSDGRPD
ARVRLDRSKIRSVGKPALE RFLRRLQVLKSTGDVAGGRALYEGYATVTDAPPECFLT LRDTVLLRKESRKLIVQP
NTHLEGSDVQLLEYEASAAGLIRSF SERFPEDGPELEEILTQLATADARFWKGPSEAPSGQA

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FIGURE 603

CCCCTCTCAGGCACTGCTGGAGAACCGAGACCGACTTCTTTCTCTTTACCTTCATTGGCGCTTCTCTCCTGCAG
TCCGCCCTCTGGGCCCTGCCGCATTTCTTGAGACTTAAAGTGGCATTCTAAAGGCAATTTAAAAATCATGTC AAGC
TCAGTTGAACAGAAAAAGGGCCTACAAGACAGCGCAAATGTGGCTTTTGTAAGTCAAATAGAGACAAGGAATGT
GGACAGTTACTAATATCTGAAAACCAGAAGGTGGCAGCGCACCATAAGTGCATGCTCTTTTCATCTGCTTTGGTA
TCATCACACTCTGATAATGAAAGTCTTGGTGGATTTTCTATTGAAGATGTCCAAAAGGAAATTTAAAGAGGCACG
AAGCTGATGTGTTCTTTGTGCCATTGTCCTGGAGCAACAATTGGTTGTGATGTGAAAACATGTCACAGGACATAC
CACTACCACTGTGCATTGCATGATAAAGCTCAAATACGAGAGAAACCTTCACAAGGAATTTACATGGCCTATTGC
CGAAAACACAAGAAAAGTGCACATAACTCCGAAGCAGCTGATTTAGAAGAAAGTTTAAATGAACATGAACTGGAG
CCCTCATCACCTAAAAGTAAAAAGAAAAGTCGCAAAGGAAGGCCAAGAAAACTAATTTTAAAGGGCTGTCAGAA
GATACCAGGTCCACATCCTCCCATGGAACAGATGAAATGGAAAGTAGTTCCTATAGAGATAGGTCTCCACACAGA
AGCAGCCCTAGTGACACCAGGCCTAAATGTGGATTTTGCCATGTAGGGGAGGAAGAAAATGAAGCACGAGGAAAA
CTGCATATATTTAATGCCAAGAAGGCAGCTGCCCATTTATAAGTGCATGTTGTTTTCTTCTGGCACAGTCCAGCTC
ACAACAACATCAAGAGCAGAATTTGGAGACTTTGATATTAAACTGTACTTCAGGAGATTAAACGAGGAAAAAGA
ATGGTCTGTAGTTTTTTATATTTGTTATGCAACATTACACTTGATTGCTGCTTTAAATTTAGAGTACATCCCAA
TTTATCCAGTCATCAGAAAATTTAAAGTAGTTCGTATGTTAAAGCAAAGTATATATTTGACTTATTTGTAATATA
ATAAAGGATGCTGATGTTACGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 604

MSSSVEQKKGPTRQRKCGFCKSNRDKECGQLLISENQVAAHHKCMLFSSALVSSHSDNESLGGFSIEDVQKEIK
RGTKLMCSLCHCPGATIGCDVKTCHRTYHYHCALHDKAQIREKPSQGIYMAYCRKHKKTAHNSEAADLEESFNEH
ELEPSSPKSKKKS RKGRPRKTNFKGLSEDTIRSTSSHGTDEMESSYRDRSPHRSSPSDTRPKCGFCHVGEEENE
RGKLHIFNAKAAAHYKCMLFSSGTVQLTTTSRAEFGDFDIKTVLQEIKRGKRMVCSFYICYATLHLICCFKFRV
HPKFIQSSENLK

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FIGURE 605

CTCGAGAGCTCCGCCATGGCCGCTCTCACCCGGGACCCCCAGTTCCAGAAGCTGCAGCAATGGTACCGCGAGCAC
CGCTCCGAGCTGAACCTGCGCCGCCTCTTCGATGCCAACAAAGGACCGCTTCAACCACTTCAGCTTGACCCCTAAC
ACCAACCATGGGCATATCCTGGTGGATTACTCCAAGAACCTGGTGACGGAGGACGTGATGCGGATGCTGGTGGAC
TTGGCCAAAGTCCAGGGGCGTGGAGGCCGCCCGGGAGCGGATGTTCAATGGTGAGAAGATCAACTACACCGAGGGT
CGAGCCGTGCTGCACGTGGCTCTGCGGAACCGGTCAAACACACCCATCCTGGTAGACGGCAAGGATGTGATGCCA
GAGGTCAACAAGTTCTGGACAAGATGAAGTCTTTCTGCCAGCGTGTCCGGAGCGGTGACTGGAAGGGGTACACA
GGCAAGACCATCACGGACGTCAACATTGGCATTGTGCGCTCCGACCTGGGACCCCTCATGGTGACTGAAGCC
CTTAAGCCATACTCTTCAGGAGGTCCCCGCGTCTGGTATGTCTCCAACATTGATGGAAGTCAATTGCCAAAACC
CTGGCCCAGCTGAACCCGGAGTCTCCCTGTTTCATCATTGCCTCCAAGACCTTTACTACCCAGGAGACCATCACG
AATGCAGAGACGGCGAAGGAGTGGTTTCTCCAGGCGGCCAAGGATCCTTCTGCAGTGGCGAAGCACTTTGTTGCC
CTGTCTACTAACACAACCAAAGTGAAGGAGTTTGGAAATTGACCCCTCAAAACATGTTTCAGATTCTGGGATTGGGTG
GGAGGACGCTACTCGCTGTGGTCCGCCATCGGACTCTCCATTGCCCTGCACGTGGGTTTTGACAACTTCGAGCAG
CTGCTCTCGGGGGCTCACTGGATGGACCAGCACTTCCGCACGACGCCCTGGAGAAGAACGCCCCCGTCTTGCTG
GCCCTGCTGGGTATCTGGTACATCAACTGCTTTGGGTGTGAGACACACGCCATGCTGCCCTATGACCAGTACCTG
CACCGCTTTGCTGCGTACTTCCAGCAGGGCGACATGGAGTCCAATGGGAAATACATCACCAAATCTGGAACCCGT
GTGGACCACCAGACAGGCCCCATTGTGTGGGGGGAGCCAGGGACCAATGGCCAGCATGCTTTTTACCAGCTCATC
ACCAAGGCACCAAGATGATACCTGTGACTTCCTCATCCCGGTCCAGACCCAGCACCCCATACGGAAGGGTCTG
CATCACAAGATCCTCCTGGCCAACCTCTTGCCCCAGACAGAGGCCCTGATGAGGGGAAAATCGACGGAGGAGGCC
CGAAAGGAGCTCCAGGCTGCGGGCAAGAGTCCAGAGGACCTTGAGAGGCTGCTGCCACATAAGGTCTTTGAAGGA
AATCGCCCCAACCACTCTATTGTGTTCAACCAAGCTCACACCATTTCATGCTTGGAGCCTTGGTCGCCATGTATGAG
CACAAGATCTTCGTTACGGGCATCATCTGGGACATCAACAGCTTTGACCAGTGGGGAGTGGAGCTGGGAAAGCAG
CTGGCTAAGAAAATAGAGCCTGAGCTTGATGGCAGTGCTCAAGTGACCTCTCACGACGCTTCTACCAATGGGCTC
ATCAACTTCATCAAGCAGCAGCGCGAGGCCAGAGTCCAATTAAACTCGTGCTCATCTGCAGCCTCCTCTGTGACTC
CCCTTTCTCTTCTCGTCCCTCCTCCCCGAGCCGGCACTGCATGTTTCCTGGACACCACCCAGAGCACCCCTCTGGT
TGTGGGCTTGGAACACGAGCCCTTAGCAGGGAAGGCTGGTCTCCCCCAGCCTAACCCCGAGCCCTCCATGTCTA
TGCTCCCTCTGTGTTAGAATTGGCTGAAGTGTGTTTGTGTCAGCTGACTTTTCTGACCCATGTTACGTTGTTTAC
ATCCCATGTAGAAAAACAAAGATGCCACGGAGGAGGT

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FIGURE 606

MAALTRDPQFQKLQQWYREHRSELNLRRLFDANKDRFNHFSLTNTNHGHIIVDYSKNLVTEDVMRMLVDLAKSR
GVEAARERMFNGEKINYTEGRAVLHVALRNRSNTP ILVDGKDVMPEVNKVLDKMKSFQQRVRSQDWKGYTGKTIT
DVINIGIVGSDLGPLMVTEALKPYSSGGPRVWYVSNIDGTHIAKTLAQLNPESLFI IASKTFTTQETITNAETA
KEWFLQAAKDP SAVAKHFVALSTNTTKVKEFGIDPQNMFEFWDWVGGRYSLWSAIGLSIALHVGFDFEQLLSGA
HWMDQHFRITPLEKNAPVLLALLGIWYINCFGCETHAMLPYDQYLHRFAAYFQQGDME SNGKYITKSGTRVDHQT
GPIVWGEPGTNGQHAFYQLIHQGTKMIPCDFLIPVQTQHP I R KGLHHKILLANFLAQTEALMRGKSTEEARKELQ
AAGKSPEDLERLLPHKVFEGNRPTNSIVFTKLTPFMLGALVAMYEHKIFVQGI IWDINSFDQWGVELGKQLAKKI
EPELDGSAQVTSHDASTNGLINFIKQQREARVQ

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FIGURE 607

GTGTATTTGCATATTTTAAGTATCTACCATCTAATATTTATTAATACAATTTTTCTTAATTTCTTAGACTTGTG
ACTATTTGAAACAAATTATAACACTGTATTGTAGGATTTATAATTTGTAGTTGTAAAATTTATAACACATGGAAT
AAGAAGATAAATGGAAGTGTCTGTAGCAAATTTTCATGTTTTATTTAAGACAGTATAGTATTAAGTCTAAA
AGTATGGTGGATATGTTAAAGATTCATATTGTATTCCCTGCAGCAACCACTAAAAATGCAAAGAAGTGTAAATGT
AAATGCTAAAAAGGAGATAATTATAAAATATTTATTTGCANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NN
NN
AGGAATATGAAAAACCAAGCACACATCCTGGATAAAATTCATAAACCTGCTCAATGAGAGAAAAGTTGGACACAA
AATTGTACTTTATGTATTTTGTATTTTATTCCAGGCAAATAATCCTATGGTGAAAAAAATCAACAAGATAATC
TCTGCATGAGAAAAAGGACCAAGACAAGTGAATTTCTGAGGGTGATGAAAGTGTGCTTCGAAAAGGGGTGAA
GTTTATATGGGTCTATTTATTTGTCTAACATGTACAGTTAAGGTTTATGCCTTGCAATGTATGTACATCTTCACA
AAAAAATCTTAAAAAATTAATGAGGTGGGGTAGGGAAAGGTTGAAGTATAGATGAAGCAGAAGTGGTACAT
GATTAGTAGTTGAAGCTGGGGGCAGGTCTATAATATTTATTTTATGTCTTTAATAGCATTTGTATAAATGTACA
ATATTCGTTTACAATGTTAGCTCAGGATCTTGTTTACCTTTGGACAGGGAGGGAGGGAGAAATTTATTTTCTGGG
TAGGAG

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FIGURE 608

MLAQDLVYLWTGREGEIYFLGR

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FIGURE 609

CGCGCCGCGGAGGAGGAGGAAGGGGAGGAGGGCGAGGCGGGAGGTGCAGGAGGGACCCTCGCCATGGGTCCACGG
GCCTAGAGTGGCGGAAGATACCGGCCTGGTGCCAACTGGCTACTGCTGCTTCCTGTGGCCTCCATGGCTGAGGA
CTGGCTGGACTGCCCGGCCCTGGGCCCTGGCTGGAAGCGCCGCGAAGTCTTTCGCAAGTCAGGGGCCACCTGTGG
ACGCTCAGACACCTATTACCAGAGCCCCACAGGAGACAGGATCCGAAGCAAAGTTGAGCTGACTCGATACCTGGG
CCCTGCGTGTGATCTCACCTCTTCGACTTCAAACAAGGCATCTTGTGCTATCCAGCCCCCAAGGCCCATCCCGT
GGCGGTTGCCAGCAAGAAGCGAAAGAAGCCTTCAAGGCCAGCCAAGACTCGGAAACGTCAGGTTGGACCCACAGAG
TGGTGAGGTGAGGAAGGAGGCCCGAGGGATGAGACCAAGGCTGACACTGACACAGCCCCAGCTTCATTCCCTGC
TCCTGGGTGCTGTGAGAACTGTGGAATCAGCTTCTCAGGGGATGGCACCCAAAGGCAGCGGCTCAAAACGTTGTG
CAAAGACTGTGAGCACAGAGAATTGCCTTCAACCGGAACAGAGAATGTTAAGCGTGTGGGCTGTGGGGAGTG
TGCAGCCTGCCAGGTAACAGAAGACTGTGGGGCCTGCTCCACCTGCCTCCTGCAGCTGCCCCATGATGTGGCATC
GGGGCTGTTCTGCAAGTGTGAACGGAGACGCTGCCTCCGGATTGTGGAAGGAGCCGAGGGTGTGGAGTATGCCG
GGGCTGTCAGACCCAAGAGGATTGTGGCCATTGCCCATCTGCCTTCGCCCTCCCCGCCCTGGTCTCAGCGGCCA
GTGGAATGTGTCCAGCGACGTTGCCTACGGGGTAAACATGCCCCGCCGAAGGGAGGCTGTGACTCCAAGATGGC
TGCCAGGCGGCGCCCCGGAGCCAGCCACTGCCTCCACCACCCCCATCACAGTCCCAGAGCCCACAGAGCCGCA
CCCCAGAGCCCTGGCCCCCTCGCCACCTGCCGAGTTCATCTATTACTGTGTAGACGAGGACGAGCTACAGCCCTA
CACGAACCGCCGCGCAGAACCAGCAAGTGCGGGGCCTGTGAGCCTGCCTACGGCGGAATGGATGTGGCCGCTGCGA
CTTCTGCTGCGACAAGCCCAAATTCGGGGGCAGCAACCAGAAGCGCCAGAAGTGTGTTGGCGCCAATGCCTGCA
GTTTGCCATGAAGCGGCTGCTGCCAGTGTCTGGTCAGAGTCTGAGGATGGGGCAGGATCGCCCCACCTTACCG
TCGTCGAAAGAGGCCAGCTCTGCCGACGGCACCATCTTGGCCCTACCTTGAAGCCCACCTTGGCTACACGCAC
AGCCCAACCAGACCATACCCAGGCTCCAACGAAGCAGGAAGCAGGTGGTGGCTTGTGCTGCCCCGCCTGGCAC
TGACCTTGTGTTTTTACGGGAAGGCGCAAGCAGTCTGTGAGGTGCCGGGGCCCTGTTGCAGCTTCCACAGAAGC
CCTGTTGCAGGAGGCCAGTGCTCTGGCCTGAGTTGGGTTGTGGCCTTACCCCAGGTGAAGCAAGAGAAGGCGGA
TACCCAGGACGAGTGGACACCAGGCACAGCTGTCTGACTTCTCCCGTATTGGTGCCTGGCTGCCCTAGCAAGGC
AGTAGACCCAGGCCTGCCTTCTGTGAAGCAAGAGCCACCTGACCCAGAGGAGGACAAGGAGGAGAACAAGGATGA
TTCTGCCTCCAAATTGGCCCCAGAGGAAGAGGCAGGAGGGGCTGGCACACCCGTGATCACGGAGATTTTCAGCCT
GGGTGGAACCCGCTTCCGAGATACAGCAGTCTGGTTGCCAAGGTCCAAAGACCTTAAAAACCTGGAGCTAGAAA
GCAGTAGACTGGAGGCTTCTACAGACTGTAGGATTCAAGTCTGCAGGGCAGGCACTCGGGAAGGGAAGATGGATG
TAAAGTGTGGGAGACCGAGGACACAGTGGAGCCCACGAGCACGAGCTGGAACCCACGAGGATGGCCTGGAACCCA
TGTCAGTCTCTCACCACTCCAGCTTCGATGATGTGGGTGCTCTGCAGAAGAAGCTGGTGCCCTTCTCACAGAG
TTAAATATGCACTCTGGCCAGGAATTAGAGAAGCTGAAAGGATGATCCTGGGGAAGGTGGAGCAGCTGCAGGCCT
GGCTGCAGGCCTGACTACTGCCACACCAACGAGGTGATCTAGCAGATACATGGCAACGTGTGAACTGCAACAAC
GCCTGGTGCCCCAGCACCAACCTTCCAAGTGTAAAAACAATGTGCTGCTGCTTCACTTCCGCCCTCCGGTTATCA
AGCAAAATGTCTCTTGTGGCCCATCTTACTGGAAGAGAGTTCGGGGAACATAGCCTCACCAGGTGACACATTA
CAAAGCCACCCTACCATGAATCCGCTCCCAAGGCTCTCACTGCTCACCTGAGGATAACTCAATATAACTATGTTG
CTGAAAATGCAAAGCTGAAGACCATGGATTTTCATGGTGATTCCAGCAAGTACAGAGATTCTATGAAGCCCACCCA
GAAAAAAGCTTGCTGGTCTGGCTATTTTTGTGTCAATTTCAAGTATTGAGAACCTGGCCTGTGGTAGGCACTG
TACTTAATACTAGGATACAGAAATGCAAAAGATACGGCCCATGCAATTTTATTAATGCAATCAATATGTATTACA
AATGGTGAATGGATTTCCAACCTTATCATGGAATTATATGCTGAATATATAGAATTCAGAAAATTGTTGGGAGGA
CAGCCCTTTTGTGAACCTTGTGTTGGGGCACAGTAGGAATTGGAAATAATTTAGTTTCTATCTCTAAGCTGTTCTA
TTTTAAATATTATTTTAAATTTTATTGTCCCACTT

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FIGURE 610

MAEDWLDCPALGPGWKRREVFRKSGATCGRSDTYYSPTGDRIRSKVELTRYLGACDLTLFDFKQGILCYPAPK
AHPVAVASKRRKKPSRPAKTRKRQVGPOSGEVRKEAPRDETKADTDAPASFPAPGCCENCGISFSGDGTQRQRL
KTLCKDCRAQRIAFNREQRMFKRVGCGECAACQVTEDCGACSTCLLQLPHDVASGLFCKCERRRCLRIVERSRGC
GVCRCGQTQEDCGHCPICLRPPRPGLRRQWKCVQRRCLRGKHARRKGGCD SKMAARRRPGAQPLPPPPPSQSPEP
TEPHPRALAPSPPAEFIIYYCVDEDELQPYTNRRQNRKCGACAACLRRNGCGRCDFCCDKPKFGGSNQKRQKCRWR
QCLQFAMKRLLPSVWSESEDGAGSPPPYRRRKRPSSARRHHLGPTLKPTLATRTAQPDHTQAPTQKEAGGGFVLP
PPGTDLVFLREGASSPVQVPGPVAASTEALLQEAQC SGLSWVVALPQVKQEKADTQDEWTPGTAVLITSPVLVPGC
PSKAVDPGLPSVKQEPDPPEEDKEENKDD SASKLAPEEEAGGAGTPVITEIFSLGGTRFRD TAVWLPRSKDLKKP
GARKQ

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FIGURE 611

CCCATTGTGTCGGACAATTATTTCTAGAGTCTTTTTCCAAACAGAATTGAACAATGCCACAAAACTTTCTTTAC
TAAAGAATATTTGAAAAATAAAACAAAGCTTTTCAGAAATCCAACCTCTGCAAAATGGCCCCCTACCAAGCTGCAGAAA
AGCATTTCATCTTTTTTGGAGGTTTTCCGCAGACATGCAGCTCCAGTTACAAGAAGGCAGTTCCCACACGGTGCACA
CAGGATGGATTACCTGCACCTTTGAGGATGATAGCCCGTGGATGGTGGTTTGACATGGATATGGTGATCATATATA
TTTATTCAGTGAACCTGGGTCATTGGATTCATTGTTTTCTGCTTTTTTTGCTATTTTTTCTTTCCGTTTTAGGAAT
TTCATACCTTACTACAATTGACCAATCATAAATGATGTAAATAACAATTGCTTAAACAATTTTT

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FIGURE 612

PLCRTIISRVFFQTELNNAKTFFTKKEYLKIKQSFQKSNSAKWPLPSCRKAFHLFGGFRRHAAAPVTRRQFP HGAH
RMDYLHFEDDSPWMVV

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FIGURE 613

AGAAGTTAGGGGCTGCAGCGCGCTGGCTTTAGGTGAACGACGTGGTGAGGAGTGGGTTTCGGGCATGAGAAGTC
ACAGGGCCGTTTCCTAGTCTCTCTTCACTTCTTTGGGTCTTCTCAGAGAAAGAAGGCTGCCGTGGGTAGGCTGGG
GGCGGAGACTATCGGGAAGAGAAAATTACTTTTCCCACTGAAACACACCCAAGTATATGCCAGCCTTCATGAAA
GTGAACAGAGAAACGAAGCGCCTTTATGTGGGTGGCCTTAGCCAGGACATTTCTGAGGCAGACCTACAAAATCAG
TTCAGCAGATTTGGAGAAGTTTCGGATGTGGAGATCATCACACGGAAGATGACCAAGGAAACCCACAGAAAGTT
TTTGCATATATCAACATCAGTGTAGCAGAAGCGGACCTGAAAAAATGTATATCTGTTTTAAATAAAACAAAATGG
AAAGGTGGAACATTACAAATTCAACTAGCAAAAGAAAGCTTTCTGCACAGATTGGCCCAAGAGAGAGAAGCAGCA
AAAGCTAAGAAAGAAGATCAACAACAGGTAACGCCAACTTGTTAGAAAAGACAGGAGGAGTGGATTTCCATATG
AAAGCTGTGCCAGGGACAGAAGTGCCAGGGCATAAGAATTGGGTTGTGAGCAAATTTGGAAGAGTCTTACCTGTT
CTTCACCTTAAAAATCAACATAAACGTAAAATCATCAAATATGATCCCTCAAAGTACTGCCACAACCTGAAGAAG
ATAGGGGAGGATTTCTCAAACACCATTCTTATATCCAGCCTGACTTGGGAATTAGAAGGAGGGAATGACCCTATG
AGTAAGAAACGGCGAGGAGAGTTCTCTGACTTTTCATGGCCCTCCCAAGAAGATAATAAAAGTGCAGAAGGATGAG
AGTTCCACTGGGTCTCTGGCCATGAGTACAAGGCCAGGAGGGTAATAGAGAGACCACCCTTAACACAGCAACAG
GCTGCACAAAAAAGAACTTGTGATTCCATTACTCCTTCTAAATCATCTCCTGTACCTGTTTCTGATACTCAGAAA
CTTAAAAATCTACCTTTTAAGACTTCTGGCTTGAAACTGCCAAGAAGAGAAACAGCATTCTTGATGATGATACT
GATTCTGAAGATGAATTGAGAATGATGATTGCGAAAGAGGAAAACTTACAGAGAACTACACAACCCTCAATAAAT
GAATCTGAAAGTGATCCTTTTGAAGTTGTAAGGGATGATTTCAAATCAGGCGTTCACAACTGCATTCTTTAATA
GGTTTAGGTATCAAAAATCGTGTCTCTTGCCATGATAGTGATGATGATATTATGAGAAATGATCGTGAGTATGAC
TCAGGAGATACAGATGAAATTATTGCGATGAAAAAAAATGTTGCTAAGGTCAAAAACAGTACAGAAATTTTCACAA
ATGGAAAAATCTACGAAGAAAACCTCTTTCAAAAATAGAGAAAACGTGAGCTTTCTGATCACTGTATTAAACTA
C

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FIGURE 614

MKVNRETKRLYVGGLSQDISEADLQNQFSRFGEVSDVEIITRKDDQGNPQKVFAVINISVAEADLKKCISVLNKT
KWKGGTLQIQLAKESFLHRLAQEREAkakKEESTTGNANLLEKTGGVDFHMKAVPGTEVPGHKNWVVSKEFGRVL
PVLHLKNQHKKRIIKYDPSKYCHNLKKIGEDFSNTIPISSLTWELEGGNDPMSKKRRGEFSDFHGPPKKIIVQK
DESSTGSLAMSTRPRRVIERPPLTQQQAAQKRTCD SITPSKSSPVVSDTQKLKNLPFKTSGLETAKKRNSISDD
DTDSEDELRMMAKEENLQRTTQPSINESESDPFEVVRDDFKSGVHKLHSLIGLGKKNRVSCHDSDDDIMRNDRE
YDSGDTDEIIAMKKNVAKVKNSTEF SQMEKSTKKT SFKNRENCELSDHCIKL

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FIGURE 615

CTTATGCATCGGATTTATTTTCCAAATCAAGAGGACAGTGATAGATGCATTTTCCCCAGGCTGTCTCAGAAAGG
TCGCTAAATGTATACTGTTGTCAGAATTGCTGAGATCTCCCCCACTTTGGTTTTTGCAGCAGTAAAACTCTTT
CCACTGTGACTTATTTTCCCCAGGCTGTCTCAGAAAGGTCGCTAAATGTATACTGTTGTCAGAATTGCTGAGATC
TCCCCCACTTTTGGTTTTTGCAGCAGTAAAACTCTTTCCACTGTGACTTATTTTCTCTCTCAGGCAGCCAGCC
ACCTGGTCCCTTGTGCTGACTCTAGCACAGTGGCCAGGATCCAATACGAGTCCAGGGGTGACCGCAGGATGGTGG
GGGCAGCGGGCTTCTCCACCTACCCAGCCACCAAGGCCCTGACGCACTGCCTCCTGCACCTTCAGCACATCCCT
GTGCACAGCTGGAAGGGTGCATGGCCGCTCACCTTTGTTTCAGATGGGTGGAAACGCTGATGATACCAGCTCCTC
CTGCCGTGCCCTGCCACGGAGCAGGCATTGTGAACTGGCTGGTGGTTTGCAGTCCACGTGGCATGGCCTCCAGC
CCAACCCACAGTGGAGACTGGAGACAGGGCAATGAGTCTGGTTCGGGGGCACGTGGACATGCCCCATAGGGGGCCC
ACCCAGACTTAACAGGCAAGGTCTGGGCATTGCGCGACGCAGGACTCAATGCTAAAGCAAGCCTGCCTGGCTCT
GTGCCAGGGCCCCCTCTTCTGATTACACATCCCATTTTTACACAGACCCTTCCTTCTTAATAAAGGCTGACAGTT
CTGTTGGCAGCCAAGAACCCACACCATGAAGACAGGGAGTGAGGGGCCTTTGTGCCAACTCCAGCACAGCTGCG
TTCTGGGGTGTGTGAGAGGCATGTTGCTGTCTGTGCGCTGGTGGTCTCGTGAGACAGTTCGAGGACGGGGAAAT
TGCAGGGTGGTGGGGCGTGAGGCTTATATGTGGAACGATGCAGAGTTCGCCTGCAGACGGATCTGGATATACA
CTATGTATAATTGTTACGTGTAATTTAAATATATCTGTTTGCCATCGTCATGAGAAGATTATATGTAAGGCTCT
GAAGGGAGAGGGAGATGTACATTCTGCCAGGCTCCTGGGGACCTTATCCGAGTCATGAAATTGATGACTGTTGAT
CCAGTGGTGCAAGAAGCTACACTCCATGTGTCACTACGCTTATGACTCCTAATGTATTTTAAAGGCAAAAAATGT
CAGCCGACTCCATCTTCACCCCTCGATTCTCGAGTCCAGCCTTTCTGTGCCAGTGCTTCACTGAGCCACAACGC
TCTCGCCATCGGGACCCGGCTGGGCCTGGAGTCTCGGGGCACAGTTGCCATGGAGCCCTCCTGGGTCATTCTACA
AATGTGCTGAGTGCCAGCTGAAAACCCACAGGAGATGGAGTACCTTGGCCAAGCTTAAAGAGAAGATTTTCTCA
GGGTATTTATTAGTGTGTCCAGCAGGGTCAGGAAGCAGGATGGAAAGATGCATTCAGACTGTTAATTTATTAACA
AGGCAATGATTTTGTGTTTCTTGATGACAGACTATTAAGTTTGGGACTTATTTCCCATTTGAGAAGTTATAAT
ATATATTTAAGATGATAAGTTTCTGCTTAAGTTGTGCCTTTAGCTTCAATGAGTTTAAAGGAGCACTAAGGGTA
ATGATACCAATGAGGGTTGGTTTATTATCAAACCTGAATAGCTGTGGTTTCTCCAGTAAATATTTTCTTCTACTG
AACATGGAGCCATTATTAAGAGTTGTGTGTTTTTTATTATGTACATTTGTATATTTTTTTGCTTGTGTTGATGTTT
TATTTTCTAATAGTTTTCTTTAGTTTTCTTAAAGTTGTGATACTAGATTTAGATTCTGATGCTAACTGCAATC
AGGTTGGTCTCTGCTGGGTCTCTCCTGCTTTTATTTTACTTTAAGGACAAGTGTAGTTGTGCTCCACCACCTTTC
AAAAATGTGAACTGCCCTGCCTCCCTTTTTGCTGACAACACTGTGTACATTGACCACTTCTACCATACTTT
ATGTTGIAAAATCAAACCTCTTTTGTGGTACATTATCTCAIGCTTCTGCAAAATTCGAATAAATTCTATGGCTTCCA
TGTGAAAAAA

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FIGURE 616

MIPMRVGLLSNLNSCGFSSKYFLLNMEPILRVVCFLLCFVYFFACLMFYFSNSFLLVSKVVILDLDSDANCKS
GWSLLGLSCFYFTLRTSVVVVHLSKNVKLPCLPFLLTTLCTLTTSYHTLCCKIKLFCGTLSHASANSNKFYGFH
VK

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FIGURE 617

CTGCTCGCGGCCGCCACCGCCGGGCCCGGCCGTCCTGGCTCCCCCTCCTGCCTCGAGAAGGGCAGGGCTTCTCA
GAGGCTTGGCGGGAAAAAAGAACGGAGGGAGGGATCGCGCTGAGTATAAAAGCCGGTTTTTCGGGGCTTTATCTAA
CTCGCTGTAGTAATTCCAGCGAGAGGCAGAGGGAGCGAGCGGGCGGCCGGCTAGGGTGGAAGAGCCGGGCGAGCA
GAGCTGCGCTGCGGGCGTCTTGGGAAGGGAGATCCGGAGCGAATAGGGGGCTTCGCCTCTGGCCAGCCCTCCCCG
CTTGATCCCCCAGGCCAGCGGTCCGCAACCCTTGCCGCATCCACGAACTTTGCCCATAGCAGCGGGCGGGCACT
TTGCACTGGAACCTACAACACCCGAGCAAGGACGCGACTCTCCCGACGCGGGGAGGCTATTCTGCCATTGTTGGG
ACACTTCCCCGCGCTGCCAGGACCCGCTTCTCTGAAAGGCTCTCCTTGACGCTGCTTAGACGCTGGATTTTTTT
CGGGTAGTGGAACCAGCAGCCTCCCGCGACGATGCCCCCTCAACGTTAGCTTCACCAACAGGAACTATGACCTC
GACTACGACTCGGTGCAGCCGTATTTCTACTGCGACGAGGAGGAGAACTTCTACCAGCAGCAGCAGCAGAGCGAG
CTGCAGCCCCCGCGGCCAGCGAGGATATCTGGAAGAAATTCGAGCTGCTGCCACCCCGCCCTGTCCCCTAGC
CGCCGCTCCGGGCTCTGCTCGCCCTCCTACGTTGCGGTACACCCCTTCTCCCTTCGGGGAGACAACGACGGCGGT
GGCGGGAGCTTCTCCACGGCCGACCAGCTGGAGATGGTGACCGAGCTGCTGGGAGGAGACATGGTGAACCAGAGT
TTCACTGCGACCCGGACGACGAGACCTTCATCAAAAACATCATCATCCAGGACTGTATGTGGAGCGGCTTCTCG
GCCCGCGCCAAGCTCGTCTCAGAGAAGCTGGCCTCCTACCAGGCTGCGCGCAAAGACAGCGGCAGCCCGAACCCC
GCCCGCGGCCACAGCGTCTGCTCCACCTCCAGCTTGACCTGCAGGATCTGAGCGCCGCCGCTCAGAGTGCATC
GACCCCTCGGTGGTCTTCCCCTACCCTCTCAACGACAGCAGCTCGCCCAAGTCTGCGCCTCGCAAGACTCCAGC
GCCTTCTCTCCGTCTCTCGATTCTCTGCTCTCCTCGACGGAGTCTCCCGCAGGGCAGCCCCGAGCCCCTGGTG
CTCCATGAGGAGACACCGCCACCACCAGCAGCGACTCTGAGGAGGAACAAGAAGATGAGGAAGAAATCGATGTT
GTTTCTGTGGAAGAGGCAGGCTCCTGGCAAAAGGTCAGAGTCTGGATCACCTTCTGCTGGAGGCCACAGCAA
CCTCCTCACAGCCCACTGGTCTCTCAAGAGGTGCCACGTCTCCACACATCAGCACAACTACGCAGCGCCTCCCTCC
ACTCGGAAGGACTATCCTGCTGCCAAGAGGGTCAAGTTGGACAGTGTCAGAGTCTGAGACAGATCAGCAACAAC
CGAAAAATGCACCAGCCCCAGGTCTCTGGACACCGAGGAGAATGTCAAGAGGCGAACACACAACGTCTTGGAGCGC
CAGAGGAGGAACGAGCTAAAACGGAGCTTTTTTGCCTGCGTGACCAGATCCCGGAGTTGGAAAACAATGAAAAG
GCCCCCAAGGTAGTTATCCTTAAAAAAGCCACAGCATAACATCCTGTCCGTCCAAGCAGAGGAGCAAAAGCTCATT
TCTGAAGAGGACTTGTTGCGGAAACGACGAGAACAGTTGAAACACAACTTGAACAGCTACGGAACCTTGTGCG
TAAGGAAGTAAGGAAAACGATTCTTCTAACAGAAATGTCTGAGCAATCACCTATGAACTGTTTCAAATGC
ATGATCAAATGCAACCTCACAACCTTGGCTGAGTCTTGAGACTGAAAGATTTAGCCATAATGTAACTGCCTCAA
ATTGGACTTTGGGCATAAAGAAGCTTTTTTATGCTTACCATCTTTTTTTTTTCTTTAACAGATTGTATTTAAGA
ATTGTTTTTAAAAATTTTAA

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FIGURE 618

MPLNVSFNRYDLDYDSVQPYFYCDEEENFYQQQQQSELQPPAPSEDIWKKFELLPTPPLSPSRRSGLCSPSYV
AVTPFSLRGDNDGGGGSFSTADQLEMVTELLGGDMVNSFICPDDETFIKNIIIQDCMWSGFSAAAKLVSEKLA
SYQAARKDSGSPNPARGHSVCSTSSLYLQDLASAAASECIDPSVVFYPLNDSSSPKSCASQDSSAFSPSSDSLLS
STESSPQGSPEPLVLHEETPPTTSSDSEEEQEDEEIDVVSVEKRQAPGKRSESGSPSAGGHSKPPHSPLVLKRC
HVSTHQHNYAAPSTRKDYPAAKRVKLDVVRVLRQISNNRKCTSPRSSDTEENVKRRTHNVLERQRRNELKRSFF
ALRDQIPELENNEKAPKVVLKKATAYILSVQAEQKLISEEDLLKRREQLKHKLEQLRNSCA

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FIGURE 619

GTGGAGCCAAGATTTAAACCCACAATCTTAGCCACTAATCTGGGGACAGTGCAGACTACTGAATCCTTGGATGGA
AGACAGACTGAGACCCTATCCAGCTGCTGCCCCATCTCCAAGAGCCTCGCCCTGCTGGAAGTGCAGTGTAGTCT
GGTTCATCAGCCACTCTGCACAGGACCCCTGCCAGGACCCAGGGTCTGCATTTTAGGCCATCCTTGCTGGATAG
GCCCAGAGCCAGGGTCCCCACCTGCCTGTAGANN
NNNNNNNNNNNNNNNNNGAATGATGGGGCATGATGAGGAAGAGGCAGAAAATGGGAAGGAAGTATAGGATCAAGA
TGGGGGCATCCTAAGGAGGGGGCAACTGCCAGCCGGTGCCAGCGTGCCTTCCAATATTCAGCCATCTCCTCATGA
AGCCTGGGATGTGATTCTTGTCCTCTAGCTCTTTCTGAGGGGCACTGGTACCTCCAGGACCTGGAGTGTACTG
GAAGAAATGGTGCAGTCCAGGTACAGCATGGACCCAGATCACCCCCACCCCACTCCCTTTAGTGATTATTGTC
TTATGAACTAGGAGGGGGAGTGGGGCAGAGATGCCCTTTTCATGGCTCCCTGCACACACAGAACCCCTTTGTACT
GGGCACTTCTACTCCCCAAGGACCCTGACTTGCACCCAGCAGCTAAGGTCATCTCACCCCCACCTCCCACCTGCCC
CTGGGCCAGCAGGAGGGGGCTTGGCCATATGTAGGCAGACAGGACTTCTTGAAGCTGAAAGATTTCCACCCCAT
AAAAGAGCCAGAATGTGACAACCAGGAGCGCTGATACCTGGGGAAGGGAGACTGGCTCTGGTCTGTGATTCCGG
GTTTAGGGCTCTGGGCCATTCCCCCTCAGCCAGCTGGTGACAGAGACTGGCCACCGCCTGCTGAGAGGGCCATC
TCACCTACAGTGAGAACAGAGCCCCCAGCCAGCTGGCTTGGACACTCTGAGGATGGGGCCAAGCAGCCACCTA
CCAGGACTCTTGGCCCCGGGGCCACACCCAGTGCTGCTAGCAGCCCCACCTTCTCCTGAAGTAGCCAGGTGTGCTC
TGCTCCAGGGCCTGCAATGGCCCCCAACACCATCTGCTCTCCCTGCAGATGCTGCAGCTGCTCCAAGCAGGCC
CCTAGTTGCTGGTGGCTCTGGCCCAGCTCTTCTGAGTCTCTTGTTACCTCAGTGAGTATCAGCAACTGCTCCTG
CAGACGGACTGTGTCTGAGCCTGGGCAGGGGTCTCAGCTGCTGGCATGGAGACTCTGGGTCCCGAAGCTCCTGG
GCCCTGCCTCCATCCCAGCTCTGCTCTTGGATCTGCAGGCCTGGCACCCAGCATCTCCTGTAGATACACTTGGTCC
AGAATCCTGGGGTCTCCTTCCAGCTTCCAGACCACACTGGGGTGGTCTTGGCAGACCGTTGATGCCTCAGGGCAT
GTTGTGGCAGGGTCTTGGCCCCAACTCAAGTTATGACTCTGAACAAGCTCTCCTCTGCTCTCTGGTCTCAGTTTT
CCCATCTGAACCAGGAGGGAAGTCACTGAATGATCCCAGGGTATTCCCAAATGTTGGAAGAGGATCCCTCTCTTG
GCTGGACTAAGCCCCCTGCGCTGCCTTCTTCTCTAGATAATGCTTCAATAATGAGGACCAGAGAATAAAGTGTGG
GGCAGAGTCAAAGGTACAGCAGGGCCAGTGCGCAGGGCCTGCCATGCACCCACTTGGGGGATCCCAGGCTGGGC
TCTGGGCCAACAGGCTGTTGGGTCAATTTGGTCCAAATGCCGCTAGGCCTTTTCCAATTCTGTCTGCAGCAGCAGG
ATCCTGTGGGTAGAAGGGATGGTCTGCCTGTTCCCTGCCACCCACCCCTCCCCACAGCCAGCCCCACTCACT
TGTCTTCTATGTTCTGGTCTGGCCTCCTCCACTCAGCCTGTCCCTGGGATCCCTGCATCTGGTGCCTCTCCTGCT
CCAGGCAGGCCAGGGAGCACTCCACCTGCTAGGAGGAGGCTGAGTGGGAGGGCTGAAGGCAGCACAGAGCCTCAG
ATAGGTAGGGCTAGCTTCCCTGCCTCCCACAGGCAGGGCAGTGTCTGCAGCCTTTGATAACGCAGGCGGACTGG
CAGCCAG

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FIGURE 620

MVCLFPATPPLPHSPAPLTCLLCGLASSTQFVPGIPASGASPAPGRPGSTPPARRRLSGRAEGSTEPQIGRAF
PASHQAGQCLOPLITQADWQ

FIGURE 621

[illegible]

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FIGURE 622

MAQAGVVGEVTQVLCAAGGALELPELRRRLRMGLSADALERLLRQGRFVVAVRAGGAAAAPERVVLAASPLRLC
RAHQGSKPGCVGLCAQLHLCRFMVYGACKFLRAGKNCRNSHSLTEHNLSVLRTHGVDHLSYNELCQLLFQNDPW
LLPEICQHYNKGDGPHGSCAFQKQCIKLHICQYFLQGECKFGTSCKRSHDFSNSENLEKLEKLGMSDDLVSRLPT
IYRNAHDIKNKSSAPSRVPPLFVFPQGTSEKDSGSGVSPNTLSQEEGDQICLYHIRKSCSFQDKCHRVHFHLPYR
WQFLDRGKWEDLDNMELIEEAYCNPKIERILCSESASTFHSHCLNFNAMTYGATQARRLSTASSVTKPPHFILTT
DWIWIWSDEFGSWQEYGRQGTVHPVTTVSSSDVEKAYLAYCTPGSDGQAATLKFOAGKHNYELDFKAFVQKNLVY
GTTKKVCRRPKYVSPQDVTTMOTCNTKFPKPSIPDYWDSSALPDPGFQKITLSSSSEYQKVWNLFNRTLFPYF
VQKIERVQNLALWEVYQWQKGOMQKQNGGKAVDERQLFHGTSAlFVDAICQQNFDWRVCGVHGTSYGKGSYFARD
AAYSHHYSKSDTQTHMFLARVLVGEFVRGNASFVRPPAKEGWSNAFYDSCVNSVSDPSIFVIFEKHQVYPEYVI
QYTTSSKPSVTPSILLALGSLFSSRQ

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FIGURE 623

TCCCTTATTCAATCAAAGGTAATGTATATTACTTCCAAAGTATAGGAGTATTAATTTAAGCTGACCAAAAAAAGA
GGACCCAGATACTCGTTTTCCAAAGATGTTTTGAATCCACCTATTTCTCAAAGGCCAAATTTTCATTTTACAGCTC
TTGTGAAACCAGGCAAGCAGIGTAAATTTTAAATGCAGCAGTGGGATATCTTCAAATGTAGCAGTGAGATTTTT
AAAATGTAGTTGTTTCAAACCTGATCAGTGACCGTCTAAATACGGGCTCCTTGAGGACATCCTGCGCCTGGTTC
ATCCTTTTTGCACTCTCAAAGTCTAGCCTTCCCAGATGGGACCTCAGTCCCAGCCCCCTACACTGCCATCCCCC
AGATCTTTAGGGCAGTGGGGTTCATTGAACAAGGTGCAGGCTACAACTTGGCAAAGTTTATAC~~TAA~~CACCTCA
TTCCATCCCACCTCCCATCTTAAAAAGGAAACCGTTAAGTATCTTATTCTAGTGACTTCAATAAAGGAACTAATT
TATAAGACAGCCAAGAACAATTAAAGTCATAAAGGGCCAAACATTTTATTTTCATCTAAGAACCGTTTGCAGGGG
TGGTCCGATCTTTTGGCTTCCCTGGGCCACACTAGAACTGTCTTGGGCCACACGTAAATACATTAAGTAGCTGA
TGAGCTTTTTTTTCC

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FIGURE 624

MGPQSQPPYTAIPQIFRAVGFIQQGRLQTWQSLY

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FIGURE 625A

GGCCACCGGAGCGGCCCCGGCGACGATCGCTGACAGCTTCCCCTGCCCTTCCCGTCGGTTCGGGCCGCCAGCCGCCG
CAGCCCTCGGCCTGCACGCAGCCACCGGCCCCGCTCCCGGAGCCAGCGCCGCCGAGGCCGAGCCGCCCGGCCA
GTAAGGCGGCGCGCCCGCGGCCACCGCGGGCCCTGCCGTTCCCTCCGCCGCGCTGCGCCATGGCGCGGCGCTGA
CTGGCCTGGCCCCGGCCCCGCCGCTCCCGCTCGCCCCGACCCGCACTCGGGCCCCCGGGGCTCCGGCCTGCCG
CCGCTCTTCCCTTCTCCAGCCGGCAGGCCCCGCGCTTAGGAGGGAGAGCCACCCGCGCCAGGAGGCCGAACGC
GGACTCGCCACCCGGCTTCAGAAATGGCAGAAAGATGATCCATATTTGGGAAGGCCTGAACAAATGTTTCATTTGGA
TCCTTCTTTGACTCATACAATATTTAATCCAGAAGTATTTCAACCACAGATGGCACTGCCAACAGATGGCCATA
CCTTCAAATATTAGAGCAACCTAAACAGAGAGGATTTCTGTTTCCGTTATGTATGTGAAGGCCCATCCCATGGTGG
ACTACCTGGTGCCTCTAGTGAAGAAGCAAGAACTTACCCTCAGGTCAAAATCTGCAACTATGTGGGACCAGC
AAAGGTTATTGTTTCAGTTGGTCACAAATGGAAGAAATATCCACCTGCATGCCACAGCCTGGTGGGAAACACTG
TGAGGATGGGATCTGCACTGTAAGTCTGGACCCAAGGACATGGTGGTTCGGCTTCGCAAACTGGGTATACTTCA
TGTGACAAAGAAAAAGTATTTGAAACACTGGAAGCACGAATGACAGAGGCGTGTATAAGGGGCTATAATCCTGG
ACTCTTGGTGCACCCTGACCTTGCCTATTTGCAAGCAGAAGGTGGAGGGGACCGGCAGCTGGGAGATCGGGAAAA
AGAGCTAATCCGCCAAGCAGCTCTGCAGCAGACCAAGGAGATGGACCTCAGCGTGGTGCGGCTCATGTTTACAGC
TTTTCTTCCGATAGCACTGGCAGCTTCACAAGGCCTGGAACCCGTGGTATCAGACGCCATCTATGACAGTAA
AGCCCCCAATGCATCCAACCTGAAAATGTAAAGATGGACAGGACAGCTGGATGTGTGACTGGAGGGGAGGAAAT
TTATCTTCTTTGTGACAAAGTTCAGAAAGATGACATCCAGATTCGATTTTATGAAGAGGAAGAAAATGGTGGAGT
CTGGGAAGGATTTGGAGATTTTCCCCCAGAGATGTTATAGACAATTTGCCATTGTCTTCAAACTCCAAAGTA
TAAAGATATTAATATTACAAAACAGCCTCTGTGTGTGTCCAGCTTCGGAGGAAATCTGACTTGGAACTAGTGA
ACCAAAACCTTTCTCTACTATCTGAAATCAAAGATAAAGAAGAAGTGCAGAGGAAACGTCAGAAGCTCATGCC
CAATTTTTCGGATAGTTTCGGCGGTGGTAGTGGTGCCGGAGCTGGAGGCGGAGGCATGTTTGGTAGTGGCGGTGG
AGGAGGGGGCACTGGAAGTACAGGTCCAGGTATAGCTTCCCACACTATGGATTTCTACTTATGGTGGGATTAC
TTTCCATCCTGGAACACTACTAAATCTAATGCTGGGATGAAGCATGGAACCATGGACACTGAATCTAAAAAGGACCC
TGAAGGTTGTGACAAAAGTATGACAAAACACTGTAAACCTCTTTGGGAAAGTTATTGAAACCACAGAGCAAGA
TCAGGAGCCCAGCGAGGCCACCGTTGGGAATGGTGAGGTCACTCTAACGTATGCAACAGGAACAAAAGAAGAGAG
TGCTGGAGTTTCAGGATAACCTCTTTCTAGAGAAGGCTATGCAGCTTGCAAGAGGCATGCCAATGCCCTTTTCGA
CTACGCGGTGACAGGAGACGTGAAGATGCTGCTGGCCGTCCAGCGCCATCTCACTGCTGTGCAGGATGAGAATGG
GGACAGTGTCTTACACTTAGCAATCATCCACCTTCATTCTCAACTTGTGAGGGATCTACTAGAAGTCACATCTGG
TTTGATTTCTGATGACATTATCAACATGAGAAATGATCTGTACCAGACGCCCTTGCACTTGGCAGTGATCACTAA
GCAGGAAGATGTGGTGGAGGATTGCTGAGGGCTGGGGCCGACCTGAGCCTTCTGGACCGCTTGGGTAACTCTGT
TTTGACCTAGCTGCCAAAGAAGGACATGATAAAGTTCTCAGTATCTTACTCAAGCACAAAAAGGCAGCACTACT
TCTTGACCACCCCAACGGGGACGGTCTGAATGCCATTATCTAGCCATGATGAGCAATAGCCTGCCATGTTTGTCT
GCTGCTGGTGGCCGCTGGGGCTGACGTCAATGCTCAGGAGCAGAAGTCCGGGCGCACAGCACTGCACCTGGCTGT
GGAGCACGACAACATCTCATTGGCAGGCTGCCTGCTCCTGGAGGGTGATGCCCATGTGGACAGTACTACCTACGA
TGGAAACCACACCCCTGCATATAGCAGCTGGGAGAGGCTCCACCAGGCTGGCAGCTCTTCTCAAAGCAGCAGGAGC
AGATCCCCTGGTGGAGAACTTTGAGCCTCTCTATGACCTGGATGACTCTTGGGAAAATGCAGGAGAGGATGAAGG
AGTTGTGCTTGAACACGCTCTAGATATGGCCACAGCTGGCAGGTATTTGACATATTAATGGGAAACCATA
TGAGCCAGAGTTTACATCTGATGATTTACTAGCACAAAGGAGACATGAAACAGCTGGCTGAAGATGTGAAGCTGCA
GCTGTATAAGTTACTAGAAATTCCTGATCCAGACAAAACCTGGGCTACTCTGGCGCAGAAATAGGTCTGGGGAT
ACTTAATAATGCCTTCCGGCTGAGTCTCTGCTCTTCCAAAACACTTATGGACAACCTATGAGGTCTCTGGGGGTAC
AGTCAGAGAGCTGGTGGAGGCCCTGAGACAAATGGGCTACACCGAAGCAATTGAAGTGATCCAGGCAGCCTCCAG
CCCAGTGAAGACCACCTCTCAGGCCCACTCGCTGCCTCTCTCGCTGCCTCCACAAGGCAGCAAAATAGACGAGCT
CCGAGACAGTGACAGTGTCTGCGACACGGGCGTGGAGACATCCTTCCGCAAACTCAGCTTTACCGAGTCTCTGAC
CAGTGGTGCCTCACTGCTAACTCTCAACAAAATGCCCATGATTATGGGCAGGAAGGACCTCTAGAAGGCAAAAT
TTAGCCTGCTGACAATTTCCACACCGTGTAACCAAAGCCCTAAATTTCACTGCGTGTCCACAAGACAGAAG
CTGAAGTGATCCAAAGGTGCTCAGAGAGCCGGCCCGCTGAATCATTCTCGATTTAACTCGAGACCTTTTCAAC
TTGGCTTCTTTCTTGGTTCATAAATGAATTTTAGTTTGGTTCACTTACAGATAGTATCTAGCAATCACAACACT
GGCTGAGCGGATGCATCTGGGGATGAGGTTGCTTACTAAGCTTTGCCAGCTGCTGCTGGATCACAGCTGCTTTCT

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FIGURE 625B

GTTGTCATTGCTGTTGTCCCTCTGC

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FIGURE 626

MAEDDPYLGRPEQMFHLDPSLHTIFNPEVFQPMALPTDGPYLQILEQPKQRGFRFRYVCEGPSHGGLPGASSE
KNKKSYPQVKICNYVGPAKIVIVQLVTNGKNIHLHAHSLVGKHCEDGICTVTAGPKDMVVGFANLGILHVTKKKVF
ETLEARMTEACIRGYNPGLLVHPDLAYLQAEGGGDRQLGDREKELIRQAALQQTKEMDLSVVRLMFTAFLPDSTG
SFTRRLEPVVSDAIYDSKAPNASNLKIVRMDRTAGCVTGGEIYLLCDKVQKDDIQIRFYEEEEENGGVWEGFGDF
SPTDVHRQFAIVFKTPKYKDNITKPASVVFVQLRRKSDLETSEPKPFLYYPEIKDKKEEVQRKRQKLMPNFSDSFG
GGSGAGAGGGGMFGSGGGGGGTGSTGPGYSFPHYGFPTYGGITFHPGTTKSNAGMKHGTMDTESKKDPEGCDKSD
DKNTVNLFVGKVIETTEQDQEPSEATVGNGEVTILTYATGTKEESAGVQDNLFLEKAMQLAKRHANALFDYAVTGDV
KMLLAVQRHLTAVQDENGDSVLHLAIHLHSQLVRDLLEVTSGGLISDDIINMRNDLYQTPHLAVITKQEDVVED
LLRAGADLSLLDRLGNSVLHLAAKEGHDKVLISILLKHKKAALLLDHPNGDGLNAIHLAMMSNSLPCLLLLVAAGA
DVNAQEQKSGRTALHLAVEHDNISLAGCLLLEGDAHVDSTTYDGTTPHLIAAGRGSTRLAALLKAAGADPLVENF
EPLYDLDDSWENAGEDEGVVPGTTPDMATSWQVFDILNGKPYEPEFTSDDLLAQGDMKQLAEDVKLQLYKLEI
PDPDKNWATLAQKLGLGILNNAFRLSPAPSKTLMNDNYEVSGGTVRELVEALRQMGYTEAIEVIQAASSPVKTTSQ
AHSPLSPASTRQQIDELRDSVCDTGVETSFRLKLSFTESLTSGASLLTLNKMPhDYGQEGPLEGKI

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FIGURE 627

AGCAAAGTATTCTGTGTTGCTGGAAGGCAGAGATGCTCTCGTGAGATCCCAGACGGGCTCAGGTAAACTCTTG
CCTATTGCATCCCTGTGGTCCAGTCCCTTCAAGCAATGGAGTCAAAAATACAGCGCAGTGATGGCCCTATGCC
TGGTGCTCGTGCCAACGAGAGAGCTAGCTCTACAAAGCTTTGACACTGTCCAGAAACTGCTTAAGCCTTTCACCT
GGATTGTGCCTGGAGTGTTAATGGGAGGAGAGAAGAGAAAATCAGAAAAGGCCAGACTCCGCAAAGGAATAAATA
TCCTTATCTCAACTCCTGGACGCCTGGTGGATCATATAAAATCCACAAAGAACATTTCATTTTAGTCGGCTGCGGT
GGTTGGTGTGTTGATGAAGCAGACAGAATCTTGGAATTTGGGTTTTGAAAAGGACATCACAGTGATACTTAATGCTG
TAAATGCTGAATGCCAAAAACGACAGAATGTCTTGCTATCAGCGACACTCACAGAAGGTGTAACGCGGCTAGCTG
ATATCAGTTTGATGATCCAGTCAGTATTTCTGTCTGGACAAGAGCCATGACCAGTTGAACCCAAAGGACAAAG
CGGTCCAGGAGGTCTGTCTCCACCAGCTGGCGACAAGCTGGACAGCTTTGCAATACCAGAGAGTCTCAAGCAGC
ATGTGACTGTGGTTCCAGCAAACCTGAGGCTCGTCTGCCTAGCGGCTTCATCCTTCAGAAATGCAAGTTTGAGG
AAGACCAGAAGATGGTTGTCTTTTTCTCAAGTTGCGAGCTGGTGGAGTTCCACTACAGCCTCTTCCTACAGACCC
TGCTGAGCAGCTCAGGGGCGCCGGCATCAGGGCAGTTGCCATCTGCCTCCATGCGATTAAAATTCCTACGGCTGC
ATGGCGGCATGGAGCAGGAGGAAAGAACAGCAGTGTTTCAGGAATTTTCACATTCCAGAAGAGGCGTCTCTCTTT
GCACGGATGTTGCAGCTCGGGGCTTAGATCTCCCTCAAGTCACGTGGATTGTTTCAGTACAACGCTCCATCTTCAC
CTGCAGAAATACATCCACCGGATTGGAAGAACCGCCCGGATTGGCTGCCATGGGAGCAGCCTGCTCATTTTGGCTC
CTTCGGAGGCAGAAATATGTCAACTCGTTGGCTTCTCACAAATCAACGTTTCTGAGATTAAGATGGAAGATATTT
TGTGTGTTCTGACAAGAGATGATTGTTTTAAAGGGAAACGATGGGGAGCCCAGAAATCCCATGCTGTTGGCCCCC
AGGAAATCCGAGAGCGAGCCACAGTCTTGACAGCGGTATTTGAAGATTACGTGCACTCCAGTGAGAGGAGGGTCT
CCTGGGCAAAGAAAGCTCTGCAGTCCTTCATCCAAGCCTACGCCACCTACCCCAGGGAGCTGAAGCACATCTTCC
ACGTCCGATCCCTCCACCTTGGGCATGTGGCGAAGAGCTTCGGACTAAGAGATGCCCCCAGGAATCTTAGTGCCT
TGACTAGAAAAGAAGAGGAAAGCACACGTGAAAAGGCCTGACCTTCATAAGAAGACCCAGAGTAAACACAGCCTCG
CTGAAATCCTACGTTCCGAATACTCAAGCGGCATGGAGGCCGACATCGCCAAGGTCAAAAAGCAAAACGCACCTG
GAGAGCCTGGTGGCCGGCCCCCTGCAGCACAGTCTGCAGCCGACACCCTGCTTTGGCCGTGGGAAAACATTAAAAAT
GGAGAAAAACCCAAAAAGGTGTACAGCGGGACAGCAAGACTTCCCAGAAAGTTTAAATCTCTCTGGGTCTTCGA
GTGGAACCTGGAAGCCCCGGGTGGCAGTGGATTGATGTCCAGTTCTGTGACAGGAGGCTTGTGAAAAATAACTG
CGCCTTTGCCTGAATACCACGTCCCCAAGAATCAGAGGGGCCACAGCCCTTCTCCTCCATGGGAGGCCCTGGAGC
CTGATAGAAATCAGTGGTGTGGGGCACTGTAGAGACTAGCCAGCTCCCGACGGAAGGGGTCTGTGTCTTGTATTG
ATCCCATCAGTGCCCGGCACTCCCTTCACCCAGGTGCTGACGTGCCGGGGTTGAGCTGGCACCCCGGGATGTGAT
GTAAGAACGCCCTGCGCGTCAGCCTGGAACGGGCTTGATTGCTGCCCTTAAGTGTGTTCTGAAGTTTCACAGCTT
GGCTTCAGCCTATCAGCGCATACATTGGCATGAATTTTGTGAATTAGGGTGTTAAAAACTGGAATTGAATTTGTA
CAAAAAGAGAATATATTTATCACTAATTATTTTCTTAATGTAGGAATGTACCGTTAAAAAGGACCAAAAGTTTTT
GGTCTGGGTCAAAAAATACGAATGTGTTCTC

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FIGURE 628

MESKIQRSDGPYALVLVPTRELALQSFDTVQKLLKPFTWIVPGVLMGGEKRRSEKARLRKGINILISTPGRLVDH
IKSTKNIHFSRLRWLVFDEADRILDLGFEEKDITVILNAVNAECQKRQNVLLSATLITEGVTRIADISLHDPVSISV
LDKSHDQLNPKDKAVQEVCPPAPAGDKLDSFAIPESLKQHVTVPVSKLRLVCLAALQKCKFEEDQKMVVFSSC
ELVEFHYSFLQTLSSSGAPASGQLPSASMRLLKFLRLHGGMEQEERTAVFQEFSHSRRGVLLCTDVAARGLDLP
QVTWIVQYNAPSSPAEYIHRIGRTARIGCHGSSLLILAPSEAEYVNSLASHKINVSEIKMEDILCVLTRDDCFKG
KRWGAQKSHAVGPFQEIIRERATVLQTVFEDYVHSSERRVSWAKKALQSFQAYATYPRELKHIFHVRSLHLGHVAK
SFGLRDAPRNLSALTRKKRKAHVKRPDLHKKTSKHS LAEILRSEYSSGMEADIAKVKKQONAPGEPGGRPLQHSL
QPTPCFGRGKTLKWRKTQKGVQRDSKTSQKV

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FIGURE 629

AGCATCTACAAAGGAGGAATAGTCAAAGCAGCAGCGGCGGCGGCGGCGGCGGCAGCAGCAGCAGCAGCAGGAGAC
CTTCTCTGATGGATGACCTCTGTGAAGCAAATGGCACTTTTGCCATCAGCTTATTTAAAAATATTGGGGGAAGAGG
ACAACCTCAAGAAACGTATTCTTCTCTCCCATGAGCATCTCCTCTGCCCTGGCCATGGTCTTCATGGGGGCAAAGG
GAAGCACTGCAGCCAGATGTCCCAGGCACCTTTGT TTATACAAAGACGGAGATATTCACCGAGGTTTTCCAGTCAC
TTCTCAGTGAAGTTAAAGAACTGGCACTCAGTACTTGTCTTAGAACTGCCAACAGACTCTTTGGAGAAAAGACGT
GTGATTTCTTCCAGACTTTAAAGAATACTGTGAGAAGTTCTATCAGGCAGAGCTGGAGGAGTTGTCCTTTGCTG
AAGACACTGAAGAGTGCAGGAAGCATATAAATGACTGGGTGGCAGAGAAGACTGAAGGTAAGATTTTCAGAGGTAC
TGGATGCTGGGACAGTCGATCCCCTGACAAAGCTAGTCCTTGTGAATGCCATTTATTTCAAGGGAAAGTGGAAATG
AGCAATTTGACAGAAAAGTACACAAGGGGAATGCTCTTTAAACCACAGAGGAAAAAAGACAGTGCAGATGATGT
TTAAGGAAGCTAAGTTTAAAAATGGGGTATGCGGATGAGGTACACACCCAGGTCCTGGAGCTGCCCTATGTGGAAG
AGGAGCTGAGCATGGTCATTCTGCTTCCCGATGACAACACGGACCTCGCCGTGGTGGAAAAAGCACTTACATATG
AGAAATTCAAAGCCTGGACAAATTGAGAAAAGTTGACAAAAAGTAAGGTTCAAGTTTTCTTCCCAGATTAAAGC
TGGAGGAGAGTTATGACTTGGAGCCTTTCTTTCGAAGATTAGGAATGATCGATGCTTTTGACGAAGCCAAGGCAG
ACTTTTCTGGAATGTCAACTGAGAAGAATGTGCCTCTGTCCAAGGTTGCCACAAAGTGCTTCGTGGAGGTCAATG
AGGAAGGCACAGAGGCTGCCGCAGCCACTGCTGTGGTCAGGAATTCCCGGTGCAGCAGAATGGAGCCAAGATTCT
GTGCAGACCACCCTTTTCTTTTCTTCATCAGGCGCCACAAAACCAACTGCATCTTGTTCTGTGGCAGGTTCTCTT
CTCCGTAAGAGGAGGCAATTGCTGTACATACCCTCCTTTCTTCTACCTATCTTGCTTAATTAACATTCCCTGT
GACCTAGTTGGTGCAGTGGCTTGAATGCCAAAATAAAGCGTGTGCACTGG

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FIGURE 630

MDDLCEANGTF AISLFKILGEEDNSRNVFFSPMSISSALAMVFMGAKGSTAAQMSQALCLYKDGD IHRGFQSLLS
EVNRTGTQYLLRTANRLFGEKTCDFLPDFKEYCQKFYQAELEELSFAEDTEECRKHINDWVAEKTEGKISEVLDA
GTVDP LTKLVLVNAIYFKGKWNEQFDRKYTRGMLFKTNEEKKTVMFMFKEAKFKMGYADEVHTQVLELPYVEEEL
SMVILLPDDNTDLAVVEKALTYEKFKAWTNSEKLT KSKVQVFLPRLKLEESYDLEPFLRRLGMIDAFDEAKADFS
GMSTEKNVPLSKVAHKCFVEVNEEGTEAAAATAVVRNSRCSRMEPRFCADHPFLFF IRRHKTN CILFCGRFSSP

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FIGURE 631

AAATCAGTTTTCTCCACCTGCACCACTGCATAGCACAGATACAGAAACCATCCTATTTTCAGGATTTGAATGCAAA
ACTTACCTTCTTACTCTAAAGATGAATGATCAGGGAGAGATTTATTCAACCCTGAGATTTTGCAGTCTCCTTCA
GAGTCACAGAATAGATTAAGGCCTGATGATACTCAAAGGCCTGGGAAAACCTGATGACAAAGAATTTTCAGTGCCC
TGGCACCTCATTGCAGTGACTCTTGGGATCCTCTGTTTACTTCTTCTGATGATAGTCACAGTGTTGGTGACAAAT
ATCTTTTCAGTGTATTCAAGAAAAACATCAACGGCAGGAAATTCTAAGAAACTGTAGTGAAAAGTACATCATGCAA
AATGACAACCTACTTAAAAGAGCAGATTTTGACAAATAAGACTTTAAATATGACGTTCTCAAAAATAGCTTTTCAG
CAGAAAAGGAACTGGATTACGCCTTATACAAAAGAACAGATGTCATAGAGAAAATGAGATCGTTTTTAAAGTT
TTGCAAAATACAGGCAAATTCTCTGAAGACCACGGGTCCTGTTGTGGAGTAACTGTTATTATTTTACCATGCAG
AAGAAAGACTGGAAGGGATGTAAACAGACTTGTCAACATTGTAGATCATCCCTTTTGAAGATAGATGACAAAGAT
GAACTCGTATTTTACATTCACTTTTATTCTCTTGGACTCTGTTTCTCAATGTTGGACCTAAGATATTGAAGACAG
GCTGGAGTCCAGAGCCTTCATTCAATCTCAGATTTATGAAATAATTACTGGATCGGATTATCATATGATGAAAG
GGAAAGTAAGTGGAAATGGATTGATAATGGCACATCTCCTGGAATTAATTCTACAATAATGCGTTTTTCTTCTGG
GAGAGGAGAATGTGCATTTTGAÇCTCAACAAGAATGGCAACTATTGATTGCATTCAAACGTACAATTGTATCTG
TGGGAAGAGAATAGACTCTATTTTCTCTGATTGCGGTGTGCGCCAAGAAGAAAAGGTGAAAATGGAATGTTTTCTT
TTTTTGTTTCCATAATAATTTCTGATTATAAATCATTGCTTTTAACTGTGGGACTTAGTTAATTCTTCAAAGA
TAAAGATGAACAGGAAGAAAAAGAAAATTATTTTGGACTATGACTTTAAAGATCAGATGCCATCTTCTTCCTGG
AGAAGAGGAGATTTTCTCTTTTGAGAGTGTTGTTTCCTTCCTT

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FIGURE 632

MNDQGEIYSTLRFLQSPSESNRLRPDDTQRPKGTDDKEFSVPWHLIAVTLGILCLLLLMIVTVLVTNIFQCIQE
KHQRQEILRNCSEKYIMQNDNYLKEQILTNTKTKYDVLKNSFQQKELDSRLIQKNRCHRENEIVFKVLQNTGKF
SEDHGSCCGVNCYYFTMQKKDWKGCKQTCQHCSSLLKIDDKDELVFYIHFYSLGLCFMSMLDLRY

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FIGURE 633

CGAGTAAAGTTTGCAAAGAGGCGCGGGAGGCGGCAGCCGCAGCGAGGAGGCGGCGGGGAAGAAGCGCAGTCTCCG
GGTTGGGGGCGGGGCGGGGGGGCGCCAAGGAGCCGGGTGGGGGCGGCGGCCAGCATGCGGCCCGCAGCGCC
CTGCCCCGCCTGCTGCTGCCGCTGCTGCTGCTGCCCGCCGCGGGCCGGCCAGTTCCACGGGGAGAAGGGCATC
TCCATCCCGGACCACGGCTTCTGCCAGCCCATCTCCATCCCGCTGTGCACGGACATCGCCTACAACCAGACCATC
ATGCCCAACCTTCTGGGCCACACGAACCAGGAGGACGCAGGCCCTAGAGGTGCACCAGTTCTATCCGCTGGTGAAG
GTGCAGTGCTCGCCCGAACTGCGCTTCTTCCTGTGCTCCATGTACGCACCCGTGTGCACCGTGTGGAACAGGCC
ATCCCCGCGTGCCGCTCTATCTGTGAGCGCGCGGCCAGGGCTGCGAAGCCCTCATGAACAAGTTCCGTTTTCAG
TGGCCCGAGCGCTGCGCTGCGAGCACTTCCCGCGCCACGGCGCCGAGCAGATCTGCGTCGGCCAGAACCCTCC
GAGGACGGAGCTCCCGCGCTACTCACCACCGCGCCGCGCCGGGACTGCAGCCGGGTGCCGGGGGACCCCGGGT
GGCCCGGGCGGGCGGCGCTCCCCGCGCTACGCCACGCTGGAGCACCCCTTCCACTGCCCGCGCTCCTCAAG
GTGCCATCCTATCTCAGCTACAAGTTTCTGGGCGAGCGTGATTGTGCTGCGCCCTGCGAACCTGCGCGGCCCGAT
GGTTCCATGTTCTTCTACAGGAGGAGACGCGTTTCGCGCGCCTCTGGATCCTCACCTGGTCGGTGCTGTGCTGC
GCTTCCACCTTCTTCACTGTCAACACGTACTTGGTAGACATGCAGCGCTTCCGCTACCCAGAGCGGCCTATCATT
TTTCTGTGCGGGCTGCTACACCATGGTGTGCGGTGGCTTACATCGCGGGCTTCGTGCTCCAGGAGCGGTGGTGTGC
AACGAGCGCTTCTCCGAGGACGGTTACCGCACGGTGGTGCAGGGCACCAAGAAGGAGGGCTGCACCATCCTCTTC
ATGATGCTCTACTTCTTCACTAGGCCAGCTCCATCTGGTGGGTATCCTGTGCTCACCTGGTTCCTGGCAGCC
GGCATGAAGTGGGGCCACGAGGCCATCGAGGCCAACTCTCAGTACTTCCACCTGGCCGCTGGGCCGTGCCGGCC
GTCAAGACCATCACCATCCTGGCCATGGGCCAGATCGACGGCGACCTGCTGAGCGGCGTGTGCTTCGTAGGCCTC
AACAGCCTGGACCCGTGCGGGGCTTCGTGCTAGCGCCGCTCTTCGTGTACCTGTTTATCGGCACGTCCTTCCTC
CTGGCCGGCTTCGTGTGCTCTTCCGCATCCGCACCATCATGAAGCACGACGGCACCAAGACCGAAAAGCTGGAG
CGGCTCATGGTGGCATCGGCGTCTTCTCCGTGCTCTACACAGTGCCCGCCACCATCGTCATCGCTTGCTACTTC
TACGAGCAGGCCTTCCGCGAGCACTGGGAGCGCTCGTGGGTGAGCCAGCACTGCAAGAGCCTGGCCATCCCGTGC
CCGGCGCACTACACGCCGCGCATGTGCCCCGACTTACGGTCTACATGATCAAATACCTCATGACGCTCATCGTG
GGCATCACGTGCGGCTTCTGGATCTGGTGGGCAAGACGCTGCACTCGTGAGGAAGTTCTTACACTCGCCTCACC
AACAGCCGACACGGTGAGACCACCGTGTGAGGGACGCCCCAGGCCGGAACCGCGCGGCGCTTTCCTCCGCCGG
GGTGGGGCCCTACAGACTCCGTATTTTATTTTTTAAATAAAAAACGATCGAAACCATTTCACTTTTAGGTTGC
TTTTTAAAGAGAACTCTCTGCCCAACACCCCC

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FIGURE 634

MRPRSALPRLLLPLLLLPAAGFAQFHGEKGISIPDHGFCQPISIPLCDIAYNQTIMPNLLGHTNQEDAGLEVHQ
FYPLVKVQCSPELRFFLCSMYAPVCTVLEQAIPPCRSICERARQGCEALMNKFGFQWPERLRCEHFPRHGAEQIC
VGQNHSEDGAPALLTTAPPPGLQPGAGGTPGGPGGGGAPPRYATLEHPFHCPRVLKVP SYLSYKFLGERDCAAPC
EPARPDGSMFFSQEETRFARLWILTWSVLCCASTFFTVTTYLVDMQRFYPERPIIFLSGCTMVS VAYIAGFVL
QERVVCNERFSEDGYRTVVQGTKKEGCTILFMMLYFFSMASSIWWVILSLTWFLAAGMKWGHEAIEANSQYFHLA
AWAVPAVKTTITILAMGQIDGDLGVCVGLNSLDPLRGFVLAPLFVYLFIGTSFLLAGFVSLFRIRTIMKHDGT
KTEKLERLMVRIGVFSVLYTVPATIVIACYFYEQAFREHWERSWVSQHCKSLAIPCPAHYTPRMSPDFTVYMIKY
LMTLIVGITSGFWIWSGKTLHSWRKFYTRLTNSRHGETTV

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FIGURE 635

CGGGCGCGGGGCTTTTGCTGACCGCCGTGTCCCCAGGCCGGCGCGACCGTGCCCCCTGGAGGTGGTGCTGCTGCG
CAAGGTGGGCGCGGCGGGCGGCGCGCGCGCGTCATCCGCCTGCTGGACTGGTTTCGAGCGGGCCGACGGCTTCCT
GCTGGTGCTGGAGCGGCCCCGAGCCGGCGCAGGACCTCTTCGACTTTATCACGGAGCGCGGCGCCCTGGACGAGCC
GCTGGCGCGCCGCTTCTTCGCGCAGGTGCTGGCCGCCGTGCGCCACTGCCACAGCTGCGGGGTCGTGCACCGCGA
CATTAAAGGACGAAAATCTGCTTGTGGACCTGCGCTCCGGAGAGCTCAAGCTCATCGACTTCGGTTCGGGTGCGCT
GCTCAAGGACACGGTCTACACCGACTTCGACGGCACCCGAGTGTAAGCCCCCGAGTGGATCCGCTACCACCG
CTACCACGGGCGCTCGGCCACCGTGTGGTTCGTGGGCGTGCTTCTCTACGATATGGTGTGTGGGGACATCCCCTT
CGAGCAGGACGAGGAGATCCTCCGAGGCCGCTGCTCTTCGGAGGAGGGTCTCTCCAGAGCGGCCGCTCGCTGGA
TCAGATTGCGGCCCCATCCCTGGATGCTGGGGGCTGACGGGGGCGTCCCGGAGAGCTGTGACCTGCGGCTGTGCAC
CCTCGACCCTGATGACGTGGCCAGCACACGTCCAGCAGCGAGAGCTTGTGAGGAGCTGCACCTGACTGGGAGCT
AGGGGACCACCTGCCTTGCCAGACCTGGGACGCCCCAGACCCTGACTTCTCCTGCGTGGGCGCTCTCCTCCT
GCGGAAGCAGTGACCTCTGACCCCTGGTGACCTTCGCTTTGAGTGCCCTTTGAACGCTGGTCCCGCGGGACTTGG
TTTTCTCAAGCTCTGTCTGTCCAAAGACGCTCCGGTCGAGGTCCCGCCTGCCCTGGGTGGATACTTGAACCCAG
ACGCCCCCTCTGTGCTGCTGTGTCCGGAGGCGGCCTTCCCATCTGCCTGCCACCCGGAGCTCTTACGCCGGCGC
AGGGTCCCAAGCCACCTCCCGCCCTCAGTCCTGCGGTGTGCGTCTGGGCACGTCTGACACACAATGCAAGTC
CTGGCCTCCGCGCCCCGCCCCACGCGAGCCGTACCCGCCGCAACTCTGTTATTTATGGTGTGACCCCTGGAG
GTGCCCTCGGCCACCCGGGGCTATTTATTGTTTAAATTTATTGTTGAGGTATTTCTCTGAGCAGTCTGCCTCT
CCCAAGCCCCAGGGGACAGTGGGGAGGCAGGGGAGGGGGTGGCTGTGGTCCAGGGACCCAGGCCCTGATTCCTG
TGCCTGGCGTCTGTCCCGCCCCCGCTGTGAGAAGATGAACATGTATAGTGGCTAACTTAAGGGGAGTGGGTGAC
CCTGACACTTCAGGCACTGTGCCCAGGGTTTTGGGTTTTAAATTATTGACTTTGTACAGTCTGCTTGTGGGCTCT
GAAAGCTGGGTGGGGCCAGAGCCTGAGCGTTTTAAATTTATTACGTACCTGTGTTTGTGTGAATGCGGTGTGTGCA
GGCATCGCAGATGGGGTTCTTTCAGTTCAAAAGTGAGATGTCTGGAGATCATATTTTTTTATACAGGTATTTCA
ATTAAATGTTTTTGTACATAGTGG

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FIGURE 636

GAGLLLTAVSPRPAPPCPWRWCCCARWARRAARAASSACWTGSSGPTASCWCWSGPSRRRTSSTLSRSAAPWTSR
WRAASSRRCWPPCATATAAGSCTATLRKICLWTCAPESSSSSTSVRVRCSTRSTPTSTAPECTAPRSGSATTA
TTGARPPCGRWACFSTIWCVGTSFSSRTRRSSEAACSSGGGSLQSGRRWIRLRPIPGCWGLTGASRRAVTCGCAP
STLMTWPAPRPAARACEELHLTGS

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FIGURE 637

ATGCTAGACAAGGTACTATGCCTGTATCTCTGCTGAAGGCTCATGAAGCTGAAATGTGGGAAGTTCACTTTCACC
CATCCAACCCAGAACATCTTTTACCTGCTCTGAAGATGGATCCCTCTGGCACTGGGATGCTTCCACAGATGTAC
CTGAAAAGTCGTCACCTCTTTCACCAAGGAGGAAGAAGCAGTACTTTTTTGTCTCATAGCATTAGTAACCAAGCTA
ATGTTTACCAGTCTGTCTAGCTCCTGGCTCAGCACTGATCCTGCAAAAGACCGAATTGAAATCACAAGCTTAC
TTCCCAGTAGGCTCTGTCTGTGAACACTTTGGATGTTTTAGGTCCTTGTCTTGTGTTGTGGAACCGATGCAGAAG
CAATTTATGTTACTAGACATCTTTTTTCGTAGAAGTACTATAATTATAAGATTTTCTAGATAGAACATGCAATTAGC
CTTTTGAAATCCAGCTTCTGTGCAAAATTTTAGTATCAGAAAATACGAGATTTGCAGGGGAAACATCAGTAAACT
ACCATTAATGTCAATGCCAGTTTTGACTTTTTGTTAGCCTGACACTCCCAAAACAGTTGTAGAATCCGATAGATGA
CTGATGGCAAAAGATTGTGAACATGTGGAAGAAAAATCAGTGGGATTCTGGTGCTGATGAATAGGTTGCCTTCAGA
GTATTATTGACAGACAGCTTGTGGAACATAATTCTTTATTTTTTGATGTTGTGGAATTAACACATCAATGGTGGTT
ATGGGAACACTACCAATGGGTTCCACAAATTTTTATCAGTAGTATGTGGCATATACACCTTCCTAGTGGCAGTTGCC
AATGTTAATGATTATTCTTTTATTGCAAGTATTTCTATGATCCTTCCACACTTTATTTCTTAATAATAATAA
ACTTTTTTCAGAAAGAATTGAGTAGAGCAAAATGACAAAGATGTGTAGCTGTGTTCAATTTTTTTTTTTTTTTT
TTTGAGGCAGAGTCTTGCTCTGCTGGAGTGGGTTGCAATCTCGGCTCACTGCAACCTCCACCTCCCAGGTTT
AAGCAATTTCTCCTGCCCTCAGTCTCCTGAGTAGCTGGAACACTACAGGTGTGCGCCACCACGCCAGCTAATTTTTGT
AATTTTAGTAGAGACAGATTTTACCATGTTGGCCAGGATGGTCTCGATCTCTTGACCTCATGATCCACCCGCCT
CGACCTCCCAAAGTGCTGTGATTACAGGTGTGAGCCACTGCACCCGGCCTGAAATTTTTTTAAGGTGAAATGTT
TTGACAAGTTCCTTTTTTCAAGATAGGTTTTTGTGAGCAGAACTCTTTCAGCTTGTAGACCCAACCTTTGCTTTTGT
TAGCTTCACAGCATAGCTGAAAGTTGCCAAACTGGACATTGTGCAATAAAGTAGAATTCTATATTGATAAGCAAA
CTATTTCCAAACTAAAAATGTGATAGATAAAAGTGTGATTAATCAAATGATATGATCAGAGTAAAGAATTTTGCC
ATTTTGATCCTTTTACTTTGTTTTAGCCACCTATAGTGTACCAACCATCTTTATCCTTGTCTGCAGGGATAATA
ATGAACATAATGTAGTGTTTAAGATAATTTAATGATACTATCTTTCCAACTTTGTTAGATTTTAAATGTATTAT
TGACCTGAGACCTTAATGACAAATCACTGCTATTAGACAATTGAAGTGTTCATTTACTTTGTAATTCCAATAATC
ATAGTTATGGAATTATGGTAAGGTTTTGCTTTTCTGTCCTAATAAATATATATATTTTTTGTAGATGGAGTTTTGC
TCTTGTGCTGAGGCAGGAGAGTTGCTCGAGCCCGGGAGGCAGAGGTTGCAGTGACCCAGGATCGTGCCACTTCA
CTCCAGCCTGGGCAAAAGAGCAAAACGCCATCTCAAAAAATATACATATATAAGGAGATAAAGTTTCCCATTTTC
CAATACAGTTTTCACATTTGAACAGCCCTAATTGATACAACCTTTATGGCAGGGTTTTAGTGTGTGAGTGGGATCCA
AAACACTCAATCCTGTAAAAGGGTACAGTCCTATTGTATGTTAGTTAACACACTGATGATGTGAGCCTGTGAGAT
GAGCCAATCACCAGTTGTTATGTTTGAATCTGCTTTGTGTTGGGACGCTTTAATGTAGGGTTTCACTAAATAAAT
GAATTTTCATATACTGAACCTG

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FIGURE 638

MPVSLKAHEAEMWEVHFHPSNPEHLFTCEDGSLWHWDASTDVPEKSSLFHQGRSSTFLSHSISNQANVHQS
V
ISSWLSTDPAKDRIEITSLLPSRSLSVNTLDVLGPCLVCGTDAEAIYVTRHLS

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FIGURE 639

GTGCTTTACTGCGCGCTCTGGTACTGCTGTGGCTCCCCGTCTGGTGCGGGACCTGTGCCCCGCGCTTCAGCCCT
CCCCGCACAGCCTACTGATTCCCCTGCCGCCCTTGCTCACCTCCTGCTCGCCATGAGTCGCTGGTTTTCGCGCG
GCGCTCCGGCCCCACTCCCTCGGCCGCAGAGCTAGCCCCGCCGCTGGCGGAAGGGCTGATCAAGTCGCCCAAGCC
CCTAATGAAGAAGCAGGCGGTGAAGCGGCACCACCACAAGCACAACCTGCGGCACCGCTACGAGTTCCTGGAGAC
CCTGGGCAAAGGCACCTACGGGAAGGTGAAGAAGGCGCGGGAGAGCTCGGGGCGCCTGGTGGCCATCAAGTCAAT
CCGGAAGGACAAAATCAAAGATGAGCAAGATCTGATGCACATACGGAGGGAGATTGAGATCATGTCATCACTCAA
CCACCCTCACATCATTGCCATCCATGAAGTGTGTTGAGAACAGCAGCAAGATCGTGATCGTCATGGAGTATGCCAG
CCGGGGCGACCTTTATGACTACATCAGCGAGCGGCAGCAGCTCAGTGAGCGCGAAGCTAGGCATTTCTCCGGCA
GATCGTCTCTGCCGTGCACTATTGCCATCAGAACAGAGTTGTCCACCGAGATCTCAAGCTGGAGAACATCCTCTT
GGATGCCAATGGGAATATCAAGATTGCTGACTTCGGCCTCTCCAACCTCTACCATCAAGGCAAGTTCCTGCAGAC
ATTCTGTGGGAGCCCCCTCTATGCCTCGCCAGAGATTGTCAATGGGAAGCCCTACACAGGCCAGAGGTGGACAG
CTGGTCCCCTGGGTGTTCTCTCTACATCCTGGTGCATGGCACCATGCCCTTTGATGGGCATGACCATAAGATCCT
AGTGAAACAGATCAGCAACGGGGCCTACCGGGAGCCACCTAAACCCTCTGATGCCTGTGGCCTGATCCGGTGGCT
GTTGATGGTGAACCCACCCGCGGGCCACCCTGGAGGATGTGGCCAGTCACTGGTGGGTCAACTGGGGCTACGC
CACCCGAGTGGGAGAGCAGGAGGCTCCGCATGAGGTGGGCACCCCTGGCAGTGAATCTGCCCCGCGCTCCATGGC
TGACTGGCTCCGGCGTTCTCCCGCCCCCTCTGGAGAATGGGGCCAAGGTGTGCAGCTTCTTCAAGCAGCATGC
ACCTGGTGGGGGAAGCACCACCCTGGCCTGGAGCGCCAGCATTCTGCTCAAGAAGTCCCGCAAGGAGAATGACAT
GGCCCAGTCTCTCCACAGTGACACGGCTGATGACACTGCCCATCGCCCTGGCAAGAGCAACCTCAAGCTGCCAAA
GGGCATTCTCAAGAAGAAGGTGTGAGCCTCTGCAGAAGGGGTACAGGAGGACCCTCCGGAGCTCAGCCCAATCCC
TGCGAGCCCAGGGCAGGCTGCCCCGCTGCTCCCCAAGAAGGGCATTCTCAAGAAGCCCCGACAGCGCGAGTCTGG
CTACTACTCCTCTCCCGAGCCAGTGAATCTGGGGAGCTCTTGAGCGCAGGCGACGTGTTTTGTGAGTGGGGATCC
CAAGGAGCAGAAGCCTCCGCAAGCTTCAGGGCTGCTCCTCCATCGCAAAGGCATCCTCAAACCTCAATGGCAAGTT
CTCCCAGACAGCCTTGAGGCTCGCGGCCCCCACCACCTTCGGCTCCCTGGATGAATCGCCCCACCTCGCCCCCT
GGCCCCGGGCCAGCCGACCCTCAGGGGCTGTGAGCGAGGACAGCATCCTGTCTCTGAGTCTTTGACCAGCTGGA
CTTGCTGAACGGCTCCCAGAGCCCCACTGCGGGGCTGTGTGTCTGTGGACAACCTCACGGGGCTTGAGGAGCC
CCCCTCAGAGGGCCCTGGAAGCTGCCTGAGGCGCTGGCGGCAGGATCCTTTGGGGGACAGCTGCTTTTCCCTGAC
AGACTGCCAGGAGGTGACAGCGACCTACCGACAGGCACTGAGGGTCTGCTCAAAGCTCACCTGAGTGGAGTAGGC
ATTGCCCCAGCCCGGTGAGGCTCTCAGATGCAGCTGGTGCACCCCGAGGGGAGATGCCTTCTCCCCACCTCCC
AGGACCTGCATCCCAGCTCAGAAGGCTGAGAGGGTTTGAGTGGAGCCCTGAGCAGGGCTGGATATGGGAAGTAG
GCAAATGAAATGCGCCAAGGGTTCAGTGTCTGTCTTCAGCCCTGCTGAACGAAGAGGATACTAAAGAGAGGGGAA
CGGGAATGCCCGCGACAGAGTCCACATTGCCTGTTTCTTGTGTACATGGGGGGGCCACAGAGACCTGGAAAGAGA
ACTCTCCCAGGGCCCCTCTCTGATCCCATGAATACTCTGTACACATGGTGCCTTCTAAGGACAGCTCCTTCCC
TACTCATTCCCTGCCCAAGTGGGGCCAGACCTCTTTACACACACATTCCCCTTCTACCAACCACCAGAACTGGA
TGGTGGCACCCTAATGTGCATGAGGCATCCTGGGAATGGTCTGGAGTAACGCTTCGTTATTTTTATTTTTATTT
TTATTTATTTATTTATTTTTTTGAGACGGAGTTTCGCTCTTGGTGGCCAGGCTAGAGTGCAATGGCGCATCTCA
GCTCACCTCAACCTCCGCCTCCCGGGTCAAGCGATTCTCCTGCCTCAGCTCCCTAGTAGCTGGGATTACAGGC
GCCCCGCCACCATGCCCCGCTAATTTTGTATTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGGTCTCA
AACTCCCAGCTCAGTGATCCACCCACCTCGGCCTCCCAAAGTGTGGGATTACAGGCGTGAGCCACCGCGCCC
CACCTAACCTTTCCTATTTAGCCTAGGAGTAAGAGAACACAATCTCTGTTTCTTCAATGGTTCTCTTCCCTTTT
CCATCCTCCAAACCTGGCCTGAGCCTCCTGAAGTTGCTGCTGTGAATCTGAAAGACTTGAAAAGCCTCCGCCTGC
TGTTGTGGACTTCATCTCAAGGGGGCCAGCCTCCTCTGGACTCCACCTTGGACCTCAGTGACTCAGAACTTCTGCC
TCTAAGCTGCTCTAAAGTCCAGACTATGGATGTGTTCTCTAGGCCTTACAGGACTCTAGAATGTCCATATTTATTT
TTATGTTCTTGGCTTTGTGTTTTAGGAAAAGTGAACTCTTGCTGTTTTCAATAATGTGAATGCTATGTTCTGGGAA
AATCCACTATGACATCTAAGTTTTGTGTACAGAGAGATATTTTGAACCTATTCCACCTCCTCCACAACCCCC
CACACTCCACTCCACACTCTTGAGTCTCTTACCTAATGGTCTCTACCTAATGGACCTCCGTGGCCAAAAAGTAC
CATTAACACAGAAAGGTGATTGGAAAAA

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FIGURE 640

MESLVFARRSGPTPSAAELARPLAEGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFLETLGKGTYGKVKKARESSG
RLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHIIAIEVFENSSKIVIVMEYASRGDLYDYISERQQLSER
EARHFFRQIVSAVHYCHQNRVVHRDLKLENILLDANGNIKIADFGLSNLYHQGKFLQTFCGSPLYASPEIVNGKP
YTGPVDSWSLGVLLYILVHGTMFPDGHDKILVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRATLEDVASH
WWVNWGYATRVGEQEAPHEGGHPGSDSARASMADWLRRSSRPLENGAKVCSFFKQHAPGGGSTTPGLERQHSLK
KSRKENDMAQSLHSDTADDTAHRPGKSNLKLPGILKKKVSASAEGVQEDPPELSPIPASPGQAAPLLPKKGILK
KPRQRESGYYSPEPSESSELLDAGDVFVSGDPKEQKPPQASGLLLHRKGILKLNGKFSQTALELAAPTTFGSLD
ELAPPRPLARASRPSGAVSEDSILSSESFDQLDLPERLPEPPLRGCVSVDNLTGLEEPPSEPGSCLRRWRQDPL
GDSCFSLTDCQEVATYRQALRVCSKLT

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FIGURE 641

GTTTTCTACTTTGCCCGCCACAGATGTAGTTTCTCTGCGCGTGTGCGTTTCCCTCCTCCCCGCCCTCAGGG
TCCACGGCCACCATGGCGTATTAGGGGCAGCAGTGCCTGCGGCAGCATTGGCCTTTGCAGCGGCGGCAGCAGCAC
CAGGCTCTGCAGCGGCAACCCCCAGCGGCTTAAGCCATGGCGTGAGTACCGGGGCGGGTCGTCCAGCTGTGCTCC
TGGGGCCGGCGCGGTTTGGATTGGTGGGGTGCGGCCTGGGGCCAGGGCGGTGCCGCCAAGGGGAAGCGATT
AACGAGCGCCCCGGGACGCGTGGTCTTTGCTTGGGTGTCCCCGAGACGCTCGCGTGCCTGGGATCGGGAAAGCGTA
GTGGGTGCCCCGACTGCTTCCCCAGGAGCCCTACAGCCCTCGGACCCCGAGCCCCGAAGGTCCCAGGGGTCTT
GGCTGTTGCCCCACGAAACGTGCAGGAACCAAGATGGCGGCGGCAGGGCGGCGGCGGGCGGTGAGTCAAGGGCG
GGCGGTGGGCGGGGCGCGGCCGCTGGCCGTATTGACGTGGGGACGGAGCGCTTTCCTCTTGGCGGCCGTTGGA
AGAATCCCTGGTCTCCGTGAGCGTCCATTTTGTGGAACCTGAGTTGCAAGCAGGGAGGGGCAAATACAACCTGCC
CTGTTCCCGATTCTCTAGATGGCCGATCTAGAGAAGTCCCGCCTCATAAGTGAAGGATGAAATTCTCAGAACAG
CTAACCTCTAATGGGAGTTGGCTTCTGATTCTCATTCAGGCTTCTCACGGCATTACGACAGCAGCGTTGCTGTAAC
CGACAAAGACACCTTCGAATTAAGCACATTCCCTCGATTCCAGCAAAGCACCGCAACATGACCGAAATGAGCTTCC
TGAGCAGCGAGGTGTTGGTGGGGGACTTGATGTCCCCCTTCGACCCGTCGGGTTTGGGGGCTGAAGAAAGCCTAG
GTCTCTTAGATGATTACCTGGAGGTGGCCAAGCACTTCAAACCTCATGGGTTCTCCAGCGACAAGGCTAAGGCGG
GCTCCTCCGAATGGCTGGCTGTGGATGGGTTGGTCAGTCCCTCCAACAACAGCAAGGAGGATGCCTTCTCCGGGA
CAGATTGGATGTTGGAGAAAATGGATTTGAAGGAGTTCGACTTGGATGCCCTGTTGGGTATAGATGACCTGGAAA
CCATGCCAGATGACCTTCTGACCACGTTGGATGACACTTGTGATCTCTTTGCCCCCTAGTCCAGGAGACTAATA
AGCAGCCCCCCCAGACGGTGAACCCAATTGGCCATCTCCCAGAAAGTTTAAACAAAACCCGACCAGGTGCCCCCT
TCACCTTCTTACAACCTCTTCCCCCTTCCCCAGGGGTCTGTCTCCTCCACTCCAGATCATTCCTTTAGTTTAGAGC
TGGGCAGTGAAGTGGATATCACTGAAGGAGATAGGAAGCCAGACTACACTGCTTACGTTGCCATGATCCCTCAGT
GCATAAAGGAGGAAGACACCCCTTCAGATAATGATAGTGGCATCTGTATGAGCCCAGAGTCTATCTGGGGTCTC
CTCAGCACAGCCCCCTTACCAGGGGCTCTCCAAATAGGAGCCTCCCATCTCCAGGTGTTCTCTGTGGGTCTGCCC
GTCCCAAACCTTACGATCCTCCTGGAGAGAAGATGGTAGCAGCAAAAGTAAAGGGTGAGAACTGGATAAGAAGC
TGAAAAAATGGAGCAAAACAAGACAGCAGCCACTAGGTACCGCCAGAAGAAGAGGGCGGAGCAGGAGGCTCTTA
CTGGTGAGTGCAAAGAGCTGAAAAGAAGAACGAGGCTCTAAAGAGAGGGCGGATTCCCTGGCCAAGGAGATCC
AGTACCTGAAAGATTTGATAGAAGAGGTCCGCAAGGCAAGGGGAAGAAAAGGGTCCCCTAGTTGAGGATAGTCA
GGAGCGTCAATGTGCTTGTACATAGAGTGCTGTAGCTGTGTGTTCCAATAAATTATTTGTAGGG

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FIGURE 642

MTEMSFLSSEVLVGDLMSPFDP SGLGAEESLGLLDDYLEVAKHFKPHGFSSDKAKAGSSEWLAVDGLVSPSNNSK
EDAFSGTDWMLEKMDLKEFDLDALLGIDDLETMPDDLTTLDDTCDLFAPLVQETNKQPPQTVNP IGHLPESLTK
PDQVAPFTFLQPLPLSPGVLSSTPDHSFSLELGSEVDITEGDRKPDYTAYVAMIPQCIKEEDTPSDNDSGICMSP
ESYLGSFQHSFSTRGSPNRS LPSPGVLCGSARPKPYDPPGEKMVA AKVKGEKLDKKLKKMEQNKTAATRYRQKKR
AEQEALTGECKELEKKNEALKERADSLAKEIQY LKDLIEEVRKARGKKRVP

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FIGURE 643

CGGCAGCCAGCTGAGAGCAATGGGAAATGGGGAGTCCCAGCTGTCTCGGTGCCTGCTCAGAAGCTGGGTTGGTT
TATCCAGGAATACCTGAAGCCCTACGAAGAATGTCAGACACTGATCGACGAGATGGTGAACACCATCTGTGACGT
CTGCAGGAACCCGAACAGTTCCCCCTGGTGCAGGGAGTGGCCATAGGTGGCTCCTATGGACGGAAAACAGTCTT
AAGAGGCAACTCCGATGGTACCCTTGTCTTTTTCTTCAGTGACTTAAACAATTCCAGGATCAGAAGAGAAGCCA
ACGTGACATCCTCGATAAACTGGGGATAAGCTGAAGTTCTGTCTGTTACGAAGTGGTTGAAAAACAATTTCGA
GATCCAGAAGTCCCTTGATGGGTCCACCATCCAGGTGTTCAAAAAAATCAGAGAATCTCTTTCGAGGTGCTGGC
CGCCTTCAACGCTCTGAGCTTAAATGATAATCCCAGCCCTGGATCTATCGAGAGCTCAAAGATCCTTGGATAA
GACAAATGCCAGTCTGTTGAGTTTGAGTCTGCTTCACTGAAGTCCAGCAGAAGTTTTTTGACAACCGTCTCGG
AAAATAAGGATTTGATCCTCTTGATAAAGCACTGGCATCAACAGTGCCAGAAAAAATCAAGGATTTACCCTC
GCTGTCTCCGTATGCCCTGGAGCTGCTTACGGTGTATGCCCTGGGAACAGGGGTGCAGAAAAGACAACCTTTGACAT
TGCTGAAGGCGTCAGAACGGTTCTGGAGCTGATCAATGCCAGGAGAAGCTGTGTATCTATTGGATGGTCAACTA
CACTTTGAAGATGAGACCATCAGGAACATCCTGCTGCACCACTCCAATCAGCGAGGCCAGTAATCTTGGATCC
AGTTGACCCAACCAATAATGTGAGTGGAGATAAAATATGCTGGCAATGGCTGAAAAAGAAGCTCAAACCTGGTT
GACTTCTCCCAACCTGGATAATGAGTTACCTGCACCATCTTGAATGTCTGCCTGCACCACTCTTCACGACCCC
AGGCCACCTTCTGGATAAGTTCATCAAGGAGTTTCTCCAGCCCAACAAATGCTTCCTAGAGCAGATTGACAGTGC
TGTTAACATCATCCGTACATTCTTAAAGAAAATGCTTCCGACAATCAACAGCCAAGATCCAGATTGTCCGGGG
AGGATCAACCGCCAAAGGCACAGCTCTGAAGACTGGCTCTGATGCCGATCTCGTCGTGTTCCATAACTCACTTAA
AAGCTACACCTCCCACAAAAACGAGCGGCACAAAATCGTCAAGGAAATCCATGAACAGCTGAAAGCCTTTTGAG
GGAGAAGGAGGAGGAGCTTGAAGTCAGCTTTGAGCCTCCCAAGTGGAAGGCTCCCAGGGTGCTGAGCTTCTCTCT
GAAATCCAAAGTCTCAACGAAAGTGTGAGCTTTGATGTGCTTCTCGCTTTAATGCACTGGGTGAGCTGAGTTC
TGGCTCCACACCCAGCCCCGAGGTTTATGCAGGGCTCATTGATCTGTATAAATCCTCGGACCTCCCGGGAGGAGA
GTTTTCTACCTGTTTACAGTCTCTGCAGCGAACTTCATTGCTCCCGCCCACTAAAGGATTTAATTCG
CCTGGTGAAGCACTGGTACAAAGAGTGTGAAAGGAACTGAAGCCAAAGGGGTCTTTGCCCCCAAGTATGCCCT
GGAGCTGCTCACCATCTATGCCTGGGAGCAGGGGAGTGGAGTGCCGATTTTGACACTGCAGAAGGTTTCCGGAC
AGTCTGGAGCTGGTCACACAATATCAGCAGCTCGGCATCTTCTGGAAGGTCAATTACAACCTTTGAAGATGAGAC
CGTGAGGAAGTTTCTACTGAGCCAGTTGCAGAAAACAGGCCTGTGATCTTGGACCCAGGCGAACCACAGGTGA
CGTGGGTGGAGGGGACCGTTGGTGTGGCATCTTCTGGACAAAGAAGCAAAGGTTAGGTTATCCTCTCCCTGCTT
CAAGGATGGGACTGGAAACCCAATACCACCTTGGAAGTGCCGACAATGCAGACACCAGGAAGTTGTGGAGCTAG
GATCCATCTTATTGTCAATGAGATGTTCTCATCCAGAAGCCATAGAATCCTGAATAATAATTCTAAAAGAACTT
CTGGAGATCATCTGGCAATCGCTTTTAAAGACTCGGCTCACCGTGAGAAAGAGTCACTCACATCCATTCTCCCT
TGATGGTCCCTATTCTCCTTCCCTTGCCTTCTTGACTTCTTGAAATCAATCAAGACTGCAAACCTTTTCATAA
AGCTGCCTTGCTGAATCCTCTCTGCAGGAGCCCTGCTTAAATAGTTGATGTCATCACTTTATGTGCATCTTAT
TTCTGTCAACTTGATTTTTTTTTCTTGTATTTTTCCAATTAGCTCCTCTTTTCTTCCAGTCTAAAAAGGA
ATCCTCTGTGTCTTCAAAGCAAAGCTCTTTACTTTCCCTTGGTTCTCATAACTCTGTGATCTTGCTCTCGGTGC
TTCCAATCATCCAGTCTGTCTGTTTCTGTATACAAAACCTTTCTGCCCCCTGCTGACACAGACATCCTC
TATGCCAGCAGCCAGGCCAACCTTTTATTAGAACTTCAAGCTCTCCAAAGGCTCAGATTATAACTGTTGTCATA
TTTATATGAGGCTGTTGCTTTTCTTCTGAGCCTGCCTTTATCCCCCACCAGGAGTATCCTCTTGCCAAAGC
AAAAGACTTTTTCTTGGCTTTAGCCTTAAAGATACTTGAAGGTCTAGGTGCTTTAACCTCACATACCCTCACTT
AAACTTTTATCACTGTTGCATATACCAGTTGTGATACAATAAAGAATGTATCTGG

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FIGURE 644

MGNGESQLSSVPAQKLGWFIQEYLKPYEECQTLIDEMVNTICDVCRNPEQFPLVQGVAIGGSYGRKTVLRGNSDG
TLVLFFSDLKQFQDQKRSQRDILDKTGDKLKFCLEFTKWLKNNFEIQKSLDGSTIQVFTKNQRISFEVLAAFNALS
LNDNPSWIIYRELKRSLDKTNASPGFAVCFTELQOKFFDNRPGLKDLILLIKHWHQCCQKKIKDLP SLSPYAL
ELLTVYAWEQGCRKDNFDIAEGVRTVLELIKCEKLCIYWMVNYNFEDETIRNILLHQLQSARPVILDPVDP TNN
VSGDKICWQWLKKEAQTWLTSPNLDNELPAPSWNVLPAPLFTTPGHLLDKF IKEFLQPNKCFLEQIDSAVNI IRT
FLKENCFRQSTAKIQIVRGGSTAKGTALKTGSDADLVVFHNSLKSYSQKNERHKIVKEIHEQLKAFWREKEEEL
EVSFEPPKWKAPRVLSFSLKSKVLNESVSFDVLP AFNALGQLSSGSTPSPEVYAGLIDLYKSSDLP GGEFSTCFT
VLQRNFIRS RPTKLKDLIRLVKHWYKECERKLKPKGSLPPKYALELLTIYAWEQSGVPDFDTAEGFRTVLELVT
QYQQLGIFWKVNYNFEDETVRKFLLSQLQKTRPVILDPGEPTGDVGGDRWCWHLLDKEAKVRLSSPCFKDGTGN
PIPPWKVPTMQTPGSCGARIHP IVNEMFSSRSRHLNNNSKRNFWRSSGNRF

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FIGURE 645

TGTTAGGCAGCAACAGTGCTGATGCTGGACTGTGGCAGGCAGAGGGTGCTATCCTGACACACTTCACCTTAGTG
AGGAAACTTCAATTTGGTGGAGAAAGGCGATTTTCAGGTTCCAATCTGGGCGACACTTCCCAGTTGGAGAGTCA
GCAAAAGGGAGAGGGCAATTCCAAGAAGAGGGAAAAGCTTGTGCACAGTGTACCTCCTTTATTCTGAAGCCCGG
GCAGTGCTTGACCTGGTCGACCAGTGCCCAAAACAGATCCAGAAAGGAAAGTTCCAGGTTGTTGCCATCGAAGGA
CTGGATGCCACGGGTAAAACCACGGTGACCCAGTCAGTGGCAGATTCACTTAAGGCTGTCTCTTAAAGTCACCA
CCCTCTTGCAATTGGCCAGTGGAGGAAGATCTTTGATGATGAACCAACTATCATTAGAAGAGCTTTTTACTCTTTG
GGCAATTATATTGTGGCTCCGAAATAGCTAAAGAATCTGCCAAATCTCCTGTGATTGTAGACAGGTACTGGCAC
AGCACGGCCACCTATGCCATAGCCACTGAGGTGAGTGGGGGTCTCCAGCACCTGCCCCCAGCCCATCACCTGTG
TACCAGTGGCCAGAGGACCTGCTCAAACCTGACCTTATCCTGCTGCTCACTGTGAGTCCTGAGGAGAGGTTGCAG
AGGCTGCAGGGCCGGGGCATGGAGAAGACCAGGGAAGAAGCAGAACTTGAGGCCAACAGTGTGTTTCGTCAAAAG
GTAGAAATGTCCTACCAGCGGATGGAGAATCCTGGCTGCCATGTGGTTGATGCCAGCCCCTCCAGAGAAAAGGTC
CTGCAGACGGTATTAAGCCTAATCCAGAATAGTTTTAGTGAACCGTAGTTACTCTGGCCAGGTGCCACGTCTAAC
TAGATTAGATGTTGTTTGAACATCTACATCCACCATTGTTATGCACTGTTCCTCAAAATTTCTGTTCTACAAGCA
TGTTGTGTGGCAGAAAACCTGGAGACCAGGCATCTTAATTTTACTTCAGCCATCGTACCCTCTTCTGACTGATGGA
CCCGTCAICACAAAGGTCCCTCTCATCATGTTCCAGTGAGAGGCCAGCGATTGCTTTCTTCTGGCATAGTAAAC
ATTTTCTTGAACATATGTTTCACTTAATCACTACCAAATATCTGGAAGACCTGTCTTACTCAGACAGCACCAGG
TGTACAGAAGCAGCAGACAAGATCTTCCAGATCAGCAGGGAGACCCCGAGCCTCTGCTTCTCCTACACTGGCAT
GCTGATGAGATCGTGACATGCCACATTGGCTTCTTCCACATCIGGTTGCACTCGTCATGATGGGCTCGCTGCAT
CTCCCTCAGTCCCAAATTTCTAGAGCCAAGTGTTTCTTGCAGAGGCTGTCTATGTGTCTGGCTGCCCAAGGACACT
CCTGCAGAGCCATTTTGGGTAAGGAACACTTACAAAGAAGGCATTGATCTTGTGTCTGAGGCTCAGAGCCCTTT
TGATAGGCTTCTGAGTCATATATAAGACATTCAAGCCAAGATGCTCCAACCTGCAAAATATACCAACCTTCTCTGA
ATTATATTTTGCTTATTTATATTTCTTTCTTTTTTCTAAAGTATGGCTCTGAATAGAATGCACATTTTCCATT
GAAGTGGATGCATTTTCAATTTAGCCAATCCAGTAATTTATTTTATATTAATCTATACATAATATGTTTCTCAGCAT
AGGAGCTATGATTCATTAATTAAGTGGAGTCAAAACGCTAAATGCAATGTTTGTGTGATTTTTCATTACACA
AACTTAATTTGTCTTGTTAAATAAGTACAGTGGATCTTGGAGTGGGATTTCTTGGTAAATTATCTTGCACTTGAA
TGTCTCATGATTACATATGAAATCGCTTTGACATATCTTTAGACAGAAAAAGTAGCTGAGTGAGGGGGAATTA
TAGAGCTGTGTGACTTTAGGGAGTAGGTTGAACCAGGTGATTACCTAAATTCCTTCCAGTTCAAAGGCAGATAA
ATCTGTAAATTATTTTATCCTATCTACCATTCTTAAAGAAGACATTACTCCAAAATAATTAAATTTAAGGCTTTA
TCAGGTCTGCATATAGAATCTTAAATTTCTAATAAAGTTTCATGTTAATGTCATAGGATTTTTAAAGAGCTATAG
GTAATTTCTATATAATATGTGTATATTAATAATGTAATTGATTTTCAAGTTGAAAGTATTTTAAAGCTGATAAATAGC
ATTAGGGTTCTTTGCAATGTGGTATCTAGCTGTATATTGGTTTTTATTTACTTTAAACATTTTGAAAAGCTTATA
CTGGCAGCCTAGAAAAACAACAATTAATGTATCTTTATGTCCCTGGCACATGAATAAACTTTGCTGTGGTTTAC
TAATCTATGCTGTCTATCCTGGGTACATATTGATTTGTCTGAAAAGTGCTTTCTCAGATTCCCTTTTTAATATTGT
GATGTAAAGGAGGGAAATTTTGGTAAAGGAAGTTGAAAGGTGTGAGCTGGCAGGCTAAGTGGAATTTGTGGTTAG
AGTGCTTTCAGAGAAA

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FIGURE 646

LGSNSADAGLWQAEGAILTHFTLVQETSIWKKGDFEVPIWATLPSWRVSKRERAIPRRGKSLCTVYLLYIPEAR
AVLDLVDQCPKQIQKGKFQVVAIEGLDATGKTTVTQSVADSLKAVLLKSPSPSCIGQWRKIFDDEPTTIIRRAFYSL
GNYIVASEIAKESAKSPVIVDRYWHSTATYAIATEVSGGLQHLPPAHPVYQWPEDLLKPDLILLTTSPEERLQ
RLQGRGMEKTREEAELEANSVFRQKVMSYQRMENPGCHVVDASPSREKVLQTVLSLIQNSFSEP

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FIGURE 647

AAGGGGTAAATACCCATTATCAGAAAGTTTATTTTCCCTCATGATGGAAGCTTAATAAAGGGTTTCTATATTTTG
GACACCCAGAGAATTGCTCAAATGTGATTTTAGTGTAATAGGTCTTTCTTTTTCATTGAGTTGATTTTAAAGCA
TTTAATACATTGCCTTGTAACAACCTCCAAGCTTCTCTATAGTCAAGAGCCCAAGCTAGATATTTTGTGGGAACTT
AACTTTAAATTCCAAACCTTTGCTGAAATTGACATTGTCACTTTTTGTGCTGTGCCTTGGATTTGTATTCTTACT
CTTCTTGAGGAAAGATAGAAGGCAGTTGAACTTTGTGACCAAGAGCGTTTCATTGGCAGTCCCTGCATGATTGAT
AATTTGTAGATACAATATTATTGCATTTCTTTACATGTATTCATTTTCTGAAGAGTATTATCTTGTGCTTTTAA
TAAATAACATGTG

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FIGURE 648

RGKYPLSESLSLMMEA

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FIGURE 649

AAGCTGCCGCAGTTAGTTGGAGTCTAAGGACTCGTGACAATCTTCGGGTGCCCTTCGAGAGAAAAGGGGAGG**ATG**

CCACTGGAGTCATCCTCTTCAATGCCACTATCCTTC⁶⁷³CATCTCTCTTACCCTCAGTACCACACAATACTAACCCT
TCCCCTCCTCTGATGTCTTACATCACCTCCCAGGAGATGAAGTGATTCTTCACTGGTTTGCCAATTGGTCAGGT
CCCCAGCGTGAACGTTTCTAGAGGACCTGGTGGCTAAGGCAGTGCCAGAAAAATTACAACCACTGCTGGATAGT
CTGGAGCAGCTTAGTGTGTCTGGGGCAGACCGACCACCTTCTATCTTTGAGTGCCAGCTACATCTTTGGGATCAG
TGGTTTCGAGGCTGGGCTGAGCAGGAGCGCAATGAATTTGTCAGACAGCTGGAGTTCAGTGAGCCAGACTTCGTG
GCAAAGTTTTACCAAGCAGTGGCTGCTACAGCTGGTAAGGACT**TGAT**AGGCATTTCAGACCAAAGAAGATAACCATA
GCTGATGGAGCCATGACTCTCTACAATGATAACTCAATTCAAATGTGTGCGCTAAAGCTCTGGAAGTGGTATTCC
AACCAGCTGACCGAACTCACTGACCAGTACAGGCATGGTTATTTCAATATTAATAGCATGTCAACTGGACTCCTA
TTTGTAATGTTATCAATCTAAGCAATCCAGCTCATCAGTCTACTAGTTTGCTTCTTTCCGAGAGATGTCAAGTC
CTCAAGAATTTGATGGCTTCTTCTGCAGCTATAACCACAAGGAACCTACACATTGTAAGTCAAGTCCACTGCTGG
CTCATGAAATGTGTAAAGTAGAACCTCCTTCCCGAGAAATAAGACAGGACAATAAAAGGTGGCGTTTTGTACT
TTACCTGGATTCCATTGGCTGGTTTTACCACTCCTATCAGATTGTAGTGTAATTGTGTGATACGCAAACCATAG
TTTACCCAGTGATGATTTAATAAAATTATGAAAAATCAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAA

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FIGURE 650

MPLESSSSMPLSFPSLLPSVPHNTNPSPLMSYITSQEMKCILHWFANWSGPQRERFLEDLVAKAVPEKLQPLLD
SLEQLSVSGADRPPSIFECQLHLWDQWFRGWAEQERNEFVRQLEFSEPDFVAKFYQAVAATAGKD

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FIGURE 651A

GGGACCGACGACACGCCCCCTCTCCTCCTTTGTTCCGGGGGTCGGCGGCCGCTCTCCTGCCAGAGCTCGGGATC
TCGGCCCCGGGAGGCGGGCGCTCGGGCGCAGCCGCCGAAGATGCGGTTGGAAGTACGCGAGAGCCGAGTGCAGAAG
ATCTGGGTGCCCCGTGGACCACAGGCCCTCGTTGCCCAGATCCTGTGGGCCAAAGCTGACCAACTCCCCACCGTC
ATCGTCATGGTGGGCCCTCCCCGCCCCGGGGCAAGACCTACATCTCCAAGAAGCTGACTCGCTACCTCAACTGGATT
GGCGTCCCCACAAAAGTGTTC AACGTCGGGGAGTATCGCCGGGAGGCTGTGAAGCAGTACAGCTCTACAACCTTC
TTCCGCCCCGACATGAGGAAGCCATGAAAGTCCGGAAGCAATGTGCCTTAGCTGCCTTGAGAGATGTCAAAAGC
TACCTGGCGAAAGAAGGGGGACAAATTGCGGTTTTTCGATGCCACCAATACTACTAGAGAGAGGAGACATGATC
CTTCATTTTTGCCAAAGAAAATGACTTTAAAGCGTTTTTCATCGAGTCGGTGTGCGACGACCCTACAGTTGTGGCC
TCCAATATCATGGAAGTTAAATCTCCAGCCCGGATTACAAAGACTGCAACTCGGCAGAAGCCATGGACGACTTC
ATGAAGAGGATCAGTTGCTATGAAGCCAGCTACCAGCCCTCGACCCCGACAAATGCGACAGGGACTTGTGCGTG
ATCAAGGTGATTGACGTGGGCCGGAGGTTCTGGTGAACCGGTGCAGGACCACATCCAGAGCCGCATCGTGTAC
TACCTGATGAACATCCACGTGCAGCCCGGTACCATCTACCTGTGCCGGCACGGCGAGAACGAGCACAACTCCAG
GGCCGCATCGGGGGCGACTCAGGCCTGTCCAGCCGGGGCAAGAAGTTTGCCAGTGTCTGTAGCAAGTTCGTGGAG
GAGCAGAACCTGAAGGACCTGCGCGTGTGGACCAGCCAGCTGAAGAGCACCATCCAGACGGCCGAGGCGCTGCGG
CTGCCCTACGAGCAGTGGAGGCGCTCAATGAGATCGACGCGGGCGTCTGTGAGGAGCTGACCTACGAGGAGATC
AGGGACACCTACCCTGAGGAGTATGCGCTGCGGGAGCAGGACAAGTACTATTACCGCTACCCACCGGGAGTCC
TACCAGGACCTGGTCCAGCGCTTGGAGCCAGTGATCATGGAGCTGGAGCGGCAGGAGAATGTGCTGGTCACTGTC
CACCAGGCCGCTCCTGCGCTGCTTGCCTACTTCTGGATAAGAGTGCAGAGGAGATGCCCTACCTGAAATGC
CCTCTTACACCGTCTGAAACTGACGCCTGTGCGTTATAGGCTGCCGTGTGGAATCCATCTACCTGAACGTGGAG
TCCGTCTGCACACACCGGGAGAGTGCAGAGGATGCAAGAAGGGACCTAACCCGCTCATGAGACGCAATAGTGT
ACCCCGCTAGCCAGCCCCGAACCCACCAAAAAGCCTCGCATCAACAGCTTTGAGGAGCATGTGGCCTCCACCTCG
GCCGCCCTGCCAGCTGCCTGCCCGGAGGTGCCACGCAGCTGCCGGACAAAACATGAAAGGCTCCCGGAGC
AGCGCTGACTCCTCCAGGAACACTGAGGCGAGACGTGTGCGTTCCATTCCATTTCCATTTCTGCAGCTTAGCTTG
TGTCTGCCCTCCGCCGAGGCAAAACGTATCCTGAGGACTTCTTCCGAGAGGGTGGGGTGGAGCAGCGGGGA
GCCTTGGCCGAAGAGAACCATGCTTGGCACCGTCTGTGTCCCCTCGGCCGCTGGACACCAGAAAGCCACGTGGGT
CCCTGGCGCTGCCTTTAGCCTGGGGGCCCCACCTCCACTCTCTGGGTTCCTAGGAATGTCCAGCCTCGGAGAC
CTTCAAAAGCCTTGGGAGGGTGATGAGTGCTGGTCTGACAAGAGGCCGCTGGGGACACTGTCCGTTTTGTTT
GTTTCTGTGATCTCCCGGCAGTTTGGAGCTGGGAAGACCACACTGGTGGCAGAATCCTAAATTAAGGAGGCA
GCCTCCTAGTTGCTGAAAGTTAAGGAATGTGTAAACCTCCACGTGACTGTTTGGTGCATCTTGACCTGGGAAGA
CGCCTCATGGGAACGAACCTGGACAGGTGTTGGGTTGACCCCTCTTCTGCAGGAAGTCCCTGAGCTGAGACGCAA
AGTTGGCTGGGTGGTGGTGGCACCTGGCTCCTGCAGGTCCACACACCTTCCAGGCCTGTGGCCTGCCTCCAAA
GATGTGCAAGGGCAGGCTGGCTGCACGGGGAGAGGGAAGTATTTGCCGAAATATGAGAAGTGGGGCCTCCTGCT
CCCAGGGAGCTCCAGGGCCCTCTCTCCTCCACCTGGACTTGGGGGGAACGAGAAACACTTTCTGGAGCTGC
TGGCTTTTGCACTTTTTTGATGGCAGAAGTGTGACCTGAGAGTCCACCTTCTCTTCAGGAACGTAGATGTCGGG
GTGTCTTGCCCTGGGGGGCTTGAACCTCTGAAGGTGGGGAGCGGAACACCTGGCATCCTTCCCCAGCACTTGCA
TTACGGTCCCTGCTCTTCCAAGGTGGGGACAGTGGCCCAAGCAAGGCCTCACACGCAGCCACTTCTTCAAGAGCT
GCCTGCACACTGTCTTGGAGCATCTGCCTTGTGCTGGCACTCTGCCGTGCTTGGGAAGGTGCGTAAGAGTGG
ACTTTGTCTGGGCTTCCCTTCATGGCGTCTAGACACTTTTGTGGTGATGGAAAGCATGGGACCTGTCGTCTCAG
CCTGTTGGTTTTCTCCTCATTGCCTCAAACCTGGGGTAGGTGGAACGGGGGTCTCGTGCCAGATGAAACCATT
TGGAAACTCGGCAGCAGAGTTTGTCCAAATGACCCTTTTTCAGGATGTCTCAAAGCTTGTGCCAAAGGTCACTTTT
CTTTCTGCTTCTGCTGTGAGCCCTGAGATCCTCCTCCAGCTCAAGGGACAGGTCTGGGTGAGGGTGGGAGA
TTTAGACACCTGAAACTGGGCGTGGAGAGAAGAGCCGTTGCTGTTTGTTTTTTGGGAAGAGCTTTTAAAGAAATGC
ATATTTTTTTTACCTGGTTGGAATTGAGTAGGAAGTGAAGCTGTGCTTCAGGTATGGTACAATCAAGTGGGGGATT
TTCATGCTGAACCCATTCAAAGCCCTCCCGTCCCGCATTTCCAGGCCACCCTTGGCTGGCGTCTGCTGGAGA
GGATGTCTCTGTGCATTCCCGTGCAGCTCAGCTCGCGCAGGTTTTCTCTCTCTCCCTGGATGTTGAGCTCTCAT
CAGAATATGTGGGTGGGGGGTGGACGTGCACGGGTGCATGATTGTGCTTAAGTTGGTTGATTTTTTCGATTGAC
ATGGAAGCCTGTTGCTTTGCTCTAGAGAATAGTTTCTCGTGTCCCTTCGCACGCCTCATTCTTTGAACCTCATC
TCTGATGTTTGATACAGATGGGGGCTTGATAGCTGTGGTCCCCTTTCCCTTCTGACTACGTGAAAATCAATACCT

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FIGURE 651B

AAATACAGAAGCCTTGGTCTAAACACCGAGACTTTTAGTTTGCGAAGGGGCTTAGATAGGGAGAGAGGTAACATG
AATCTGGACAGGGGAGGGAGATACTATAGAAAGGAGAACACTGCATACTTTGCAAAGCCAGTGACCTCCTTTTGA
AGGGGACATTGGACGGGGGCGGGGGCGGGGGTTCGGTTTGACTACCGTCATGAACTTTTGGCGTATACTGATT
CTCCAACCTCTCCACCCCAAAAATAACGGGGACCAATATTTTTAACTTTGCCTATTTGTTTTTGGGTGAGTTTCC
CCCCTCCATTATTCTGTCCTGAGACCACGGGCAAAGCTCTTCCATTTTGAGAGAGAAGAAAACTGTTTGAACC
ACACCAATGATATTTTCTTTGTAATACTTGAAATTTATTTTTTTATTATTTTGATAGCAGATGTGCTATTTATT
TATTTAATATATGTATAAGGAGTCCTAAACAATAGAAAGCTGTAGAAGCTGTAGAGATAGGCTTCAGTTGTTAAT
TGGTTTGGAGCCTCCTATGTGTGACTTATGACTCTCTGTGTTCTGTGTATTTGTCTGAATTAATGACCTGGGATA
TAAAGCTATGCTAGCTTTCAAACAGGAGATGCCTTCAGAAAGCTTTGTATATTTTGCAGTTGCCAGACCAATAAA
ATACCTGGTTGAAATACATGGACGAAAAAAAAAAAAAAAAAAAAA

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FIGURE 652

MPLELTQSRVQKIWVPVDHRPSLPRSCGPKLTNSPTVIVMVGLPARGKTYISKKLTRYLNWIGVPTKVFNVGEYR
REAVKQYSSYNFFRPDNEEAMKVRKQCALAALRDVKSYLEGGQIAVFDAATNTTRERRHMILHFAKENDFKAFF
IESVCDDPTVVASNIMEVKISSPDYKDCNSAEAMDDFMKRISCYEASYQPLDPDKCDRDLSLIKVIDVGRRLVN
RVQDHIQSRIVYYLMNIHVQPRTIYLCRHGENEHNLOGRIGGDSGLSSRGKKFASALSKEVEQNLDLRVWTSQ
LKSTIQTAELRLPYEQWKALNEIDAGVCEELTYEEIRDTYPEEYALREQDKYYRYPTGESYQDLVQRLEPVM
ELERQENVLVICHQAVLRCLLAYFLDKSAEEMPYLKCPHVLKLTVPVAYGCRVESIYLNVESVCTHRERSEDAK
KGNPPLMRNSVTPLASPEPTKKPRINSFEEHVASTSAALPSCPPEVPTQLPGQNMKGSRSSADSSRKH

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FIGURE 653

AGTCGCTGTTTGGGACGCTGGGTGTGCGGTGTTCTGTCTCCGCTCCCGTTTTCGCTGTCACAGCCGTTCCCTTCCC
GGAGCCCCGGGACAGGCTGGGCGCGCGCCCGTGTGAGTGAGCGGGACTCAGGGCAGAAGTGTCCCTCACTGCGTT
TTTTTTTCTTTTATCCAAAGAACGGGGCAGTTAGTAGCCTTGCCCTTCTGTGCCCCGGTTGGGAGCGGGGTGG
TGTGCGGAGTGGTTGCGCTTTTTTTCTTTAGAACTGTGAGCCTTTTTTTTTTTTTTTTTTTCTTTCTTTTTTT
AGGCTCAGTGCTGTCCGGGCTGGTTTGCCCGGTCCCTGACTAACGGCTTTCTGCCCTTCTCTGCCACCCCTGC
CCAAGGTCGCCCCCTCTGCCTTCGCCCCGTGCCGGGAGGGTGGGAAGCTTTGACCCCGCCCTGCCACTCGCGTC
TCCGAGCCGTAGCCGCGCCTGTCCCAATATGAATAGGGTCAACGACCCACTTATTTTTATAAGAGATATTAAGC
CCGGACTGAAAACTTAAATGTCGTCTTTATTGTCTGGAGATAGGACGCGTGACCAAACCAAAGACGGCCATG
AAGTGAGATCGTGCAAAGTAGCAGATAAAACGGGCAGCATCACTATTTCCGTGTGGGATGAGATCGGAGGTCTTA
TACAGCCAGGGGATATTATTCCGTTGACCAGAGGGTATGCATCCATGTGGAAAGGATGTCTGACACTTTATACTG
GAAGGGGTGGTGAACCTTCAAAAAATTGGGGATCTAGGTGCGGTGCAGGCAGCCGAATGCGAGATTCCATACACT
ACTACCCTGGTAATGATCTCCACCCTGACCTGGAGGAGCCATCCTCTCTAGGGGTGTAAGATTTTGTATGGTTTA
TTCAGAAGTGCCAAATTTCACTGAACCCAACCCAGATTATCGAGGACAGCAGAACAAGGGGCACAGAGTGAACA
GAAGAATAATTCCATGAATAGTAATATGGGTACAGGTACATTTGGACCAGTGGGAAATGGTGTTCACACTGGCCC
TGAATCAAGGGAACACCAGTTTTACATGCTGGCAGAAGCAATGGCCGGGGACTTATAAATCCACAACATAAAGG
AACAGCTAGTAATCAACAGTGATGACCACAATAAGTAATGGCAGGGACCCTCGGAGAGCCTTTAAAGATGACC
TATGCTAAATACTCATGTGTAGTTTTTATACTACATGCCCTACTTGAACACTTATTGCACTTTATTTATTGTTA
ACTGTGAAAAGTACGTCCTTTATTGGGTTTCCCTTTATATTCTTGGTTTGTAAAGAAGATGGTTTGTTTTTATA
GCAAACTGTTAAGCTGCTCGAGTCTCCTGTTGAAGAATGGGAACACTGAAAAGTAGGGGCATTATTTTTAGAG
TAAAAAGATTATTGGATAGCCTTTAAAAAACCTGCACCCATTTTCATGGGTGAGTTACTTAAGACATCAGCTTTAT
AGCCTCTATGAGTCTATCTTCTGTATAAGTTTTGTAAATATTTAACATAAGGCTTAATGGGAGATGTTCTTTTGTCT
TTGTATTAGATATTGCCAACTAAAGCAATAACCATCAAAAAACACAAGAACTTGTCAATGCTAGCAGTAATTTT
TGAGTGTGTTGTGGCTCTCGGAATGATTGACTTCGTTGAGTGACTACTATTAAGATTTTCCAAGGACTGACTCATC
CCAAATTTTTGTTGTATTACCAAAAAACAGATTTCCTTATCAGAATTTGGAATAGAATGTGATCTCTATTGCAAC
AAGTAATTTTTAAAGAAAGCTACATTTATTTAGAGTAGTGCTCCTAACATGTATTATCAACTTTGTGGATTACA
TTGGAGGAAAATTTAAACTGGGCCTTGAATATTATTTTTTGAACACTACCATGTAAATACTGAAGTATAATT
TGGGGGAGTTATAAAGTTATGATAAACATTCATCTGATTATTTAAACAATAGTTGTGGTAGATAAACATACTGG
AGGTGAGTAAATTTGAATTCATATAGTAACATGCAGTCTGAAGTCTAGTTACTTAATAGGTACTCAGCCTGGAG
TGAAATCCTGGGTACTGACTTTGAGAGGAGTGAGTGTGCATGTTGTCAAAGTTTCTGAACACAGTTTCACATAGC
CTTATTAGCAAAAGTTTTAAGAAATGGCTCTATCAAGAAGCAATTGCAGCTTTATTAGAAAATATAAAGTGGA
ATTTATGTACATGTATAAGTGGTACCCACTTCCCCTTTTTACTGTAGGGTGGATAACTCTTAGGATTTAACTCT
TTGAATATTATCTCTTGAATAAAGCATGTGTTAATGTTAACAAACCTACGTAATTTTTGCCCTTTCAATGACTTA
CAGTGGAGAGCCAGTACATCTTAAGTACTGTTGTAGTGATGGTATCAACCTCATGGTTACTTAGCTCTGCATTTG
TTGCTTTGTTTTTTTTTCCACTTCAAATCACAAAATAAGTAGATTTTGTCTTCTGAAAACCTCATAGCATTTGAAT
ACAAAAAGTTGTGCCAGATTGTTGCCCTAATTCAGTGTGTTTAAACAATATTTAGTACACACTATGTATTAGG
CACTGTGTGGAAGTGTAAAGGGGTAGACAAGATACCGAATAATCTCCACAAGTTTATTTGTGGTCTATAGTACT
TTTGTAAGTGGGGTTACAAAAATTATAGAAATTTTTCTCTTTGTTTCATATGCATATTCATGATTATAATTTGGC
TTTGTGTTGTGATTAATGTTTTCTTAAGATTTTCACATTATAGAATACCTCAAAAGAAGTTGTCTAAGGACTGGGA
TAGAGAGTATGTTTCATAAAATTGTAGATGTTTAGAATTTTTAAAAACCCTACAAATTAGTATATGATTGTTTTA
TATAAGTAAGATAGGAGCAACACTTTAAATTATTTGTGGGAGAATACAGCATTAAAGGTGATTTTAAAGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 654

MNRVNDPLIFIRDIKPGLKLNLVFIVLEIGRVTKTKDGHEVRSCKVADKTGSITISVWDEIGGLIQPGDIIRLT
RGYASMWKGCLTLYTGRGGELQKIGDLGAVQAAAMRDSIHYYPGNDLHPDLEEPSSLGV

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FIGURE 655

CCATCTCAAAACAACAAAAACAACAAAAAACACATGCCTGGCGGAGAACAAAGAGATCATTTAGTCCAATCTC
TTCATGGAGATGAGGGCTCCTGGGAGCCCCCTCTTCATGTCTCAGGTTCTTAGTTGACTATGTTTATCCAAATGAT
TCCAGATTCTGTGGAAACAAGGAATCGATGTACAAATGGGGTAGGGTGGCAAGGAAAACCTCTTAAGAGAGAAAC
ATCAAGGTTTTACATTAGGTTAAAGACAAGAAGGTTTCTAGGCAGGTAGTGTAAATGTCTAGGTGATTTTGAAGT
GAACTTAAGCCACTAGGTTTGAGGGACAAAGGACAGTAGAAAATGGTGAAGACTGCAGATCACCTGCTATACCTC
AAGGAGCAGCGGACCCAGCAGAATATGGCCAAAAAGGAGGCAGGTCTCCTGTTGCAAGAGCCTCTGTTTTTTTA
AAGAGAAAACAAGAATCCTGGTTTTATGTGAAATCTCTAATTTTAAAATAATAACTCATTAAAAATATTGTAA
TGTCAAAAGTATCTTTCCATTAACTTCTAAAAATCTCTTAAATGTTTTTTTTTAAATAATTGTAAAGTGAGTTT
TTGTTAAGCTTATAGGAATGGGCCAGTTAACTAAGGTAGACAGATGTAGGAAATTAAATATTGATTTACTTAGG
GATCTATATGACATCAGTTATCAAAGAATACATTTTAAACCCAAAAGTATACCATGCTCATTGTATCTTTGATCGT
TCTTCAAGTATTTCTCAATCTTTTTAATCTATCAGGAACATTACTATCAAGAGCAGATTGTTGTAACATAATACTC
AGGATACATGAAATGTATGTGAGAGATAAATAGATAATAGAAAGTTTTATTGTTATAAAAAATGACCTACAACCTTAT
ATAAAAAAATTCTGAAATGTTGACTTTTTTTGGACTGAAGGCTGCAAAATAAATGGCTTCTCAAAGTAAATTCC
TATTTACTTAAATTGCCTTCTTGATTGTTACACCTGGAAAAATATATTCATCTACTTTTTCTTTTAAATTATGTT
AGTAGACTGAATTAACCAGCTACATAGACACTCTCTCATTGAAGCTGTTGGGATCCTTGAGTTGCCTCTTTCA
TTGGTACGTTTTATCCATTGTCACAACTGTGGTCTTCATTAATAACTCATTTTAATGTCTTAGGAGTAGAATGTG
TTTCCTATTTTTTTTCAAATAAGAGTCAGTTAATTTGAAATGGCAAATTATTTACCTGAATGTGTATCATTGTT
CATTGCAAGGTTTAAAGCTCAGGCAGATCCAATAATTAGGTAAAGGTTGCATCTTTGGTCCTCTGCACATTTTT
TCTGGTAATCAAATCTGAAGCGACATCTCAGCAAGCAGACTTGGGTATTTTTCCACTAGGATGGGAATGGAAAAC
AGTGCTGGGAGACTGGGAAGTGGCTATTTCTGTGTCTCACTGGGGAATTGCAAGATCAAAGAATGTTGTTACTTT
TATGTGATGAAAAAATAGGGCAAGAAAGATATACCTGAATCATCAGACTGCTTAAATTTGGGAGGAAAAAATTC
TATTTTACTACTAACCATAAATCACTTTTGCTAGATAGTACTTTAAAGATTCTGAATTAATGTATCTTTAAAAA
CAACAATATAATATTACTAAAAATGCAGACATACTTAACTTGCTAGAATAAATTCTGTGAGGTCTTCGTTTGG
TATTTTCATAGGATTTCTTACTGTTAAGTTATTGGAAAATGAAAATATAAAGTGCTTTCAGAAGTTATAGTATTT
TCCAATTCATTGAATTACTTTGCTTGTGAAAATATATTAACATATTTAAATGAGACCTATCCTACATTTAAAAA
CCAGTTTTGTTTATATAAAATTGTATTTGAAAGGTCCTGAACATTAAAAATGTGAAAATTTATAATGTTGATGAT
CAAAAGTAACGTGTTGAGACTCTGAGCTTAATCCATTAAATGGATTTTAGAATCTAGTAGAAGTTA

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FIGURE 656

ISKQQKQQKNHMPGGEQRDHLVQSLHGDEGSWEPLFMSQVLS

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FIGURE 657

GGGGCGGCCCTGGCCAGAAGCGGAGGAGGTGGCACCCGGGACCGAGCTGGGGTCTTGGAGGAAGAGAGGATGGCG
TCGTCGAGCCCTGACTCCCCATGTTCTGCGACTGCTTTGTCTCCGTGCCCCGGCCTCAGCCATCCCGGCTGTG
ATCTTTGCCAAGAACTCGGACCGACCCCGGGACGAGGTGCAGGAGGTGGTGTGTTGTCCCCGACGGCACTCACACT
CCTGGGAGCCGGCTCCAGTGCACCTACATTGAAGTGAACAGGTGTGCAAGACGCACGCTGTGATTCTGAGCCGT
CCTTCTTGGCTATGGGGGGCTGAGATGGGCGCCAACGAGCATGGTGTCTGCATTGGCAACGAGGCTGTGTGGACG
AAGGAGCCAGTTGGGGAGGGGGAAGCCCTGCTGGGCATGGACCTACTCAGGCTGGCTTTGGAACGGAGCAGCTCT
GCCCAGGAGGCCTTGATGTGATCACAGGTTACTGGAGCACTATGGGCAGGGGGGCAACTGCCTGGAGGATGCT
GCGCCATTCTCCTACCATAGCACCTTCTGCTGGCTGACCGCACTGAGGCGTGGGTGCTGGAGACAGCTGGGAGG
CTCTGGGCTGCACAGAGGATCCAGGAGGGGGCCGCAACATCTCCAACCAGCTGAGCATTGGCACGGACATCTCG
GCCCCAACACCCGGAGCTGCGGACTCATGCCCAGGCCAAGGGCTGGTGGGATGGGCAGGGTGCCTTTGACTTTGCT
CAGATCTTCTCCCTGACCCAGCAGCCTGTGCGCATGGAGGCTGCCAAGGCCCGCTTCCAGGCAGGGCGGGAGCTG
CTGCGGCAACGGCAAGGGGGCATCACGGCAGAGGTGATGATGGGCATCCTCAGAGACAAGGAGAGTGGTATCTGT
ATGGACTCGGGAGGCTTTTCGCACCACGGCCAGCATGGTGTCTGTCTGCCCCAGGATCCACGCAGCCCTGCGTG
CACTTTTCTTACCGCCACGCCAGACCCATCCAGGTCTGTGTTCAAACCTTTTCATCTTCGGGTGGGGGTGGCCAG
GCCCCCAGGTGCTGTCCCCACTTTTGGAGCACAAGACCCTGTTTCGGACCCTGCCCCGATTCCAGACTCAGGTA
GATCGTCGGCATACCCTCTACCGTGGACACCAGGCAGCCCTGGGGCTGATGGAGAGAGATCAGGTATCCCCAGG
GAGTAGGGGCTACCTTGAGGGGATGATAGACCTCCCCACTCCAGTGGGACTCTGGAAATATGAAGGAAGTAGG
GAGTGGAAGAGATTTAGAGCTGGGGAGAGGAGTTCTCCCTTCAAAGCCAGCAACTGCCTTTGGGGAATGTGCG
GGGGTCTCTCCTTTCTCCTGCTTGTGTGAGGTGGTACACAGTCCCCCTTACCTGGCGGGAAGCCTGTCCCGGA
CAGACTCATCTCAGCTTTCCCTTGGGGCAGGATCGGGGGCAGCAGCTCCAGCAGAAACAGCAGGATCTGGAGCAG
GAAGGCCTCGAGGCCACACAGGGGCTGCTGGCCGGCGAGTGGGCCCCACCCCTCTGGGAGCTGGGCAGCCTCTTC
CAGGCCTTCGTGAAGAGGGAGAGCCAGGCTTATGCGTAAGCTTCATAGCTTCTGCTGGCCTGGGGTGGACCCAGG
ACCCCTGGGGCCTGGGTGCCCTGAGTGGTGGTAAAGTGGAGCAATCCCTTACGCTCCTTGGCCATGTTCTGAGC
GGCCAGCTTGGCCTTTCCTTAATAAATGTGCTTTATTTTCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 658

GAALARSGGGGTRDRAGVLEEERMASSSPDSPCSCDCFVSVPFASAIPAVIFAKNSDRPRDEVQEVVFPAGTHT
PGSRLQCTYIEVEQVSKTHAVILSRPSWLWGAEMGANEHGVCIGNEAVWTKEPVGEGEALLGMDLLRLALERSSS
AQEALHVITGLLEHYGQGGNCLEDAAPFSYHSTFLLADRTEAWVLETAGRLWAAQRIQEGARNISNQLSIGTDIS
AQHPELRTHAQAKGWWDGQGAFFAQIFSLTQQPVRMEAAKARFQAGRELLRQRQGGITAEVMMGILRDKESGIC
MDSGGFRTTASMVSVLPQDPTQPCVHFLTATPDPSRSVFKPFFIGVGVAQAPQVLSPTFGAQDPVRTLPRFQTQV
DRRHTLYRGHQAALGLMERDQVSPRE

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FIGURE 659

GCGGCCGCGCGGCTCCCGGGCGGGCCTACAGCCATGTCCCGGGACCCGGGGTCGGGCGGCTGGGAGGAGGCCCC
GCGCGCAGCTGCCGCGCTCTGCACCCTGTACCACGAGGCCGGACAGCGGCTGCGCCGCTGCAGGACCAGCTCGC
TGCCCGCGACGCCCTCATCGCTCGCCTCCGCGCCCGCCTGGCCGCGCTGGAGGGGGACGCCGCGCCGAGGCCCA
GGACGCGCTGCTGGAGCAGGTTGCGCGCTTCCGGGAGCAGCTGCGAAGGCAGGAGGGCGGCGCCGAGGCCCA
GATGCGCCAGGAAATTGAGAGGCTGACTGAGCGACTAGAAGAAAAAGAGAGGGAGATGCAGCAGCTGCTGAGCCA
GCCCCAACACGAGCGAGAGAAGGAAGTCGTCTGTACGGAGGAGCATGGCAGAAGGGGAGCGCGCCCGGGCCGC
CAGTGACGTCCTGTGCCGCTCCTTGGCCAACGAGACCCATCATCTGCGGAGGACGCTGACCGCCACCGCCACAT
GTGTCAGCATCTGGCCAAGTGTCTGGATGAACGACAGCATGCACAAAGGAATGTGGGGGAGAGAAGTCCTGACCA
GTCGGAACACACAGATGGGCACACCTCTGTCCAGAGTGTATTGAGAAGTTGCAGGAAGAAAATCGACTGTTAAA
ACAGAAGGTGACTCACGTTGAAGACCTCAATGCCAAGTGGCAGCGCTACAACGCCAGCAGGGACGAATACGTGAG
GGGGCTCCATGCGCAGCTCAGGGGGCTGCAGATCCCCACGAGCCGAGCTGATGAGGAAGGAGATCTCCCGGCT
CAACAGACAGTTGGAAGAGAAAATAAATGACTGTGCCGAAGTGAAGCAGGAGCTGGCGGCCCTCAGGACGGCCCCG
GGATGCTGCGTTGGAGCGGGTGCAGATGCTGGAACAGCAGATTCTCGCTTACAAGGATGACTTCATGTCAGAAAG
GGCCGATCGGGAACGGGCTCAAAGTAGGATTCAAGAACTGGAGGAAAAGGTCGCCTCTTTGCTGCACCAGGTGTC
CTGGAGACAGGATTCTCGAGAGCCAGACGCCGGCCGATTACGCTGGGAGCAAACTGCCAAGTATTTGGCCGC
CGACGCATTAGAGCTTATGGTGCCTGGTGGCTGGAGGCCTGGGACTGGGTCCCAGCAGCCAGAACCCCTGCAGA
GGGCGGGCATCCTGGCGCGGCCAGAGAGCCAGGGGGACCTTCAGTGCCCTCACTGCCTGCAGTGCTTCAGTGA
CGAGCAAGGGGAAGAGCTCCTCAGGCATGTGGCCGAGTGCTGCCAGTGAACCGAGACTACCCGTGCCCTTGCGGC
CTCCTGGCCCGGTGCAGCTGCCCTCAGGGACAGGGTGGGTGCTCTCAGATGCCATGGGTTGAGCTCTACTGAGAG
CCAAGGCCCCCTAGAATAGTTGCGGGGCACTCTGATCGTTCACTTTGGTCCCTTTGGCTATGGAACAGGCTGGGT
ACAGGGAAGTGCAGTGAGGCTGGAGGCTGGAGGTGGAGATGGGGTCAGGAACATCTGGCAGAGGGAGGTCCAG
TCTGTGTCTCCATCAGGCTTAAGCCAGAGCTATCTGGTGCTGGTGTGCCAGCCCCCTCCCCAGCCTGCCTAGAAA
GGGGTGGCTGCCTGAGGGAGTCACTTGATGGTCCCCAGGGTGGGAGCCCCATCCTGTTCTATGGAATAAAGCGT
CGCCTCTCTGCCTCGAACCAGTCAAATGGAGTATTGCGGCTGCACGTACACTAGGGTGGCCACCCCCGCCATTG
CGAGCCACATGTCTGC

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FIGURE 660

MSRDPGSGGWEEAPRAAAALCTLYHEAGQRLRRLQDQLAARDALIARLRARLAALLEGDAAPSLVDALLEQVARFR
EQLRREQEGGAAEAQMRQEIETRLTERLEEKEREMQQLSQPQHEREKEVVLLRRSMAEGERARAASDVLCSRSLANE
THHLRRTL TATAHMCQHLAKCLDERQHAQRNVGERSPDQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLNA
KWQRYNASRDEYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEEKINDCAEVKQELAASRTARDAALERVQMLE
QQILAYKDDFMSEERADREERAQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLAADALELMVPGGW
RPGTGSQQPEPPAEGGHPGAAQRGQDLQCPHCLQCFSDQGEELLRHVAECCQ

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FIGURE 661

CCTGTTTCTTAATGGCTCTTTTTCAAAGGTTAATGTAAGCTTTTTGGAAATTCACATTGTCTTCCTGACAGTTAT
AGGGCAAAGTAGTATCTACACCCTGGGAACACCTAGCACATCTGTTCTTAGAAGCCCTTAGCAGTTGTTTCATGAG
CTTTGATTTTTAAAAAACTCCTTTGGCCTTGCTTTTGATGCCTTGATGTGTTTTTTTCATCACCTTTGGTTATAT
CAGTAAGCATTGAAGCACCCCTCTCTGCTGGTACTTGGTGTCTTAGCCTGAAGCTCCCTTTGACGTTCCCTGGAGG
TGGAAGCACTCTTTTTATTTTGAATGTACCATTTTGTTTTGCTTTGATGGCATTGCGGCTGGAATATAGACC
CTCTATTGGCACCGGTAGCCTTTATGTGCCTACGAGGCTCAAAGCCCTGCCTGTGCCCACCGGGCCTGTCTCATA
CCAGGAGGCTATTTCTCTGTCTGTCTGGGGAAGCCACAGAACCAGTGCAAAGGAGTTGAGGGGTAGTTTTTTAT
TGTTGCTGTTGTTGGGTGCCCTTCTCAATCATTGCCTTTCTAGATTAGCCATCTGGATCACCTTTCTTCCTAAAA
TGTGAAAAGGCCACACCCCTATGCATTTTATTGTTCCCAAGTATTATATGTTTGTGTCATATATCATATGTATA
TATTCACATATATATATGTTTTTTTTTAACC

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FIGURE 662

MSPFCFCFDGIWAWNIDPLLAPVAFMCLRGSKPCLCPPGLSHTRRLFCLSWGSHRTSAKELRGSFLLLLLLGAL
LNHCLSR

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FIGURE 663

GTCCATGGGGAAGCTGCCATTTTCTTGAAAAAGCCAGAATTGCACAGAAAAGGAGGTGCTGAAGCAATGTTAGTTG
TCAATAACAGTGTCCATTTTCCCTCCCTCAGGTGACAGATCTGAATTTCCCTGATGTGAAAATACTGATTGCATTTA
TAAGCTACAAAGACTTTAGAGATATGAACCAGACTCTAGGAGATAACATTACTGTGAAAATGTATTCTCCATCGT
GGCCTAACTTTGATTATACTATGGTGGTTATTTTTGTAATTGCGGTGTTCACTGTGGCATTAGGTGGATACTGGA
GTGGACTAGTTGAATTGGAAAACCTTGAAAGCAGTGACAACCTGAAGATAGAGAAATGAGGAAAAAGAAGGAAGAAT
ATTTAACTTTTAGTCCTCTTACAGTTGTAATATTTGTGGTCATCTGCTGTGTTATGATGGTCTTACTTTATTCT
TCTACAAATGGTTGGTTTATGTTATGATAGCAATTTTCTGCATAGCATCAGCAATGAGTCTGTACAACCTGTCTTG
CTGCACTAATTCATAAGATACCATATGGACAATGCACGATTGCATGTGCTGGCAAAAACATGGAAGTGAGACTTA
TTTTTCTCTCCGGACTGTGCATAGCAGTAGCTGTTGTTTGGGCTGTGTTTCGAAATGAAGACAGGTGGGCTTGGA
TTTTACAGGATATCTTGGGGATTGCTTTCTGTCTGAATTTAATTAACCACTGAAGTTGCCCAACTTCAAGTCAT
GTGTGATACTTCTAGGCCTTCTCCTCCTCTATGATGTATTTTTTGTTCATAACACCATTTCACAAAAGAATG
GTGAGAGTATCATGGTTGAACTCGCAGCTGGACCTTTTGGAATAATGAAAAGTTGCCAGTAGTCATCAGAGTAC
CAAACTGATCTATTTCTCAGTAATGAGTGTGTGCCTCATGCCTGTTTCAATATTGGGTTTTGGAGACATTATTG
TACCAGGCCTGCTGATTGCATACTGTAGAAGATTTGATGTTTCAGACTGGTTCTTCTTACATATACTATGTTTGT
CTACAGTTGCCTATGCTATTGGCATGATACTTACATTTGTTGTTCTGGTGCTGATGAAAAGGGGCAACCTGCTC
TCCTCTATTTAGTACCTTGCACACTTATTACTGCCTCAGTTGTTGCCTGGAGACGTAAGGAAATGAAAAAGTTCT
GGAAAGGTAACAGCTATCAGATGATGGACCATTGGATTGTGCAACAAATGAAGAAAACCTGAGATATCTGGTG
AACAGATTGTCCAGCAATTAATATTATGTGGAACCTGCTATAATGTGTGTCATTGATTTTCTACAAATAGACTTCGACT
TTTTAAATTGACTTTTGAATTGACAATCTGAAAGAGTCTTCAATGATATGCTTGCAAAAATATATTTTATGAGC
TGGTACTGACAGTTACATCATAAATACTAAAACGCTTGTCTTTAATGTTAAAGTTGTGCCTTCACATTAAATA
AAACATATGGTCTGTGTAGTTTCCGAGATGTACTATATACAGTATATTTTTCT

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FIGURE 664

MLVVNNSVLFPPSGDRSEFPDVKILIAFISYKDFRDMNQTLDNITVKMYSWPNFDTMVFVIAVFTVALG
GYWSGLVELENLKAVTTEDREMRKKKEEYLTFSPLTVVIFVVICVMMVLLYFFYKWL VYVMIAIFCIASAMSLY
NCLAALIHKIPYGQCTIACRGKNMEVRLIFLSGLCIAVAVVWAVFRNEDRWAWILQDILGIAFCLNLIKTLKLPN
FKSCVILLGLLLLYDVFFVFITPFITKNGESIMVELAAGPFGNNEKLPVIRVPKLIYFSVMSVCLMPVSILGFG
DIIVPGLLIAYCRRFDVQTGSSYIYYVSSTVAYAIGMILTFVVLVLMKKGPALLYLVPCTLITASVVAWRRKEM
KKFWKGSYQMDHLDCATNEENPEISGEQIVQQ

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FIGURE 665

ATATTCCCATCTGATTCCACTATGAGCAGTNCCATGCATGCCCTACTAGAACTGTGGATACGCTTTAAACAAG
TGGAAGATGATAGGGTGGGACTCATTACGTCTAATCTTGGGGAACACTGATAACGTGTCCAGGAGAGACAGCACA
AGGGGCTCCATCTTCATCACACAACATCATCGCATGCTTCCAGAGATATTCTGGCGCTGCCACCTAGAGGAAGTA
TTTTGGAAGGTTGAGCAAGCATTGTGAAAGTCCGGAGGCAACAGTCCAAATGCCACCATAGAACGAGTGTCCATG
ACAAGATATTTCTACCTCTTTCCTGGCAACTGAAAATGGTTAAGCATTGAGAGTTGTTGGTGGTGTATGAAATAA
ATGAAAGTGTGATATTGGAGGAAACCACAAGCAGCCAGCCCTCCTTTATCAACTTCAAGAAACACCTTTACTAG
TACAGATTGAATGCTTAACATTTTGTATTTCAATAAAGGTGAAGACAAATG

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FIGURE 666

MIGWDSLRLILGNTDNVSRRDSTRGSIFITQLIACFQRYSWRCHLEEVFWKVQQAFESPEATVQMPTIERVSMTR
YFYLFPGN

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FIGURE 667

TTGATGCTTCGCTTTCTGGGTGAAAAAGCTGCAGCAAAGAGACAAGTCCTAAATGCCGACTCAGTGGAACAATCT
TTTGTGGATTGAAACAGCTAATCAGCTGCAGAAACTGGAGGGCAGCAGTGACCTGTGCGGACGTCTCCTCACA
GCCCACGGCCAGGGCTACGGCAAGAGCGGGCTGCTCACCAGCCACACGACAGATTCACTGCAGCTCTGGTTTGTC
AGGCTGGCACTACTAGTGAAGTTGGGCCTTTTCCAGAATGCTGAGATGGAATTTGAGCCCGTCGGAAATCTTGAT
CAGCCAGATCTTTATTACGAGTACTACCCGCACGTGTACCCTGGGCGCAGGGGCTCCATGGTCCCCTTCTCGATG
CGCATCTTGACGCGGATTTGCAGCAGTACCTGGGGAACCCACAGGAGTCGCTGGATAGACTGCACAAGGTGAAG
ACTGTCTGCAGCAAGATCCTGGCCAATTTGGAGCAAGGCTTAGCAGAAGACGGCGGCATGAGCAGCGTGACTCAG
GAGGGCAGACAAGCCTCTATCCGGCTGTGGAGGTCACGTCTGGGCCGGGTGATGTACTCCATGGCAAACCTGTCTG
CTCCTGATGAAGGATTATGTGCTGGCCGTGGAGGCGTATCATTGGTTATCAAGTATTACCCAGAGCAAGAGCCC
CAGCTGCTCAGCGGCATCGGCCGGATTTCCCTCCAGATTGGAGACATAAAAAACAGCTGAAAAGTATTTTCAAGAC
GTTGAGAAAAGTAACACAGAAATTAGATGGACTACAGGGTAAAAATCATGGTTTTGATGAACAGCGCGTTCCTTCAC
CTCGGGCAGAATAACTTTGCAGAAGCCCACAGGTTCTTCACAGAGATCTTAAGGATGGATCCAAGAAACGCAGTG
GCCAACAAACAACGCTGCCGTGTGTCTGCTCTACCTGGGCAAGCTCAAGGACTCCCTGCGGCAGCTGGAGGCCATG
GTCCAGCAGGACCCAGGCACTACCTGCACGAGAGCGTGCTCTTCAACCTGACCACCATGTACGAGCTGGAGTCC
TCACGGAGCATGCAGAAGAAACAGGCCCTGCTGGAGGCTGTGCGCCGCAAGGAGGGGGACAGCTTCAACACACAG
TGCCCTCAAGCTGGCCTAGCTGCCTCCAACACACTACGTGAGAAGGACCCGGGTCTTTGAACTGTGTCTTGAAGC
TAATGTATTAATGTGACATGGAGGAACCTCAATAAACTCCTGCTTCACTGGTGAAAAA

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FIGURE 668

MLRFLGEKAAAKRQVLNADSVESFVGLKQLISCRNWRAAVDLCGRLLTAHGQGYGKSGLLTSHTTDSLQLWFVR
LALLVKLGLFQNAEMEFEPVGNLDQPDLYEYYPHVYPGRRGSMVPPFSMRILHADLQQYLGNPQESLDRHKKVT
VCSKILANLEQGLAEDGGMSSVTQEGRQASIRLWRSRLGRVMYSMANCLLLMKDYVLAVEAYHSVIKYYPEQEPQ
LLSGIGRISLQIGDIKTAEKYFQDVEKVTQKLDGLQKIMVLMNSAFLHLGQNNFAEAHRFFTEILRMDPRNAVA
NNNAAVCLLYLGKLDKSLRQLEAMVQQDPRHYLHESVLFNLTMYELESSRSMQKKQALLEAVAGKEGDSFNTQC
LKLA

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FIGURE 669

AATGGAGGAAGACTGGACCTACTGATTCAACTTGGAGATGAGCGGGTCTGTCCTCTTCACGGCGGGAGAGAGGTG
GAGATGCTTTCTGACCCCGTTCGAGGTCATCCCTGTACTGGGCCTTACATAATTTCTGCTGTCGGAAAAATCCAC
TACACCTAAGAAAAATTACTCCCAATGTTACTTTTTGTGATGAAAAATGCAAAGGAGCCCGAAAATGCACCTTGACAA
GCTCTTCTCTTCAGAACAGCAGGCTTCCATCTTGCATGTGTTGAATACAGCATCTACTAAAGAACTTGAAGCTTT
CCGATTGCTTCGTGGAAGAAGGTCCATCAATATCGTAGAGCACAGAGAAAACCTTTGGGCCATTTTCAAGATTTTAGA
GAGTTTAAATGAATGTGCCCTTGTTTAAGTATAAAAAGTACAGTTCAAGTTTGTAACCTCATACTTTGTCCAAAGAC
TGGACGGGAAAAAAGAAAGTCACCGGAAAACCGGTTCTTGAGAAAGCTCCTCAAACCAGACATAGAAAGAGAAAG
ACTTAAGAATTGCCTGGGCTCACCTTGATCGTAAGTTGACAGTGCTGGACTGGCAGCAAAGTGACCGTTGGAGTT
TAATGAGAGGAATATACTCATCATCAGTCTATTTAGAAGAGATTTCTCGATCATTTCAAAGATGCCTAAAGCAG
ATTTCTATGTTCTGGAAAAACAGGACTATCCATTCAGAACTCATCTCTGTTTCCAATACTGTTACATTTTCATA
TCATGGAAGCCATGCTGTATGCCTTATTAATAAAACTTTTGCCAGGATGGGCAGCATCAGGTGCTGAGCATGA
ATCGAAATGCAGTGGGGAAGCATTTTGAAGTATGATTGGTGACTCCCGGACTAGTGGAAAAGAGCTAGTGAAGC
AGTTTCTCTTCGATTCTATACTGAAGGCGGATCCTCGGGTGTCTTCCCATCAGATAAAATAGTTCACTACAGAC
AGATGTTTTTATCTACTGAAGTACAAAGAGTAGAAGAGCTTTATGATTCAATTATTACAAGCTATTGCCTTCTATG
AATTAGCAGTGTGTTGACTCTCAGCCTTAGAATTCTGAGGTTAACGTGCTAAAGTATAATTATTAGCTTAACGTA
ACACCAACTGTTGTGAACATCCATGTTATTGGAAAAGAACACATTTTCAGTGTATTTTAGATGTTTAAATTCTGA
CTTTTGGCTATTAAATGGTTTACACAATAAGCCAAGACCAATCAATAAACATTTTATGAGAAAAAAAAAAAAAA
AAA

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FIGURE 670

MRGIYSSSVYLEEISSIISKMPKADFYVLEKTGLSIQNSSLFPILLHFHIMEAMLYALLNKTF AQDGOHQVLSMN
RNAVGKHFELMIGDSRTSGKELVKQFLFDSILKADPRVFFPSDKIVHYRQMFLSTELQRVEELYDSSLQAIAFYE
LAVFDSQP

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FIGURE 671

CCTTCCGGTCGTAAACGCCCACGGGCTCGCGCGGCGCCGCTCCTGGGCTCAGTTACCGCGGACGCCAGTGCCGG
GCTCCAGGAGACGCAGGGCGACGCCACACGCCGGGTGGCCGACTGGGTCAGCGCGGGCTGCGCTCCTCGCCAT
GGGCCCCCTCTCGGCGCGGCTGCTAATGCAGCGCGGGCGCCCCAAGAGCGACCGGCTGGGGAAGATCCGGAGTCT
GGACCTGTGTCAGGATTGGAGCTGCTTTCCGAGCACCTGGACCCCCAACTCCTGTGCGCGCTGACGCACTGTCAGGA
GCTTGACCTGTCTAACAACCACCTGGAGACGCTGCCGACAACCTGGGCCTGTCCACCTGCGTGTCTCCGCTG
CGCCAACAACCAGCTGGGGGATGTTACTGCCTTGTGCCAGTTCCCCAAGCTCGAGGAACCTCAGCCTGGAGGGCAA
CCCCCTCCTGACGGTCAATGACAACCTGAAAGTCTCCTTTCTCCTGCCCACGCTCCGTAAGGTCAATGGCAAGGA
TGCGTCTCAACTTACTCTCAGGTGGAGAACCTGAATCGGGAGCTGACCAGCAGGGTCACAGCTCACTGGGAGAA
GTTTCATGGCCACACTGGGTCTGAAGAGGAGGCTGAGAAGGCCCCAGGCGGACTTTGTGAAGTCGGCTGTCAGGGA
TGTCGCTACGGGCCCCGAGTCCCTCAGCGAGTTCAACAGTGGCGGGTGCGGATGATCTCTGAGGAGCTGGTGGC
CGCCAGTAGGACCCAGGTGCAAAAGGCTAACAGCCAGAGAAGCCCCAGAAGCTGGAGCTGCCACAAGCCAG
GGCCAGACTGGCGGCCTTGAAACGGCCAGACGACGTCCCACTCAGCCTCTCTCCAGCAAGCGGGCGTGTGCCTC
CCCGTCGGCCAGGTGGAGGGCAGCCCTGTGGCAGGCTCCGATGGCAGCCAGCCTGCTGTGAAGCTGGAGCCCCCT
GCACTTCTGTCAGTGCCACAGCAAGAACAACAGCCCCAGGACCTCGAGACCCAGCTGTGGGCCCTGTGCCTTCGA
GCCGGCCTGGGAGGAGGGGGCCACATCCAGACCGTGCCACGTGCGGCGGGGAGGCTGTGTGCGTAATTGATTG
CCAGACGGGCATCGTGCTCCACAAGTACAAGGCACCCGGCGAGGAGTTCTTTTCTGTGGCCTGGACCGCTCTGAT
GGTGGTCACACAGGCTGGCCACAAGAAGCGCTGGAGTGTGCTGGCGGCTGCAGGCCTACGGGGCCTGGTCCGGCT
GCTGCACGTGCGTGCCGGCTTCTGCTGCGGGGTCA TCCGAGCCCACAAGAAGGCCATCGCCACCCTGTGCTTCAG
CCCCGCCCACGAGACCCATCTCTTCACGGCCTCCTATGACAAGCGGATCATCCTCTGGGACATCGGGGTGCCCAA
CCAGGACTACGAATTCCAGGCCAGCCAGCTGCTCACTGGACACCACCTCTATCCCCCTGCGCCTCTGCCCTGT
CGCCTCCTGCCCCGACGCCCGCTGTGGCCGGCTGCGAGGGCGGCTGCTGCTGCTGGGACGTGCGGCTGGACCA
GCCCCAAAAGAGGAGGGTGTGTGAAGTGAATTCGTCTTCTCTGAGGGCTCCGAGGCATCTGGACGGAGAGTGGA
TGGGCTGGCATTGTGAATGAGGACATCGTGGCCTCCAAGGGGAGCGGCCTGGGCACCATCTGCCTGTGGAGCTG
GAGGCAGACGTGGGGGGGGCGGGGCAGCCAGTCCACAGTGGCAGTGGTGGTCTGGCGCGGCTGCAATGGTCTCTC
CACCGAGTTGGCCTACTTCTCGCTCAGCGCTGCCCTGATAAGGGGATTGTGCTCTGTGGGGATGAGGAGGGCAA
CGTGTGGCTCTACGACGTGACGAACATCTGAAGCAGCCACCCCTGCTGCCGGCAGCCCTGCAGGCCCCCACACA
GATCCTGAAGTGGCCCCAGCCCTGGGCCCTTGCCAGGTGGTGACCAAGACCATGGTGAACACAGTGGTGGCCAA
TGCCCTCCTTACCTACCTACCGCCCTGACGGAATCCAACATCGTAGCCATCTGGGGGAGGATGTAGCCTCACAC
CATCGCAAAGGACCAGGGACACAGCTAACTAACTTATTAGCTTTGGGCCGATGGGGGTGGGGGGGGTCTTTTTCAG
TGAATATTTTTATTAACTCTACTGTGGACAAGAAA
AAAA

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FIGURE 672

LPVVNAHGLARRRLGSVTADASAGLQETQGDATRRGGRLGQRLRLLAMGPLSARLLMQRGRPKSDRLGKIRSL
DLSGLELLSEHLDPKLLCRLTQLQELDLSNNHLETLPDNLGLSHLRVLRRCANNQLGDVTALCQFPKLEELSLEGN
PFLT VNDNLKVSFLLPTLRKVNGKDASSTYSQVENLNRELT SRVTAHWKFMATLGPEEEAEKAQADFVKS AVR
VRYGPESLSEFTQWRVRMISEELVAASRTQVQKANSPEKPPEAGAAHKPRARLAALKRPDDVPLSLSPSKRACAS
PSAQVEGSPVAGSDGSQPAVKLEPLHFLQCHSKNNSPQDLETQLWACAFEPAWEEGATSQTVATCGGEAVCVIDC
QTGIVLHKKYKAPGEEFFSWAWTALMVVTQAGHKKRWSVLAAAGLRGLVRL LHVRAGFCCGVIRAHKKAIATLCFS
PAHETHLFTASYDKRIILWDIGVPNQDYEFQASQLLTLDTTSIPLRLCPVASC PDARLLAGCEGGCCCWDVRLDQ
PQKRRVCEVEFVFSEGEASGRRVDGLAFVNEDIVASKGSLGTICLWSWRQTWGGGRGSQSTVAVVVLARLQWSS
TELAYFSLSACPDKGIVLCGDEEGNVWLYDVSNIKQPPLLPAALQAPTQILKWPQPWALGQVVTKTMVNTVVAN
ASFTYLTALTDSNIVAIWGRM

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FIGURE 673A

GAATTCGGGGGGCGAGTAAGCCAGCGGCAGGACCAGCGGGCGGGGGCCACAACAAAAGCTGGCAGGCTGACAGAG
GCGGCCTCAGGACGGACCTTCTGGCTACTGACCGTTTGGCTGTGGTTTTCCCGATTGTGTGTAGGTGTGAGATC
AACCATGAGTTCCGTTGCAGTTTTGACCCAAGAGAGTTTTGCTGAACACCGAAGTGGGCTGGTTCGCCAACAAAT
CAAAGTTGCCACTCTAAATTCAGAAGAGGAGAGCGACCCTCCAACCTACAAGGATGCCTTCCCTCCACTTCCTGA
GAAAGCTGCTTGCTGGAAAGTGCCAGGAACCCGCTGGAGCCTGGGGGAACAAGATCCGACCCATCAAGGCTTC
TGTCATCACTCAGGTGTTCCATGTACCCCTGGAGGAGAGAAAAATACAAGGATATGAACCAAGTTTGGAGAAGGTGA
ACAAGCAAAAATCTGCCTTGAGATCATGCAGAGAACTGGTGCTCACTTGGAGCTGTCTTTGGCCAAAGACCAAGG
CCTCTCCATCATGGTGTGAGGAAAGCTGGATGCTGTATGAAAGCTCGGAAGGACATTGTTGCTAGACTGCAGAC
TCAGGCCTCAGCAACTGTTGCCATTCCCAAGAACACCATCGCTTTGTTATTGGCAAAAATGGAGAGAAAAGTGA
AGACTTGGAGCTAAAACTGCAACCAAAATCCAGATCCCACGCCAGATGACCCAGCAATCAGATCAAGATCAC
TGGCACCAAGAGGGCATCGAGAAAGCTCGCCATGAAGTCTTACTCATCTCTGCCGAGCAGGACAAACGTGCTGT
GGAGAGGCTAGAAGTAGAAAAGGCATTCCACCCCTTCATCGCTGGGCCGTATAATAGACTGGTTGGCGAGATCAT
GCAGGAGACAGGCACGCGCATCAACATCCCCCACCAGCGTGAACCGGACAGAGATTGTCTTCACTGGAGAGAA
GGAACAGTTGGCTCAGGCTGTGGCTCGCATCAAGAAGATTTATGAGGAGAAGAAAAAGAACTACAACCATTGC
AGTGAAGTGAAGAAATCCCAACACAAGTATGTCAATTGGGCCCAAGGGCAATTCATTGCAGGAGATCCTTGAGAG
AACTGGAGTTTCCGTTGAGATCCCACCCTCAGACAGCATCTCTGAGACTGTAATACTTCGAGGCGAACCTGAAAA
GTTAGGTGAGGCGTTGACTGAAGTCTATGCCAAGGCCAATAGCTTCACCGTCTCCTCTGTGCGCCGCCCTTCCTG
GCTTCACCGTTTCATCATTGGCAAGAAAGGGCAGAACCTGGCCAAAATCACTCAGCAGATGCCAAAGGTTACAT
CGAGTTCACAGAGGGCGAAGACAAGATCACCTGGAGGGCCCTACAGAGGATGTCAATGTGGCCCGAGGAACAGAT
AGAAGGCATGGTCAAAGATTTGATTAACCGGATGGACTATGTGGAGATCAACATCGACCACAAGTTCCACAGGCA
CCTCATTGGGAAGAGCGGTGCCAACATAAACAGAAATCAAAGACCAGTACAAGGTGTCCGTGCGCATCCCTCCTGA
CAGTGAGAAGAGCAATTTGATCCGCATCGAGGGGGACCCACAGGGCGTGACAGGCGCAAGCGAGAGCTGCTGGA
GCTTGATCTCGCATGGAAAATGAGCGTACCAAGGATCTAATCATTGAGCAAAGATTTTCATCGCACAATCATTGG
GCAGAAGGGTGAACGGATCCGTGAAATTCGTGACAAATTCAGAGGTCATCATTAACTTTCCAGACCCAGCACA
AAAAAGTGACATTGTCCAGCTCAGAGGACCTAAGAATGAGGTGGAAAAATGCACAAAATACATGCAGAAGATGGT
GGCAGATCTGGTGGAAAATAGCTATTCAATTTCTGTTCCGATCTTCAAACAGTTTCACAAGAAATATCATTGGGAA
AGGAGGCGCAAACATTAAAAAGATTCTGTGAAGAAAGCAACACCAAAATCGACCTTCAGCAGAGAATAGCAATTC
AGAGACCATTATCATCACAGGCAAGCGAGCCAACTGCGAAGCTGCCCGGAGCAGGATTCTGTCTATTAGAAAGA
CCTGGCCAACATAGCCGAGGTAGAGGTCTCCATCCCTGCCAAGCTGCACAACTCCCTCATTGGCACCAAGGGCCG
TCTGATCCGCTCCATCATGGAGGAGTGCGGGCGGGTCCACATTCACTTTCCCGTGGAAAGGTTAGGAAGCGACAC
CGTTGTTATCAGGGGCCCTTCTCGGATGTGGAGAAGGCCAAGAAGCAGCTCCTGCATCTGGCGGAGGAGAAGCA
AACCAAGAGTTTCACTGTTGACATCCGCGCCAAGCCAGAATACCACAAATTCCTCATCGGCAAGGGGGGCGGCAA
AATTGCAAGGTGCGCGACAGCACTGGAGCACGTGTATCTTCCCTGCGGCTGAGGACAAGGACCAGGACCTGAT
CACCATCATTGGAAGGAGGACGCCGTCCGAGAGGCACAGAAGGAGCTGGAGGCCTTGATCCAAAACCTGGATAA
TGTGGTGGAAAGACTCCATGCTGGTGGACCCCAAGCACCACCGCCACTTCGTATCCGAGAGGCCAGGTCTTGCG
GGAGATTGCTGAAGAGTATGGCGGGGTGATGGTCAGCTTCCCACGCTCTGGCACACAGAGCGACAAAGTCACCC
CAAGGGCGCAAGGACTGTGTGGAGGCAGCCAAGAAACGCATTTCAGGAGATCATTGAGGACCTGGAAGCTCAGGT
GACATTAGAATGTGCTATACCCAGAAATTCATCGATCTGTATGGGCCCCAAAGGTTCCAGAATCCAGCAGAT
TACTCGGGATTTCACTGTTCAAATTAATTCAGACAGAGAGGAGAACGCAGTTTACAGTACAGAGCCAGTTGT
CCAGGAGAATGGGGACGAAGCTGGGGAGGGGAGAGAGGCTAAAGATTGTGACCCCGGCTCTCCAAGGAGGTGTGA
CATCATCATCTCTGGCCGGAAGAAAAGTGTGAGGCTGCCAAGGAAGCTCTGGAGGCATTGGTTCTGTCTAC
CATTGAAGTAGAGGTGCCCTTTGACCTTACCGTTACGTTATTGGGCAGAAAGGAAGTGGGATCCGCAAGATGAT
GGATGAGTTTGAGGTGAACATACATGTCCCGGCACCTGAGCTGCAGTCTGACATCATCGCCATCACGGGCCTCGC
TGCAAAATTTGGACCGGGGCCAAGGCTGGACTGCTGGAGCGTGTGAAGGAGCTACAGGCCGAGCAGGAGGACCGGGC
TTTAAGGAGTTTTAAGCTGAGTGTCACTGTAGACCCCAAATACCATCCCAAGATTATCGGGAGAAAGGGGGCAGT
AATTACCCAAATCCGTTGGAGCATGACGTGAACAATCAGTTTCTGATAAGGACGATGGGAACCGACCCAGGA
CCAAATTACCATCACAGGGTACGAAAAGAACACAGAAGCTGCCAGGGATGCTATACTGAGAATTGTGGGTGAAGT
TGAGCAGATGGTTTCTGAGGACGTCCCGCTGGACCACCGGTTACGCCCCGCATCATTGGTGCCCGGGCAAAGC

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FIGURE 673B

CATTTCGCAAAATCATGGACGAATTCAAGGTGGACATTTCGCTTCCCACAGAGCGGAGCCCCAGACCCCAACTGCGT
CACTGTGACGGGGCTCCCAGAGAATGTGGAGGAAGCCATCGACCACATCCTCAATCTGGAGGAGGAATACCTAGC
TGACGTGGTGGACAGTGAGGCGCTGCAGGTATACATGAAACCCCCAGCACACGAAGAGGCCAAGGCACCTTCCAG
AGGCTTTGTGGTGCGGGACGCACCCTGGACCGCCAGCAGCAGTGAGAAGGCTCCTGACATGAGCAGCTCTGAGGA
ATTTCCCAGCTTTGGGGCTCAGGTGGCTCCCAAGACCCTCCCTTGGGGCCCCAAACGATTAATGATCAAAAAGAAC
AGAACCCTCTCCAGCCTGCTGACCCGAACCCAACCACACAATGGTTTGTCTCAATCTGACCCAGCGGCTGGACCC
TCCGTAAATTGTTGAGCGCTCTTCCCCTTCCCGAGGTCCGCAGGGAGCCTAGCGCCTGGCTGTGTGTGCGGCCGC
TCCTCCAGGCCTGGCCGTGCCCGCTCAGGACCTGCTCCACTGTTTAAACAATAAACCAAGGTCATGAGCATTTCGAG
CTAAGATAACAGACTCCAGCTCCTGGTCCACCCGGCATGTTCAGTCAGCACTCTGGCCTTCATCACGAGAGCTCCG
CAGCCGTGGCTAGGATTCCACTTCCTGTGTCTATGACCTCAGGAAATAAACGTCCTTGACTTTATAAAAGCCCCGA
ATTC

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FIGURE 674

MSSVAVLTOESFAEHRSGLVPPQIKVATLNSEESDPPTYKDAFPPLPEKAACLESQAQEPAGAWGNKIRPIKASV
ITQVFHVPLEERKYKDMNQFGEQAKICLEIMQRTGAHLELSIAKDQGLSIMVSGKLDVAMKARKDIVARLQTQ
ASATVAIPKEHHRFVIGKNGEKLQDLELKTATKIQIPRPDDPSNQIKITGTKEGIEKARHEVLLISAEQDKRAVE
RLEVEKAFHFFIAGPYNRLVGEIMQETGTRINIPPSVNRTEIVFTGEKEQLAQAVARIKKIYEEKKKKTTTIAV
EVKKSQHKYVIGPKGNSLQEILERTGVSVEIPPSDSISETVILRGEPEKLGQALTEVYAKANSFTVSSVAAPSWL
HRFIIGKKGQNLAKITQQMPKVHIEFTEGEDKITLEGPTEDVNVAQEQIEGMVKDLINRMDYVEINIDHKFHRHL
IGKSGANINRIKDQYKSVRIPPDSEKSNLIRIEGDPQGVQQAQKRELLELASRMENERTKDLIEQRFHRTIIGQ
KGERIREIRDKFPEVIINFPDPAQKSDIVQLRGPKNEVEKCTKYMQKMVADLVENSYSISVPIFKQFHKNIIIGK
GANIKKIREESNTKIDLPAENSNETIIITGKRANCEAARSRIISIQKDLANIAEVEVSIPAKLHNSLIGTKGRL
IRSIMEECGGVHIHFPVEGSGSDTVIRGPSSDVEKAKKQLLHLAEKQTKSFTVDIRAKPEYHKFLIGKGGGKI
RKVRDSTGARVIFPAAEDKDQDLITIIIGKEDAVREAQKELEALIQNLNDNVVEDSMLVDPKHHRHFVIRRGQVLRE
IAEEYGGVMVSFPRSGTQSDKVTLKGAKDCVEAAKKRIQEIIEDLEAQVTLECAIPQKFHRSVMGPKGSRIQQIT
RDFSQVIKFPDREENAVHSTEPVVQENGDEAGEGREAKDCDPGSPRRCDIIISGRKEKCEAAKEALEALVPVTI
EVEVPFDLHRYVIGQKSGIRKMMDEFEVNIHVPAPELQSDIIAITGLAANLDRAGLLERVKELQAEQEDRAL
RSFKLSVTVDPKYHPKIIIGRKGAVITQIRLEHDVNIQFPDKDDGNQPDQITITGYEKNTEAARDAILRIVGELE
QMVSEDVPLDHRVHARIIGARGKAIRKIMDEFKVDIRFPQSGAPDPNCVTVTGLPENVEEAIDHILNLEEYLLAD
VVDSEALQVYMKPPAHEEAKAPSRGFVVRDAPWTASSEKAPDMSSSEEFPSFGAQVAPKTLPGPKR

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FIGURE 675

AAAATGGTGGTGTTCGGGTATGAGGCTGGGACTAAGCCAAGGGATTTCAGGTGTGGTGCCGGTGGGAAGTGGAGAA
GCGCCCAAGGAAATGAAACACGATTTCCAAAATGAACTTAATCTTTTCATGAGAACTGAGGATAGAGATGTCAAT
AAGCAGCCACTGTTTCCACCTCCCCACCTGAAGAGCTAGGAGCGCCCAAGCTTTTCGGTTCAGCTCGGACTAAG
CCATGTGGATTTCAGGTGTGGATGACGGTGGGAAGTGGGAAGCGCCCAAGGTTTTCAAGATGGCAGCATCTATGC
ATGGTCAGCCCAGTCCTTCTCTAGAAGATGCAAACTCAGAAGACCAATGGTCATAGAAATCATAGAAAAAATT
TTGACTATCTTAGAAAAGAAATGACACAAAATATATATCAAATGGCGACATTTGGAACAACAGCTGGTTTCTCTG
GAATATTTCTCAAACCTCCTGTTTCAGACGCTGCTTCAAGGTTAAACATGATGCTTTGAAGACATATGCATCATTGG
CTACACTTCCATTTTTGTCTACTGTTGTTACTGACAAGCTTTTTGTAATTGATGCTTTGTATTTCAGATAATATAA
GCAAGGAAAAGTGTGTTTTGAGAAGCTCACTGATTGGCATAGTTTGTGGTGTGTTTTCTATCCCAGTTCTTTGGCTT
TTACTAAAAATGGACGCCTGGCAACCAAGTATCATACCGTTCCACTGCCACCAAAGGAAGGGTTTTAATCCATT
GGATGACGCTTTGTCAAACACAAATGAAATTAATGGCGATTCTCTAGTCTTTTCAGATTATGTTTGAATATTAA
ATGGTCTATACCATTTATGCAGTATTTGAAGAGACACTTGAGAAAAGTATACATGAAGAGTAAACCAAAAAAATGAA
TGGTTGCTAACTTAGCAAAATGAAGTTTCTATAAAGAGGACTCAGGCATTGCTGAAAGAGTTAAAGTAAGTGTG
AACAATAATTTGTTCTGTGCCTTTTGCCTGGTATATAGCAAATACTCAAAAAGTATTCAATAATTCAATCAATA
AATATAAGTTTCATCTTACACGTAAGATACAGGCTTATCTCCTGATGGTGTGTCCATTTTGCCTGGTATATAAC
AGATAATAAATATCCAGTGTCAATAAATGTAACAATAAAAAAAAAA

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FIGURE 676

MWIQVWMTVGTEEAPKVFKMAASMHGQSPSPSLEDAKLRRPMVIEIEKNFDYLRKEMTONIYQMATFGTTAGFSG
IFSNFLFRRCFKVKHDALKTYASLATLPFLSTVVTDKLFVIDALYSDNISKENCVFRSSLIGIVCGVFYPSSLAF
TKNGRLATKYHTVPLPPKGRVLIHWMTLCQTQMKLMAIPLVFQIMFGILNGLYHYAVFEETLEKTIHEE

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FIGURE 677

GGAAAAGATGGCGGCTGCCGCACAATCCCGGGTTGTCCGGGTCCTGTCAATGTCACGTTCTGCCATTACTGCAAT
AGCCACATCTGTGTGTACGGCCCCACCCTGTGCGCCAGCTTCATCATGCCCTCATGCCTCATGGGAAAGGTGGACG
TTCTTCAGTCAGTGGGATTGTGGCCACTGTGTTTGGAGCAACAGGATTCTGGGGCGATATGTTGTCAACCACCT
TGGACGCATGGGGTCACAGGTAATCATACCCTATCGGTGTGATAAAATATGACATCATGCACCTTCGTCCCATGGG
TGACCTGGGCCAGCTTCTGTTTCTGGAATGGGACGCGAGAGATAAAGATTCTATCCGACGAGTAGTACAACACAG
CAATGTGGTCATCAATCTTATTGGACGAGACTGGGAAACCAAAACTTTGATTTTGAGGATGTTTTGTGAAGAT
TCCCCAAGCAATTGCTCAACTGTCCAAGGAAGCTGGAGTTGAAAAATTCATTCATGTTTCACATCTGAATGCGAA
TATTAAAAGCTCTTCTAGATATTTGAGAAATAAGGCTGTTGGAGAGAAAAGTAGTGAGAGATGCATTCCGGAAGC
CATTATCGTAAAGCCGTCGGACATCTTTGGAAGAGAGGATAGATTCTTAATTCTTTTGCAAGTATGCATCGGTT
TGGTCCTATACCCCTTGTTTCCTTGGGCTGGAAGACAGTTAAACAACCAGTATATGTCGTAGATGTATCCAAAGG
AATTGTTAATGCAGTTAAGGATCCTGATGCCAATGGGAAAACCTTTGCTTTCGTTGGGCCAAATCGATATCTCCT
CTTTGACCTGGTGAAGTACATCTTGCTGTGGCTCACAGCAAAGGGTACTTCTCCCGTACCCCTTGCCACCTT
TTGCCTATCAGTGGGTAGCAAGAGACTTTGAAATAAGCCCATTTGAGTCCTGGACAACAAGGGATAAAGTGGAGC
GTATTCACATCACAGACATGACCTTGTCTCACCTGCCAGCTTAGAAGACCTTGGTATTCAGGCAACACCACTGG
AACTCAAGGCCATTGAGGTGCTGCGGCTTCATCACACTTACTGCTGGCTGTCTGCTGAAATTGAGGATGTGAAGC
TGGCCAAGACCGTCAACATTTAGTGCTCCCGAGCAACTCTTGGTTTTGGTGTCTTTTGGGTCAGCCCGTGTGGT
TTGAGCACCCAGCCAGGTGGTCTCTTTAGAGAATCCTGTACACAGTGAATAAGATCCCACCATTAAACATTTGA
GGTT

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FIGURE 678

EKMAAAQSRVVRVLSMSRSAITAIATSVCHGPPCRQLHHALMPHGKGGRSSVSGIVATVFGATGFLGRYVNNHL
GRMGSQVIIPYRCDKYDIMHLRPMGDLGQLLFLEWDARDKDSIRRVVQHSNVVINLIGRDWETKNFDFEDVFVKI
PQAIAQLSKEAGVEKFIHVSHLNANIKSSRYLRNKAVGEKVVRDAFPEAIVKPSDIFGREDRFLNSFASMHRF
GPIPLGSLGWKTVKQPVYVVDVSKGIVNAVKDPDANGKTFAFVGPNRYLLFDLVKYIFAVAHSKGVLPVPVPLATF
CLSVGSKRL

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FIGURE 679

AGGTTTCGGCGGGGCTGCACGTGCGCAGGGGTGTGGAACTTACCGGCTGAGCCATGGGATACACCGTTAAGGCG
CAGCCGACGGCTGGGAGGCCCTAAGGCCGAATCCCCGAGAGCCTCACCTCAGTTTCGCGGACGAGACGGGCCCT
TGTGGAGTTCGAGTCGAACCCAGAAGAAACGAGGGAGCCCGGGTCTCCTCCGAGTGTGCAGCGGGCTGGCCTGGG
GTCCCCGAAAGGCCGCCGAAGACAAGCCCAGGATCACCCCGTCTGCAGCAGGGTGCAGGCTTGGAGTCAACCCCA
AGGGCAGCCAGACCCAGGCGCAGCGTCCCCCAGCGTCAGCAAGACCTACACCTGGAGTCGCCTCAAAGACAGCC
AGAGTACAGTCTGAATCCCCACGATGTCAGCCGAAGCCAAGTGAGGAGGCACCAAAGTGTCTCAGGACCAGGG
AGTACTGGCCTCGGAGTTGGCCCAGAATAAGGAGGAGCTGACCCCGGGGGCCCCCAGCATCAGCTACCGCCGGT
CCCAGGATCACCCAGAGCCTTACCCCGGTGAGCAAGCTCCCGGTCCGGAGCCCTCTCAGCCACTACTGGAGCTGAC
ACCCAGGGCACCTGGCTCCCCCGGGGTGAGCATGAGCCGAGCAAGCCACCTCCAGCTGGGGAGACGGTGACAGG
CGGCTTCGGGGCAAAGAAGCGAAAAGTTCTTCATCCCAGGCCCCAGCGTCCAAGAAGTTGAATAAAGAGGAGCT
TCCTGTAATCCCGAAGGGGAAGCCCAAATCGGGGCGAGTGTGGAAAGGACCGCTCCAAGAAAAGATTCTCCAGAT
GCTTCAGGACAAGCCCCTGCGCACATCGTGGCAGCGGAAGATGAAGGAACGACAGGAGAGGAAGCTGGCCAAGGA
CTTTGCCCCGTACCTGGAGGAGGAGAAGGAGAGGCGCCGCCAGGAGAAGAAACAGCGCCGGGCTGAGAACCTGAA
ACGCCGCCCTGGAGAATGAGCGGAAGGCAGAGGTCGTCCAAGTGATCCGAAACCCCGCCAAGCTCAAGCGGGCAAA
GAAGAAGCAGCTGCGCTCCATTGAGAAGCGGGACACCCTGGCCCTGCTGCAGAAGCAGCCGCCCCAGCAGCCGGC
AGCCAAGATCTGAGCTCAGGACGGCCCCGAGGCCTTCCATGGCCAACGACCATGTCAGACACAGCACCTCAGGCCG
CTGCTCAGATGCCTCTGCTGGAGCTGGCACTCCAAACCCATGGCTCCAGAACGGGGACCCCCACCCGACCGGGG
CTCCTCGGCCTTTGAAGGCTTCCAGGCAGGTCTGTGTGGGACAGAAGCCCAGAGGGGGCCTGGGACCTGGCAGAG
ATGGGGGCGGGAAGAGATTTCAGCTCCCATCCCTCCTTCTCCTTCTCCAAGTGCCTTCAAACCAAGAACTGTA
CATTCTTCTGGTTCCTCAGTGAGCTGGTGACTGGCAGGTGACTCCCTCAGCAGTGTATGCCCTTTCTCAGCATCC
TAGGTCCATCCCAGGCCTGGAGGCTGACAGTTGGGAATCCAGCTTCCCCCACACCTTCCCAAAGGCTGCTCTGAG
CACCTCCACACCCCACTGCCTCTGTCCCCAGCAAACTGAATCCGGTTCTCTCCACTTTTCAATACTGAAAGATT
AAAATGGGGAGGTTGCAGGGAGCAGAGCTTTTCCCTAGCACCCACTTTCCCAAACCAAGTCTCTGCAGAAGCCCCA
GAGAATCTAACTCATGCCTGTCCAGTCTACAGCAAAAATATTTATTGAGTGCCTGTTGCATACAGGCACAATCCT
AGGCACCGGCAAATACAGACAATAGACCAAAGTCCCTGCCCTCGAGGAGCTTTCATTCTGATGGAGAGAAAACAT
AATAACAAGCAAAATGCAAAAAAAAAAAAAAAAAA

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FIGURE 680

MDTPLRRSRRLGGLRPESPELTSVSRTRRALVEFESNPEETREPGSPPSVQRAGLGSPERPPKTSPGSPRLQQG
AGLESPQGQPEPGAASPORQDLHLESPQRQPEYSPESPRCQPKPSEEAPKCSQDQGVLAELAQNKEELTPGAP
QHQLPPVPGSPEPYPGQQAPGPEPSQPLLELTPRAPGSPRGQHEPSKPPAPAGETVTGGFGAKKRKGSSSQAPASK
KLNKEELPVIPKGKPKSGRVWKDRSKKRFSQMLQDKPLRTSWQRKMKERQERKLAKDFARHLEEEKERRRQEKKQ
RRAENLKRRENERKAEVVQVIRNPAKLKRAKKKQLRSIEKRD TLALLQKQPPQPPAAKI

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FIGURE 681

GTCGACTACCAGAAAATACTTTCAACATAAATGAACTCTCCAAC TTATTAACTTTTATATAGATAGAGGAAGAC
AGCTCTTTTCGGGATAACCACCTGATACCTGCAGAAACCCCGAGTCCTGTTATTTTCAGTGATTTTCCATTTATCT
TTAATTCGCTATCCAAAATTAAATTATTGCAAGCTGATTCACATATAAAGATGCAGATGTCAGAAAAGAAAGCAT
ACATGCTTATGCATGAAACAATTCTGCAAAAAAAGGATGAATTTCTCCATCACCCAGATTTATACTTAGAGTCA
GACGAAGTCGCCTGGTTAAAGATGCTCTGCGTCAATTAAGTCAAGCTGAAGCTACTGACTTCTGCAAAGTATTAG
TGGTTGAATTTATTAATGAAATTTGTCCTGAGTCTGGAGGGGTTAGTTCAGAGTTCTTCCACTGTATGTTTGAAG
AGATGACCAAGCCAGAATATGGAATGTTTCATGTATCCTGAAATGTGTTCTGCATGTGGTTTCTGCCAAGCCTA
AACCTGAGAAGAAAAGATATTTCTCTTTGGAATGCTGTGTGGACTCTCCTTATTCAATTTAAATGTTGCTAACCC
TTCCTTTCCCACTGGCTCTGTATAAAAAAAGCTTCTGGACCAAAAGCCATCATTGGAAGATTTAAAGAAGCTCAGTC
CTCGGTTGGGGAAGAGTTTGCAAGAAGTTCTAGATGATGCTGCTGATGACATTGGAGATGCGCTCTGCATACGCT
TTTCTATACACTGGGACCAAAATGATGTTGACTTAATTCCAAATGGGATCTCCATACCTGTGGACCAACCAACA
AGAGAGACTATGTTTCTAAGTATATTGATTACATTTTCAACGCTCTCTGTAAAAGCAGTTTATGAGGAATTTCAGA
GAGGATTTTATAGAGTCTGTGAGAAGGAGATACTTAGACATTTCTACCCTGAAGAACTAATGACAGCAATCATTG
GAAATACTGATTATGACTGGAAACAGTTTGAACAGAATTCAAAGTATGAGCAAGGATACCAAAAATCACATCCTA
CTATACAGTTGTTTTGGAAGGCTTTCCACAAGCTAACCTTGGATGAAAAGAAAAAATTCCTCTTTTTCCTTACAG
GACGTGATAGGCTGCATGCAAGAGGCATACAGAAAATGGAATAGTATTTTCGCTGTCCTGAAACTTTCAGTGAAA
GAGATCACCCAAACATCAATAACTTGTCTATAATATTCTCTCCCTCCCTAAGTATTCTACAATGGAAGAATGGAGG
AAGCACTCCAAGTAGCCATCAACAACAACAGAGGATTTGTCTCACCCATGCTCACACAGTCAATAACCTCTGA
GAGACTCAGGGTGGGCTTTCTCACACTTGGATCCTTCTGTTCTTCTTACACCTAAATAATACAAGAGATTAATG
AATAGTGGTTAGAAGTAGTTGAGGGAGAGATTGGGGGAATGGGGAGATGATGATGATGGTCAAAGGGTGCAAAAT
CTCACACAAGACTGAGGCAGGAGAATAGGGTACAGAGATAGGGATCTAAGGATGACTTGGACACACTCCCTGGCA
CTGAAGAGTCTGAACACTGGCCTGTGATTGGTCCATTCCAGGACCTTCATTTGCATAAGGTATCAAACCACATCA
GCCTCTGATTGGCCATGGGCCAGACCTGCACTCTGGCCAATGATTGGTTCATTCCAGGACATTCATTTGCATAAG
GAGTCAAACCACACCAGTCTTGGATTGGCTGTGAGCCAATTCACCTCAGTCTCTAATTGGCTGTGAGTCAGTCTT
TCATTTACATAGGGTGTAAACATCAAGAAACCTCTACAGGGTACTTAAGCCCCAGAAGATTTTGCTACCAGGGCT
CTTGAGCCACTTGCTCTAGCCCACTCCCACTGTGGAATGTACTTTCACTTTTGCTGCTTCACTGCCTTGTGCT
CCAATAAATCCACTCCTTCAACCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 682

MQMSEKKAYMLMHETILQKKDEFPPSPRFILRVRRSRLVKDALRQLSQAEATDFCKVLVVEFINEICPESGGVSS
EFFHCMFEEMTKPEYGMFMYPEMCSCMWFPAPKPKPEKKRYFLFGMLCGLSLFNLNVANLPFPLALYKKLLDQKPS
LEDLKELSPRLGKSLQEVLDDAADDIGDALCIRFSIHWDQNDVDLIPNGISIPVDQTNKRDYVSKYIDYIFNVSV
KAVYEEFQRGFYRVCEKEILRHFYPEELMTAIGNTDYDWKQFEQNSKYEQGYQKSHPTIQLFWKAFHKLTLDK
KKFLFFLTGRDLRHARGIQKMEIVFRCPETFSERDHPTSITCHNILSLPKYSTMERMEEALQVAINNNRGFVSPM
LTQS

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FIGURE 683

TCGAATTCCTAATTTTTGTGGGACTCCTTAAGACCCACAAGTGACTTCTGTCTACACTACAGATGAACTGAATTG
ATCATCTAAAATACGTTTATAGCGTTCATTGTGCCAGTTGCTCATGGTTCTGCTAATTGGCCCAGGACTAGTTGT
GATCTGCAGACTGAAGCCAGAGTAAGTAAGAGAATTCAAGGCACTAAGACAACCAGGAACAGTTTTACCAAGGCA
AGTGGAAGCTGCTAGGCTCAGTGGTTGCATGCCTATAGATGGGGTAAATCATCCTGGTGCAAATATGGTATTAC
ACCATAAATGTGTAGTGCAAGTTTCCTCTGTGGCCAATCACAGGGCTGCAAGCTGAAGCCCCAGTTTAGCTTATT
CTCCATACATAACTTCAAGGGGACTTTCTGGTGAACTTTCCAAGAAGCTCCAAGCACAGATGGTTCAAATTTGC
AGTTTGGCTAGACTTTGTGACTGGATGTACATTAAATTAA

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FIGURE 684

MVQICSLARLCDWMIK

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FIGURE 685

GGGGGGTGGCTGGGCTGCGCTTGGGTCCGTCGCTGCTTCGGTGTCCCTGTGCGGGCTTCCCAGCAGCGGCCTAGCG
GGAAAAGTAAAAGATGCTCTGAATATATTCCGGTAACCGAAGATGAGAACGATGAGCCCATGAAATACCATCGGA
AGACGATGGGACGGTGTCTCTCCACGGTTACAGCCCAGTTTCCAGGGGCGTGTGGGCTTCGCTACAGGAATCC
AGTGTCTCAGTGTATGAGAGGTGTCCGGCTGGTAGAAGGAATTCTGCATGCCCCAGATGCTGGCTGGGGAAATCT
GGTGTATGTTGTCAACTATCCAAAAGATAACAAAAGAAAATGGATGAGACAGATGCTTCATCAGCAGTGAAAGT
GAAAAGAGCAGTCCAGAAAACATCCGATTTAATAGTGTGGGTCTCCCATGGAAAACAACCGAACAGGACCTGAA
AGAGTATTTTAGTACCTTTGGAGAAGTTCTTATGGTGCAGGTCAAGAAAGATCTTAAGACTGGTCATTCAAAGGG
GTTTGGCTTTGTTTCGTTTTACGGAATATGAAACACAAGTGAAAGTAATGTACAGCGACATATGATAGATGGACG
ATGGTGTGACTGCAAACCTTCCATAATTCTAAGCAAAAGCCAAGATGAGCCTTTGAGAAGCAGAAAAGTGTTTGGG
GCGCTGTACAGAGGACATGACTGAGGATGAGCTGCGGGAGTTCTTCTCTCAGTACGGGGATGTGATGGATGTCTT
CATCCCCAAGCCATTTCAGGGCCTTTGCCTTTGTTACATTTGCAGATGATCAGATTGCGCAGTCTCTTTGTGGAGA
GGACTTGATCATTAAAGGAATCAGCGTTCATATATCCAATGCCGAACCTAAGCACAATAGCAATAGACAGTTAGA
AAGAAGTGGAAGATTTGGTGGTAATCCAGGTGGCTTTGGGAATCAGGGTGGATTTGGTAATAGCAGAGGGGGTGG
AGCTGGTTTGGGAAACAATCAAGGTAGTAATATGGGTGGTGGGATGAACTTTGGTGCCTTCAGCATTAAATCCAGC
CATGATGGCTGCCGCCAGGCAGCACTACAGAGCAGTTGGGGTATGATGGGCATGTTAGCCAGCCAGCAGAACCA
GTCAGGCCCATCGGGTAATAACCAAAACCAAGGCAACATGCAGAGGGAGCCAAACCAGGCCTTCGGTTCTGGAAA
TAACTCTTATAGTGGCTCTAATTCGGTGCAGCAATTGGTTGGGGATCAGCATCCAATGCAGGGTTCGGGCACTGG
TTTTAATGGAGGCTTTGGCTCAAGCATGGATTCTAAGTCTTCTGGCTGGGGAATGTAGACAGTGGGGTTGTGGTT
GGTTGGTATAGAATGGTGGGAATTCAAATTTTCTAAACTCATGGTAAGTATATTGTAAAATACATATGTACTAA
GAATTTTCAAATTTGGTTTGTTCAGTGTGGAGTATATTTCAGCAGTATTTTTTGACATTTTTCTTTAGAAAAAGGAA
GAGCTAAAGGAATTTTATAAGTTCTGTTACATGAAAGGTTGAAATATTGAGTGGTTGAAAGTGAAGTCTGTTTG
CCTGATTGGTAAACCAACACACTACAATTGATATCAAAGGTTTCTCCTGTAATATTTTATCCCTGGACTTGTCA
AGTGAATTCCTTGCATGTTCAAACGGAAACCATGATTAGAACACATTCTTTACCCCTTGTTTAATTTGAAC
CCCACCATATGGATTTTTTTCCTTAAGAAAATCTCCTTTTAGGAGATCATGGTGTACAGTGTGGTTCTTTTG
TTTTGTTTTTTAACACTTGTCTCCCTCATACACAAAAGTACAATATGAAGCCTTCATTTAATCTCTGCAGTTCA
TCTCATTTCAAATGTTTATGGAAGAAGCACTTCACTGAAAGTAGTGCTGTAAATATTCTGCCATAGGAATACTGT
CTACATGCTTTCTCATTCAAGAATTCGTCATCAGCATCACAGGCCGCGTCTTTGACGGTGGGTGTCCCATTTTT
ATCCGCTACTCTTTATTTTCATGGAGTCGTATCAACGCTATGAACGCAAGGCTGTGATATGGAACCAGAAGGCTGT
CTGAACTTTTGAAACCTTGTGTGGGATTGATGGTGGTGCCGAGGCATGAAAGGCTAGTATGAGCGAGAAAAGGAG
AGAGCGCGTGCAGAGACTTGGTGGTGCATAATGGATATTTTTTAACTTGGCGAGATGTGTCTCTCAATCCTGTGG
CTTTGGTGAGAGAGTGTGCAGAGAGCAATGATAGCAAATAATGTACGAATGTTTTTGCATTCAAAGGACATCCA
CATCTGTTGGAAGACTTTTTAAGTGAGTTTTTGTCTTAGATAACCCACATTAGATGAATGTGTTAAGTGAAATGA
TACTTGTAATCCCCCTACCCCTTTGTCAACTGCTGTGAATGCTGTATGGTGTGTGTTCTCTCTGTTACTGATAT
GTAAGTGTGGCAATGTGAAGTGAAGCTGATGGGCTGAGAACATGGACTGAGCTTGTGGTGTGCTTTGCAGGAGGA
CTTGAAGCAGAGTTCAACAGTGAGCTCAGGTGTCTCAAAGAAGGGTGGAAGTTCTAATGTCTGTAGCTACCCAT
AAGAATGCTGTTTGTGTGAGTTCTGTGTCTGTGCTTGGATGCTTTTTTATAAGAGTTGTCAATGTGTGGAAATTC
TAAATAAGACTGATTTAAATAATAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 686

MSEYIRVTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGILHAPDAGWGNLVYVV
NYPKDNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTTEQDLKEYFSTFGEVLMVQVKDLKTGHSGFGFV
RFTEYETQVKVMSQRHMIDGRWCDCKLENSKQSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIKKP
FRAFAFVTFADDQIAQSLCGEDLIIGISVHISNAEPKHNSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLG
NNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMMGLASQQNQSGPSGNNQNQGNMQREFNQAFGSGNNSYS
GSNSGAAIGWGSASNAGSGSGFNNGGFGSSMDSKSSGWGM

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FIGURE 687

AAGAGATGATTTCTCCATCCTGAACGTGCAGCGAGCTTGTCTAGGAAGATCGGAGGTGCCAAGTAGCAGAGAAAGC
ATCCCCCAGCTCTGACAGGGAGACAGCACATGCTCTAAGGCCCAAGCCTTGGCCCTACCGGAGGAGAAGTCAAT
TTTCTTCTCGAAAATACCTGAAAAAGAAATGAATTCCTTCCAGCAACAGCCACCGCCATTCCGGCACAGTGCCAC
CACAAATGATGTTTTCTCCAACTGGCAGGGGGCAGAGAAGGACGCTGCTTTCTCGCCAAGGACTTCAACTTTT
TCACTTTGAACAATCAGCCACCACCAGGAAACAGGAGCCAACCAAGGGCAATGGGGCCCAGAAACAACCTGTACA
GCCAGTACGAGCAGAAGGTGCGCCCTGCATTGACCTCATCGACTCCCTGCGGGCTCTGGGTGTGGAGCAGGACC
TGGCCCTGCCAGCCATCGCCGTATCGGGGACCAGAGCTCGGGCAAGAGCTCTGTGCTGGAGGCACTGTCTAGGAG
TCGCGCTTCCCAGAGGCAGCGGAATCGTAACCAGGTGTCCGCTGGTGCTGAACTGAAAAAGCAGCCCTGTGAGG
CATGGGGCCGAAGGATCAGCTACCGGAACACCGAGCTAGAGCTTCAGGACCCTGGCCAGGTGGAGAAAGAGATAC
ACAAAGCCCAGAAGCTCATGGCCGGGAATGGCCGGGGCATCAGCCATGAGCTCATCAGCCTGGAGATCACCTCCC
CTGAGGTTCCAGACCTGACCATCATTGACCTTCCCGGCATCACCAGGGTGGCTGTGGACAACCAGCCCCGAGACA
TCGGACTGCAGATCAAGGCTCTCATCAAGAAGTACATCCAGAGGCAGCAGACGATCAACTTGGTGGTGGTTCCCT
GTAACGTGGACATTGCCACCACGGAGGCGCTGAGCATGGCCCATGAGGTGGACCCGGAAGGGGACAGGACCATCG
GTATCCTGACCAACCAGATCTAATGGACAGGGGCACTGAGAAAAGCGTCATGAATGTGGTGCGGAACCTCACGT
ACCCCTCAAGAAGGGCTACATGATTGTGAAGTGCCGGGGCCAGCAGGAGATCACAAACAGGCTGAGCTTGGCAG
AGGCAACCAAGAAAGAAATTACATTCTTTCAAACACATCCATATTTAGAGTTCTCCTGGAGGAGGGGTCAGCCA
CGGTTCCCCGACTGGCAGAAAGACTTACCACTGAACTCATATGCATATCCAAAATCGCTCCCGTGTGTAGAAG
GACAAATAAGGGAGAGCCACCAGAAGGCGACCGAGGAGCTGCGGCGTTGCGGGCTGACATCCCCAGCCAGGAGG
CCGACAAGATGTTCTTTCTAATTGAGAAAATCAAGATGTTTAAATCAGGACATCGAAAAGTTAGTAGAAGGAGAAG
AAGTTGTAAGGGAGAATGAGACCCGTTTATACAACAAAATCAGAGAGGATTTTAAAACTGGGTAGGCATACTTG
CAACTAATACCCAAAAGTTAAAAATATTATCCACGAAGAAGTTGAAAAATATGAAAAGCAGTATCGAGGCAAGG
AGCTTCTGGGATTTGTCAACTACAAGACATTTGAGATCATCGTGCATCAGTACATCCAGCAGCTGTTGGAGCCCCG
CCCTTAGCATGCTCCAGAAAGCCATGGAAATTATCCAGCAAGCTTTTATTAACTGGCCAAAAAACATTTTGGCG
AATTTTTCAACCTTAACCAAAGTTCAGAGCAGGATTGAAGACATAAAAGTGAAACACACAGCAAAAGGCAGAAA
ACATGATCCAACCTTCAGTTTCAAGATGGAGCAGATGTTTGTGTCAGATCAGATTTACAGTGTGTCTGAAGA
AAGTCCGAGAAGAGATTTTTAACCTCTGGGGACGCCTTACAGAATATGAAGTTGAAGTCTCATTTTCCAGTA
ATGAGTCTTCGGTTTCTCTTTACTGAAATAGGCATCCACCTGAATGCCTACTTCTTGGAACACAGCAAACGTC
TCGCCAACCAGATCCCATTATATAATTAGTATTTATGCTCCGAGAGAATGGTGACTCCTTGAGAAAGCCATGA
TGCAGATACTACAGGAAAAAATCGCTATTCCTGGCTGCTTCAAGAGCAGAGTGAGACCGCTACCAAGAGAAGAA
TCCTTAAGGAGAGAATTTACCGGCTCACTCAGGCGCGACACGCACTCTGTCAATTCTCCAGCAAAGAGATCCACT
GAAGGGCGGCGATGCCTGTGGTTGTTTTCTTGTGCGTACTCATTCTAAGGGGAGTCGGTGCAGGATGCCGC
TTCTGCTTTGGGGCCAACTCTTCTGTCACTATCAGTGTCATCTCTACTGTACTCCCTCAGCATCAGAGCATGC
ATCAGGGGTCCACACAGGCTCAGCTCTCTCCACCACCAGCTCTTCCCTGACCTTACGAAGGGATGGCTCTCCA
GTCCTTGGGTCCCGTAGCACACAGTTACAGTGTCTAAGATACTGCTATCATCTCTCGCTAATTTGTATTTGTAT
TCCCTTCCCCCTACAAGATTATGAGACCCAGAGGGGAAGGTCTGGGTCAAATTCTTCTTTTGTATGTCCAGTC
TCCTGCACAGCACCTGCAGCATTGTAAGTGTCTAATAAATGACATCTCACTGAACGAATGAGTGTGTGTAAAGTG
ATGGAGATACCTGAGGCTATTGCTCAAGCCAGGCCTTGGACATTTAGTGACTGTTAGCCGGTCCCTTTCAGATC
CAGTGGCCATGCCCCCTGCTTCCCATGGTTCACTGTCAATTGTGTTTCCAGCCTCTCCACTCCCCGCCAGAAAG
GAGCCTGAGTGATTCTCTTTCTTCTTGTTCCTGATTATGATGAGCTTCCATTGTTCTGTAAAGTCTTGAAGA
GGAATTTAATAAAGCAAAGAACTTTTTAAAAACGT

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FIGURE 688

MSKAHKWPYRRRSQFSSRYLKKEMNSFQQQPPPFQGTVPQMMFPPNWQGAEKDAAFLAKDFNFLTLLNNQPPPG
NRSQPRAMGPENNLYSQYEQKVRPCIDLIDSLRALGVEQDLALPAIAVIGDQSSGKSSVLEALSGVALPRGSGIV
TRCPLVLKLLKKQPCEAWAGRISYRNTELELQDPGQVEKEIHKAQNVMAGNRGISHELISLEITSPEVPDLTIID
LPGITRVAVDNQPDRDIGLQIKALIKKYIQRQQTINLVVPCNVDIATTEALSMAHEVDPEGDRITIGILTKPDLM
RGTEKSVMNVVRNLTYPLKKGYMIVKCRGQQEITNRLSLAEATKKEITFFQTHPYFRVLLEEGSATVPRLAERLT
TELMHIQKSLPLEGQIRESHQKATEELRRCGADIPSQEADKMFFLIEKIKMFNQDIEKLVEGEEVVRENETRL
YNKIREDFKNWVGILATNTQKVKNIIHEEVEKEYEKQYRGKELLGFVNYKTFEIIIVHQQYIQQLVEPALSMLOKAME
IIQQAFINVAKKHFGFEFFNLNQTVQSTIEDIKVKHTAKAENMIQLQFRMEQMVFCQDQIYSVVLKKVREEIFNPL
GTPSQNMKLNSHFPSNESSVSSFTEIGIHLNAYFLETSKRLANQIPFIIQYFMLRENGDSLQKAMMQILQEKNR
SWLLQEQSETATKRRLKERIYRLTQARHALCQFSSKEIH

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FIGURE 689

CGAGCACTAAGTCCTCTGAGTTCCGCAGCGCAGCACCGGAAGCGGCCGAGCGCGCTCAGCCCGGCGACCCCTGCCG
GGCTCCAGACCCCTGCGCCGCTGCGCCCCGGGTTTTCGCCGCAACCAAGACCCAGCGAGTGCAGCGGCGGCCGCTG
AGGAGGTTTCGAAAACATGGCCAAAAGAAATGCCGAGAAGGAAGTACAGATAGGAATTGGGATCAAGAAGATGAA
GCTGAAGAGGTGGGAACATTCTCCATGGCCAGTGAGGAAGTCTTGAAGAATAGAGCCATAAAGAAAGCAAAGCGC
AGAAATGTTGGATTTGAATCTGACACTGGAGGAGCCTTTAAAGGTTTTAAAGGTTTGGTGTTACCTTCTGGAGGA
GGACGCTTTTCTGGATTTGGTAGTGGCGCTGGAGGGAAGCCTTTGGAAGGACTGTGAATGGAAACAACATAACC
AGTGCCCTCCCTTCGCCAGTGCAAAGGCAGCGGCAGATCCCAAGGTAGCCTTTGGTTCTCTTGCTGCAAATGGC
CCTACCACCTTGGTTGATAAAGTTTCAAATCCCAAACTAATGGGGACAGTCAGCAGCCCTCCTCCTCTGGCCTT
GCTTCCAGTAAAGCTTGTGTGCGAAATGCCTATCACAAGCAGTTGGCCGCCTTGAAGTGTCCGTGCGGGATTGG
ATAGTGAAGCACGTGAATACAAACCCCTCTGTGATCTGACACCTATCTTTAAAGACTATGAGAAATATTTAGCA
AACATTGAACAGCAACACGGGAACAGTGGCAGGAATTCTGAAAGTGAATCTAACAAAGTGGCAGCTGAAACACAG
TCTCCTTCCCTTTTTTGGCTCAACAAAATTACAGCAAGAGTCAAGCTTTTTGTTTCATGGCAACAAAAGTGAAGAT
ACACCTGACAAGAAGATGGAGGTGGCATCTGAAAAGAAAACGGACCCATCATCACTAGGAGCGACAAGTGCCTCA
TTTAATTTTCGGCAAGAAAGTTGATAGCTCTGTTTTGGGCTCATTAAAGCTCTGTCCCCCTGACTGGATTTTCTTTC
TCCCCTGGAAACTCCAGTTTATTTGGCAAAGATACTACCCAGAGTAAACCAGTCTCTTCACCATTTCCCACTAAA
CCATTGGAGGGCCAAGCAGAAGGTGACAGTGGTGAATGCAAAGGTGGAGATGAAGAAGAGAATGATGAGCCACCC
AAAGTAGTAGTTACCGAAGTAAAGAAGAAGATGCTTTTTACTCCAAAAGTGTAAGTGTGTTTACAAGAAGGAC
AATGAGTTTAAAGAGAAAGGCATAGGTACTCTGCAATTTAAACCTACAGCAAATCAGAAGACACAGCTTTTGGTG
CGGGCAGACACCAATTTAGGCAACATATTGCTGAACGTTCTGATTCCACCCAATATGCCATGTACGCGAACAGGG
AAGAATAACGTTCTTATCGTCTGTGTTCCAAATCCACCAATTGACGAGAAGAATGCCACCATGCCAGTCACCATG
TTGATTTCGGGTAAAAACCAGCGAGGATGCAGACGAGTTGCACAAAATTTTACTGGAGAAAAAGGATGCCCTGAACA
CGCAAAGTCGGCTGCAGAATTATTGCCAAGTTGCTGCTGCTTCCACCGCCCCCTTAAAGTTAGTCAGTTTTTCTTC
TCTTCTTTGACATTCTAAGAAGTTATAGATAACTTAAACTTTTGTGAGGAAGATTAAATGTGGCCAATAAAACCT
TTAAATGTTAAGTGTCAAAAAAAAAAAAAAAAAA

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FIGURE 690

MAKRNAEKELTDRNWDQEDAEAEVGTFSMASEEVLKNRAIKKAKRRNVGFESDTGGAFKGFKGLVVPSSGGGRFSG
FGSGAGGKPLEGLSNGNNITSAPPFASAKAAADPKVAFGSLAANGPTTLVDKVSNPKTNGDSQQPSSSSGLASSKA
CVGNAYHKQLAALNCSVRDWIVKHVNTNPLCDLTPIFKDYEKYLANIEQQHGNSGRNSESESNKVAAETQSPSLF
GSTKLQQESSFLFHGNKTEDTPDKKMEVASEKKTDPSLGGATSASFNFGKKVDSSVLGSLSSVPLTGFSPGNS
SLFGKDTTQSKPVSSPFPTKPLEGQAEGDSGECKGGDEEENDEPPKVVVTEVKEEDAFYSKKCKLFYKKDNEFKE
KGIGTLHLKPTANQKTQLLRADTNLGNILLNVLIIPNMPCTRTGKNNVLIVCPNPPIDEKNATMPVTMLIRVK
TSEDADELHKILLEKKA

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FIGURE 691

AAGCTTTCCTCTTTGCATTTTGGCATTGAAAACTCCGAAGAGCGGTTTTTGTGTTTTTATTTAAAGAAGATGATA
CATATGTGTACCCGATTCAAACCTAGAGAATAGAATTTAAACATAATTTCAAAGTCTTCAAATATGCCTAAAG
GTAACAATGTCACTCTTTAATTGCCAATTTCTCTACCACTTTCAAAAAATTACTTCCAAGGATTTAATGAGCTCC
TTCCTTTCAACAGAAAATGGACTATTTTCCTTTTCAGATTTACTATATGCTGTCACTCCAGCTTTATAACCGCATG
TGCATACACAAACATTTCTTTCTCTCTTGCAGGTGGCACAACCAGGAAGGGGAAATCTGTGGTTTAAATCTTT
ATGCCTCATCCTCTGAGTGCTGAAGGCTTGCTGTAGGCTGTATGCTGTTAATGCTAATCGTGATAGGGGTTTTTG
CCTCCAACCTGACTCCTACATATTAGCATTAAACAGTGTATGATGCCTGTTACTAGCATTACATGGAACAAATTGC
TGCCGTGGGAGGATGACAAAGAAGCATGAGTCACCCTGCTGGATAAACTTAGACTTCAGGCTTTATCATTTTTCA
ATCTGTTAATCATAATCTGGTCACTGGGATGTTCAACCTTAAACTAAGTTTTGAAAGTAAGGTTATTTAAAAGAT
TTATCAGTAGTATCCTAAATGCAAACATTTTCATTTAAATGTCAAGCCCATGTTTGTGTTTTTATCATTAAACAGAAA
ATATATTCATGTCACTCTTAATTGCAGGTTTTGGCTTGTTCAATTATAATGTTTCATAAACACCTTTGATTCAACTG
TTAGAAATGTGGGCTAAACACAAATTTCTATAATATTTTGTAGTTAAAAATTAGAAGGACTACTAACCTCCAGT
TATATCATGGATTGTCTGGCAACGTTTTTTAAAAGATTTAGAACTGGTACTTTCCCCCAGGTAACGATTTTCTG
TTCAGGCAACTTCAGTTTAAAATTAATACTTTTATTTGACTCTTAAAGGGAACTGAAAGGCTATGAAGCTGAAT
TTTTTTAATGAAATATTTTAAACAGTTAGCAGGGTAAATAACATCTGACAGCTAATGAGATATTTTTCCATACA
AGATAAAAAGATTTAATCAAAAAATTTCAATTTGAAATGAAGTCCCAAATCTAGGTTCAAGTTCAATAGCTTAG
CCACATAATACGGTTGTGCGAGCAGAGAATCTACCTTTCCACTTCTAAGCCTGTTTCTTCTCCATATGGGGATA
ATACTTTACAAGTTGTTGTGAGGCTTAGATGAGATAGAGAATTATTCCATAAGATAATCAAGTGCTACATTAAT
GTTATAGTTAGATTAAATCCAAGAACTAGTCACCCTACTTTATTAGAGAAGAGAAAAGCTAATGATTTGATTTGCA
GAATATTTAAGGTTTGGATTTCTATGCAGTTTTTCTAAATAACCATCACTTACAAATATGTAACCAAACGTAATT
GTTAGTATATTTAATGTAAACTTGTTTTAACAACCTCTTCTCAACATTTTGTCCAGGTTATTCACTGTAACCAAAT
AAATCTCATGAGTCTTTAGTTGATTTAAAAAA

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FIGURE 692

MSSFLSTENGLFSFQIYYMLSLQLYNRMCIHKHFFLSCRWHKPGRGNLWFKFFMPHPLSAEGLL

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FIGURE 693

GGCACTTTTTAAAAATGTTTATATGAGGAAACAAAGAAGACTTGCTGTGATCCAGCGACATGCCCAGTGAGTCGA
AGAGAAGAAACTGGAATTAAGCTAATCTGTGTGCCACTTAGGTCAGGCCCTCCACTACATGGTCCTGCTTCTCTT
GCATGAGTTAGCTACTCATATCATGAGAGCATCCCTTTCTTAATTTCTGCGCTAGTGGAGCAGAGCCATGTATG
TGCTATGGCCCATATGTTGAAACTTGTTTATCTACAGCTAGCCAGATGGTCTGTAACAGCACACAAAGAAGCCAT
TTGGAAACTTTTCAGAGGGTCAGCACGTTTGGAAAACAACTCAGAGTAATGCATATTGTGATGTCATTGCTTACTT
TAAGCTTACAGTGAGGAATATCTTGTTAGGTACTGAATGTGAAACATGCAGACTTTGAGAACCAACTCAGAGGTC
CTAGCCCCCAGAGACAGAAATTTATTTAATTGGATCACCTTTAGACTTGTTTTGTCTACATGTTCTCTGAAAAA
GGAATATAATGTCTTAATTTAAAATACTTTGTTTTTAAAGTTGCTGCTGGGTAAATACATTTTTTTTTTAAAGAA
AACCTGCTTATGCAGTACATGTTAACAGATATGATGTGGTCATCAATAAAAAATGTAAAATA

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FIGURE 694

ALFKNVYMRKQRR LAVIQRHAQ

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FIGURE 695

GAGACATTCTCAATTGCTTAGACATATTCTGAGCCTACAGCAGAGGAACCTCCAGTCTCAGCACCAATGAATCAA
ACTGCGATTCTGATTGCTGCCTTATCTTTCTGACTCTAAGTGGCATTCAAGGAGTACCTCTCTCTAGAACCGTA
CGCTGTACCTGCATCAGCATTAGTAATCAACCTGTTAATCCAAGGTCTTTAGAAAACTTGAAATTATTCTGCA
AGCCAATTTTGTCCACGTGTTGAGATCATTGCTACAATGAAAAAGAAGGGTGAGAAGAGATGTCTGAATCCAGAA
TCGAAGGCCATCAAGAATTTACTGAAAGCAGTTAGCAAGGAAATGTCTAAAAGATCTCCTTAAAACCAGAGGGGA
GCAAATCGATGCAGTGCTTCCAAGGATGGACCACACAGAGGCTGCCTCTCCCATCACTTCCCTACATGGAGTAT
ATGTCAAGCCATAATTGTTCTTAGTTTGAGTTACACTAAAAGGTGACCAATGATGGTCACCAAATCAGCTGCTA
CTACTCCTGTAGGAAGGTTAATGTTTCATCATCCTAAGCTATTTCAGTAATAACTCTACCCTGGCACTATAATGTAA
GCTCTACTGAGGTGCTATGTTCTTAGTGGATGTTCTGACCCTGCTTCAAATATTTCCCTCACCTTTCCCATCTTC
CAAGGGTACTAAGGAATCTTCTGCTTTGGGGTTTATCAGAATTCTCAGAATCTCAAATAACTAAAAGGTATGCA
ATCAAATCTGCTTTTTTAAAGAATGCTCTTTACTTTCATGGACTTCCACTGCCATCCTCCCAAGGGGGCCAAATTCT
TTCAGTGGCTACCTACATACAATTCCAAACACATACAGGAAGGTAGAAATATCTGAAAAATGTATGTGTAAGTATT
CTTATTTAATGAAAGACTGTACAAAGTATAAGTCTTAGATGTATATATTTCTATATTGTTTTTCAGTGACATGG
AATAACATGTAATTAAGTACTATGTATCAATGAGTAACAGGAAAATTTAAAAATACAGATAGATATATGCTCTG
CATGTTACATAAGATAAATGTGCTGAATGGTTTTCAAATAAAATGAGGTACTCTCCTGGAAATATTAAGAAAGA
CTATCTAAATGTTGAAAGATCAAAGGTTAATAAAGTAATTATAACT

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FIGURE 696

MNQTAILICCLIFLTLSGIQGVPLSRTVRCTCISISNQPVNPRSLEKLEIIPASQFCPRVEIIATMKKKGKRCI
NPESKAIKNLLKAVSKEMSKRSP

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FIGURE 697

ATGATTGCAACAGTGGATT TAAAAGTCAATGAATATGAGAAAACCAAAAATGGCTTGAGATCCTAAATAAGATT
GAAAACAAAACATACACGAAGCTCAAAAATGGACATGTGTTTAGGAAGCAGGCACTGATGAGTGAAGAAAGGACT
CTGTTATATGATGGCCTTGTTTACTGGAAAAGTGTACAGGTCGTTTCAAAGATATCCTAGCTCTACTTCTAACT
GATGTGCTGCTCTTTTTACAAGAAAAGACCAGAAATACATCTTTCAGCCGTTGATCAGAAGCCATCAGTTATT
TCCCTTCAAAGCTTATTGCTAGAGAAGTTGCTAATGAGGAGAGAGGAATGTTTCTGATCAGTGCTTCATCTGCT
GGTCTGAGATGTATGAAATTCACACCAATTCCAAGGAGGAACGCAATAACTGGATGAGACGGATCCAGCAGGCT
GTAGAAAGTTGTCTGAAGAAAAGGGGGAAGGACAAGTGAATCTGATGAAGACAAGAGGAAAAGCTGAAGCCAGA
GTGGCCAAAATTAGCAATGTCAAGAAATACTACTAACCAGACCAACAAATTTGTGCGTATTTGGAGGAGAAG
CTGCATATCTATGCTGAAGTTGGAGAACTGAGCGGATTGAGGACGTCCATCTAGAGCCCCACCTCCTTATTTAAA
CCTGACCCAGGCGAGCCTCCCCAGGCAGCCTCATTACTGGCAGCAGCACTGAAAGAAGCATTAGTCACAGGAGGG
AGAGAAGGAAGAGGCTGTTCCGGATGTGGATCCCGGGATCCAGGCTGTGGTAACCGACTTGCGCGTCTCTGATGCA
GGGGAGAAGGTGGAATGTAGAAATTTCCAGGTTCTTACAATCAGAGATTATACAAGCCATACAGAATTTAACC
CGTCTCTTATACAGCCTTCAGGCCGCCTTGACCATTAGGACAGCCACATTGAGATCCACAGGCTGGTTCTCCAG
CAGCAGGAGGGCCTGTCTCTCGGCCACTCTATCTCCGAGGCGGGCCCTTGAGGACCCAGAGTCTCGCGACGCG
GACAGGCAGCATGAGGAGCTGGCCAATGTGCACCAAGCTTCAGCACCAGCTCCAGCAGGGGCAGCGGCGCTGGCTG
CGCAGGTGTGAGCAGCAGCAGCGGGCGCAGGCGACAGGGAGAGCTGGCTGCAGGAGCGGGAGCGGGAGTGCCAG
TCGAGGAGGAGCTGCTGCTGCGGAGCCGGGGCGAGCTGGACCTCCAGCTCCAGGAGTACCAGCACAGCCTGGAG
CGGCTGAGGGAGGGCCAGCGCCTGGTGGAGAGGGAGCAGGCGAGGATGCGGGCCCAGCAGAGCCTGCTGGGCCAC
TGGAAGCACGGCCGGCAGAGGAGCCTGTCCGCGGTGCTCCTTCCGGGTGGCCCCGAGGTAATGGAACCTTAATCGA
TCTGAGAGTTTATGTCATGAAAATCATTCTTTCATCAATGAAGCTTTAGTACAAATGTCATTTAACACTTTCAAC
AAACTGAATCCATCAGTTATCCATCAGGATGCCACTTACCCTACAACCTCAATCTCATTCTGACTTGGTGAGGACT
AGTGAACATCAAGTAGACCTCAAGGTGGACCCCTTCTCAGCCTTGAATGTCAGTCACAACTGTGGACAGCCGCT
GGTTCCGGCCATCAGATACTTCTTCCATGAAAGCAGCAAGGATTCTTGTAATAATGGCTCCAGTATGACAAAG
TGCAGTTGTACGTTGACATCTCCCCGGGACTGTGGACTGGAACCACATCTACTTTGAAGGATTTGGACACCTCC
CACACTGAGTCCCCAACCCCCATGACTCAAATTCACACCGCCCTCAACTGCAGGCGTTTATAACAGAAGCAAAG
CTAAATCTACCGACAAGGACAATGACCAGACAAGATGGGGAACTGGAGATGGAGCCAAAGAAAATATTGTTTAC
CTCTAAATTGTTGTGTCATTTTCCAAACAAAACAAAACACTGGCACTTTTGGGAGAACTTTTGTCTCCATTCC
TTATGTATGTGTGATTGTCTGTGTCCAAATTGCTTTAAGAATAATATTTAATATTTCTGGAAGCTCATTTTTTT
GGCATGAGTCTAATTAATATTGAAAGCCACCCTGTTGTATAATCTTTAACTTATCAAATCTAATTTAGATT
TCTGGAGGAGAACTAACTTGAATAAGCAGGACTATTTTAAAAGTTGTTTGGACGCTAGAGTAAAATTCATGTC
ACATTTTCTACCCAATCATCTGGATTTCAGATTTCCTTTAAGATCTCAATGAAGCAATTTGGATTTAAAGAGTG
GTATTCACAAGGGGTGAACCTTTCACAGTCAGGGCAGTTGCCTCAGTGCCACATAGGCAGAGGAGGATGTGGGAA
AGGGCTTTTCTCAGCTAGTTTTTGTGTGCTCATTTCTTCTGGGAGCATTAAAAGTGGTGATCTGTTACAGTCACT
ATTCAACTGGGCACGTGTTGTGATTGGTCAGTCAGTACAGCCAGGGATACAGTCCGGACTTGCTTAGTACCTAAGC
CTAATGCTGGTGGGTTTCAAGACATGGTTTCAGCATCATCTTTTAAACAGGCCAGAGGCCAGAGCCCGCATCA
AGTCATTTTGATGTAAATAGTGAACCTTGTAGAGCCCTCACTTCTATCAATCAGCTGTCCTGTCCCTGCCAGCA
CCTGGAGCACCACCTACCCTCCCTGGAAAGAACCCTCCCTGCAGTTTTTAAAGGACAAAACCTGCCACTCCTC
ATTAAGTTTGCTGCCTGGATACACTTTTCCACAAAGGAAAACCTGGCATATCCTGCCTTCCGAGTAGTATGGGCTC
CTGTGTGAGAAACCAGGAGATATTTTCATCTTGTTCCGAAATACTTGTATGTATTTTGGTGTCAATAAATATCTT
GTACCTCATTTAAAAA

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FIGURE 698

MIATVDLKVNEYEKNQKWLEILNKIENKTYTKLKNHVFVRKQALMSEERTLLYDGLVYWKATATGRFKDILALLLT
DVLLFLQEKDQKYIFAAMDQKPSVISLQKLIAREVANEERGMFLISASSAGPEMYEIHNTSKEERNNWMRRIQQA
VESCPEEKGGRTSESEDEDKRKAARVAKIQQCQEILTNQDQQICAYLEEKLHIYAEELGELSGFEDVHLEPHLLIK
PDPGEPPQAASLLAAALKEALVTGGREGRGCSVDVPGIQGVVTDLAVSDAGEKVECRNFPGSSQSEIIQAIQNL
RLLYSLQAALTIQDSHIEIHLVLQQQEGLSLGHSLRGGPLQDQKSRDADRQHEELANVHQLQHQLQQGQRRWL
RRCEQQQRAQATRESWLQERERECQSQEELLLRSRGELDLQLQEYQHSLERLREGQRLVEREQARMRAQQSLLGH
WKHGRQRLSAVLLPGGPEVMELNRSESLCHENSFFINEALVQMSFNTFNKLNP SVIHQDATYPTTQSHSDLVRT
SEHQVDLKVDPSPQPSNVSHKLWTAAGSGHQILPFHESSKDSCKNGSSMTKCSCTLTSPPGGLWTGTTSTLKDLDTS
HTESPTPHDSNSHRPQLQAFITEAKLNLPTRTMTRQDGETGDGAKENIVYL

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FIGURE 699

GCGGCGCTAGGCCTGGGCACGCTGGCGCTGTGCGGGGCGGCGCTGCTCTACCTGGCGCGCTGCGCGGGCCGAGCCC
GGGGACCCCAGGGCGATGTCGGGCGCGAGCCCGCCTCCCCCGCGCCCGCGCGCGCCCGCCCTTCCTGGCAGTG
CTGGTGGCCAGCGCGCCCCGCGCCGCGCGAGCGCCGAGCGTGATCCGCGACACGTGGCTTGCGCGGGCGGGGC
CCCGGGCGACGTGTGGGCGCGCTTTGCCGTGGGCACGGCCGGCCTGGGCGCCGAGGAGCGGGCGGCCCTGGAGCG
GGAGCAGGCGCGGCACGGGGACCTGCTGCTGCTGCCGCGCTGCGCGACGCCTACGAAAACCTCACGGCCAAGGT
GCTGGCCATGCTGGCCTGGCTGGACGAGCACGTGGCCTTCGAGTTCGTGCTCAAGGCGGACGACGACTCCTTCGC
GCGGCTGGACGCGCTGCTGGCCGAGCTGCGCGCCCGCGAGCCCGCGCGCCGCCGCTCTACTGGGGCTTCTTC
TCGGGCGCGGGCCGCTCAAGCCGGGGGGGCGCTGGCGCGAGGCGCCTGGCAACTCTGCGACTACTACCTGCC
TACGCGCTGGGCGCGGCTACGTGCTCTCGGCCGACCTGGTGCCTACCTGCGCCTCAGCCGCGACTACCTGCGC
GCCTGGCACAGCGAGGACGTGTCTCTGGGCGCCTGGCTGGCGCCGGTGGACGTCCAGCGGGAGCACGACCCGCGC
TTCGACACCGAATACCGTCCCCGCGGCTGCAGCAACCAGTACCTGGTGACGCACAAGCAGAGCCTGGAGGACATG
CTGGAGAAGCACGCGACGCTGGCGCGGAGGGCCGCTGTGCAAGCGCGAGGTGCAGCTGCGCCTGTCTACGTG
TACGACTGGTCCGCGCCGCCCTCGCAGTGCTGCCAGAGAAGGGAGGGCATCCCCTCAGCCCGCGGGCCCGGCC
TCCGGGACACCTGCTTACCCGGCGGGCGCCTTGGGGCAGGTGCCGAGCGGGCGCACTACGCCCGGGCCCCAAGGC
CCCCGTCCCGCAGCCACGCTTGTGGTCTGCTGCGTCCGGTCTGCGTTTGGGAGACCCCTGGGGGTTGCCGGGGCA
GCGCGCCGTGTCCAGGTGGAGGTGCCCCGTTCTTGACCTCAGCGAGCCTGAGCCGGGGCCGCGCACGCTGACC
CCGTGCTGTCCCCGACCGGCTCACGGGGCTGGGCTCCGATCTTCCGTGCTCTTATCAGTGGCGTTTCTCACGT
CTGCGTCTCAGATCTAACGTGGTTTACATCAATCCGCTTTCATGGGATTTTGGTCTCTGTCCAGTGACTTCGTG
GTAAATGTAACCTCAGTGTGTTGCTTGCAGCTTATTTATAAATATTGTAAGTTTGTGTCGATGAGTGTAAAGTTGGCA
GTGCGCACGTCTCGGTTTTTTTACATGATTTAAGGAAAGACTTTTATGTCAGAACTTGGTGCCTGTACCGTCAAC
CCGCTGCTGCCGTGTTTAAACGCAGGACAACCTTTAAACTGGCCATCTATCTTTTCAGTGTACAAGTCACTGA
ACCCATTGTTTCTTTCTGAAGAGACTTTCTTTTCAAGGCTTCCCATGGGTCCGCGCCACACAGGGCCGGTGTGTC
TTTATTTTCAGACTCTGCCCCAGGTTCCAGGAATCCGAACCCCGGAGTGCTGACGCGGTTCCCCAAGTTCCGCCCTT
AAGAAAACAGGACCAGCCGGCACCAGGCCCGTCTCTCACGTACTTTAACACATCCTTGAAAGCCCCTCGTTTAAT
GAGAAAAGCGAACACTGCGGTCCCTTGCCAAAGTAAATGAAGCTGCCCCAGGACAAGGGGTTACCATGAGCTCCC
TGGAGTCCGACGCGGGTTTTCTCTCTGGGGACCTGGGTGGTCCCCGCTGTGGTCTTTGTTGTCCCACTTTGGGA
CCGGGTCCAGTCTGGGTCTAGTCTCGAGCATCAGGGTCAGGCTCGGGGACGGGCTGGGTAGGCTCCGGGTGAG
TCTTGCCATGGGTTTGGGAGCAGGTTTGGGTACTTGCCTTTGAAGGCAGCAGTGGTCTCAGGAGGAAGAAACGG
GGGCGGGAGAGAGTGGTGATCTGTGGTCACTGGGTGAGTACCTGCACGGTGATTCTCCACCTCCAAAAGGTAG
GGGTGGGACTGGAGGCGTCCCTAGGTGAGGCCGTTGAGTTCGAGCTCCGATGGGCCACCTTGAATCCAGGACTGA
CCGCCCCGTGTGTGCACAGTTTGTCTTGGACGAGGACTCGTGAGGATCGAGGGCTGGGGACCCGGTGTGAGCAG
GATGGGGCCCTGCCCTCCCGTGGGAGTTGTGGACTCGAGCCCAGGGGCTGCCCGTACAGCGGTGTCCAGGTCC
CTGCCATCCGATTTTACCTGGGATGTCTTCTCTGGAGTTTGAATTGCTTGAGGAACCTGCGTGTGCTTGAGA
GGCCAGAGGGCTTGTGAGAACCCCATGGACAGTGGAGAGCGGGATTGGAACCAAGGGCTGGACTCCACACCTC
TGGCCTGCGTCCCGAGTTCTTTGTGGCTCTGAAGAATTGGCCGCTGTGAAAAGAGCAATGTCCGAGACCCCC
AACAGGAAGAGTCTAAAAATCCAGTTTGCAACCATTCTGACCTACAAAAAATGGAAATTTAGTGTTCAGC
CTAAGACATTAAATTCATATCAGAACAGAA

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FIGURE 700

AALGLGTLALCGAALLYLARCAAEPGDPRAMSGRSPPPAPARAAFLAVLVASAPRAGRAPQRDPQHVACAARG
PGRRVGALCRGHGRPGRGAARPGAGAGAARGPAAAAARAARRLRKPHGQGAGHAGLAGRARGLRVRAQQGGRLLR
AAGRAAGRAARPRARAPPLYWGFFSGRGRVKPGGRWREAAWQLCDYYLPYALGGGYVLSADLVHYLRLSRDYLR
AWHSEDVSLGAWLAPVDVQREHDPRFDTEYRSRGCSNQYLVTHKQSLEDMLEKHATLAREGRICKREVQLRLSYV
YDWSAPPSQCCQRREGIP

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FIGURE 701

CCGAGGCCAAGTCCCGGGCGCTAGCCACCTCCCACCCGCCTCTTGGCTCCTCTCCTCTAGGCCGTCGCTTTTCGG
GTTCTCTCATCGCTTCGTGCTTCGCCAATGTTTGAGGAGAAGGCCAGCAGTCCTTCAGGGAAGATCGGAGGCGAG
GAGAAGCCGATTGGTGCTGGTGAAGAGAAGCAAAAGGAAGGAGGCCAAAAGAAGAACAAGAAGGATCTGGAGAT
GGAGGTCCAGCTGAGTTGAATCCTTGGCCTGAATATATTTACACACGTCTTGAGATGTATAATACTAAAAGCA
GAACATGATTCCATTCTGGCAGAAAAGGCAGAAAAAGATAGCAAGCCAATTAAAGTCACTTTGCCTGATGGTAAA
CAGGTTGATGCGGAATCTTGGAAAACCTACACCATATCAAAATTGCCTGTGGAATTAGTCAAGGCCTGGCCGACAAC
ACCGTTATTGCTAAAGTAAATAATGTTGTGTGGGACCTGGACCGCCCTCTGGAAGAAGATTGTACCTTGGAGCTT
CTCAAGTTTGAGGATGAGGAAGCTCAGGCAGTGTATTGGCACTCTAGTGCTCACATAATGGGTGAAGGCATGGAA
AGAGTCTATGGTGGATGTTTATGCTACGGTCCGCCAATAGAAAATGGATTCTATTATGACATGTACCTCGAAGAA
GGGGGTGTGTCTAGCAATGATTCTCTTCTCTGGAGGCTTTGTGTAAGAAAATCATTAAAGAAAAACAAGCTTTT
GAAAGACTGGAAGTTAAGAAAGAACTTTACTGGCAATGTTTAAAGTACAACAAGTTCAAATGCCGGATATTGAAT
GAAAAGGTGAATACTCCAACCTACCACAGTCTATAGATGTGGCCCTTTGATAGATCTCTGCCGGGTCTCATGTT
AGACACACGGGCAAAATTAAGGCTTTAAAAATACACAAAATTCCTCCACGTAAGTGGGAAGGCAGAGATATG
GAGACTCTCCAGAGAATTTATGGCATTTCATTCCAGATCCTAAAATGTTGAAAGAGTGGGAGAAGTTCCAAGAG
GAAGCTAAAAACCGAGATCATAGGAAAATTGGCAGGGACCAAGAACTATATTTCTTTTCACTGAAGTCAAGCCTGGA
AGTTGCTTTTTTCTGCCAAAAGGAGTCTATATTTATAATGCATTATTGAATTCATTAGGAGCGAATATAGGAAA
AGAGGATTCCAGGAGGTAGTCACCCCAACATCTTCAACAGCCGACTCTGGATGACCTCGGGCCACTGGCAGCAC
TACAGCGAGAACATGTTCTCCTTTGAGGTGGAGAAGGAGCTGTTTGCCCTGAAACCCATGAAGTGGCCAGGACAC
TCCCTTATGTTTGATCATCGGCCAAGGTCTGGCGAGAAGTGCCTCTGCGGCTAGCTGATTTTGGGGGTCTTCAT
AGGAACGAGCTGTCTGGAGCACTCACAGGACTCACCCGGGTACGAAGATTCCAACAGGATGATGCTCACATATTC
TGTGCCATGGAGCAGATTGAAGATGAAATAAAAGGTTGTTTGGATTTTCTACGTACGGTATATAGCGTATTTGGA
TTTTCTTTTAACTAAACCTTTCTACTCGCCCCGAAAAATTCCTTGAGATATCGAAGTATGGGATCAAGCTGAG
AAACAACCTTGAAAACAGTCTGAATGAATTTGGTGAAAAGTGGGAGTTAACTCTGGAGATGGAGCTTTCTATGGC
CCAAAGATTGACATACAGATTAAAGATGCGATTGGGCGGTACCACAGTGTGCAACCATCCAGCTGGATTTCAG
TTGCCCATCAGATTTAATCTTACTTATGTAAGCCATGATGGTGGAGATAAGAAAAGGCCAGTGATTGTTTCATCGA
GCCATCTTGGGATCAGTGGAAGAATGATTGCTATCTCACAGAAAACCTATGGGGGCAAATTGGCCCCCTTTTGG
CTGTCCCCTCGCCAGGTAATGGTAGTTCCAGTGGGACCAACCTGTGATGAATATGCCCAAACGTACGACAACAA
TTCCACGATGCCAAATTCATGGCAGACATTGATCTGGATCCAGGCTGTACATTGAATAAAAAGATTGCAATGCA
CAGTTAGCACAGTATAAATTCATTTTAGTTGTTGGTGAAAAAGAGAAAAATCACTGGCACTGTTAATATCCGCACA
AGAGACAATAAGGTCCACGGGGAACGCACCATTTCTGAAACTATCGAGCGGCTACAGCAGCTCAAAGAGTTCCGC
AGCAAACAGGCAGAAGAAGAATTTTAAATGAAAAAATTACCCAGATTGGCTCCATGGAAGGAGGAACAGCGTTT
CCGTAAAATTGACTTTGTACTCGAAAACGTCAATTTATATTGAACTTGGAGGAGGAGTTTGGCAAAGTCTGAAAT
AGGTCAACCTGCAGGCGTAACTATTTTGTACCTAGTCAGTTTTTAAACAATGTGCATTGGAAGGAGTTAATTA
AGAGAGCCAATAAAATGATTTTACTCATTCACTATCTGAGTACTGGAAGTGAAACATGAGGAATGCTTTAGTGTA
ATGTGGGAGAATTTTTTGTAAATTTAATGCAATTGAAAAAGTTTTCAAATTCATTAAGATACTAGAATTGGT
TATGGTGTAACCGAATTC

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FIGURE 702

MGGEKPIGAGEEKQKEGGKKKNKEGSGDGGRAELNPWPEYIYTRLEMYNILKAEHDSILA EKA EKDSKPIKVTL
PDGKQVDAESWKTPPYQIACGISQGLADNTVIAKVN NVVWDLDRPLEEDCTLELLKFEDEEAQAVYWHSSAHIMG
EGMERVYGGCLCYGPPIENGFFYD MYLEEGGVSSNDFSSLEALCKKIIKEKQAFERLEVKKETLLAMFKYNKFKC
RILNEKVNTPTTTTVYRCGPLIDLRCRGPVHRHTGKIKALKIHKNSSTYWEGKADMETLQRIYGISFPDPKMLKEWE
KFQEEAKNRDHRKIGRDQELYFFHELSPGSCFFLPKGVYIYNALIEFIRSEYRKRGFQEVVTPNIFNSRLWMTSG
HWQHYS ENMFSFEVEKELFALKPMNCPGHSLMFDHRPRSWRELPLRLADFGGLHRNELSGALTGLTRVRRFQDD
AHIFCAMEQIEDEIKGCLDFLRTVYSVFGFSFKLNLSTRPEKFLGDI EVWDQAEKQLENSLNEFGEKWELNSGDG
AFYGP KIDIQIKDAIGRYHQCATIQ LDFQLPIRFNLTYVSHDGEDKKRPVIVHRAILGSVERMIAILTENYGGKL
APFWLSPRQVMVVPVGPTCDEYAQNVRQQFHDAKFMADIDLDPGCTLNKKIRNAQLAQYNFILVVGEKEKITGTV
NIRTRDNKVHGERTISETIERLQQLKEFRSKQAE EEF

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FIGURE 703

ACGTA CTCC ATG CGCTACCTGCTGCCCAGCGTCGTGCTCCTGGGCACGGCGCCACCTACGTGTTGGCCTGGGGG
GTCTGGCGGGCTGCTCTCCGCCCTTCCTGCCCCCGCGCTTCTACCAAGCGCTGGACGACCGGCTCTACTGCGTCTAC
CAGAGCATGGTGCTCTTCTTCTCGAGAATTACACCGGGGTCCAGATATTGCTATATGGAGATTGCCAAAAAAT
AAAGAAAATATAATATATTTAGCAAATCATCAAAGCACAGTTGACTGGATTGTTGCTGACATCTTGGCCATCAGG
CAGAATGCGCTAGGACATGTGCGCTACGTGCTGAAAGAAGGGTTAAAATGGCTGCCATTGTATGGGTGTTACTTT
GCTCAGCATGGAGGAATCTATGTAAAGCGCAGTGCCAAATTTAACGAGAAAGAGATGCGAAACAAGGTGCAGAGC
TACGTGGACGCAGGAACCTCCAATGTATCTTGTGATTTTTCCAGAAGGTACAAGGTATAATCCAGAGCAAAACAAA
GTCCTTTTCAGCTAGTCAGGCATTGTCTGCCCCAACGTGGCCTTGCAAGTATTAAAACATGTGCTAACACCACGAATA
AAGGCAACTCACGTTGCTTTTGATTGCATGAAGAATTATTTAGATGCAATTTATGATGTTACGGTGGTTTATGAA
GGGAAAGACGATGGAGGGCAGCGAAGAGAGTCAACCGACCATGACGGAATTTCTCTGCAAAGAATGTCCAAAAAAT
CATATTCACATTGATCGTATCGACAAAAAAGATGTCCCAGAAGAACAAGACATATGAGAAGATGGCTGCATGAA
CGTTTCGAAATCAAAGATAAGATGCTTATAGAATTTATGAGTCACCAGATCCAGAAAGAAGAAAAAGATTTCTCT
GGGAAAAGTGTTAATTCCAAATTAAGTATCAAGAAGACTTTACCATCAATGTTGATCTTAAGTGGTTTGACTGCA
GGCATGCTTATGACCGATGCTGGAAGGAAGCTGTATGTGAACACCTGGATATATGGAACCCCTACTTGGCTGCCTG
TGGGTTACTATTAAAGCA TAG ACAAGTAGCTGTCTCCAGACAGTGGGATGTGCTACATTGTCTATTTTTGGCGGC
TGCACATGACATCAAATTTGTTCTGAATTTATTAAGGAGTGTAAATAAAGCCTTGTTGATTGAAGATTGGATAA
TAGAATTTGTGACGAAAGCTGATATGCAATGGTCTTGGGCAACATACCTGGTTGTACAACCTTTAGCATCGGGGC
TGCTGGAAGGGTAAAAGCTAAATGGAGTTTCTCCTGCTCTGTCATTTCCTATGAACATAATGACAACCTTGAGAAG
GCTGGGAGGATTGTGATTTTGCAAGTCAGATGGCTGCATTTTGTGAGCATTAAATTTGCAGCGTATTTCACTTTT
CTGTTATTTTCAATTTATTACAACCTTGACAGCTCCAAGCTCTTATTACTAAAGTATTTAGTATCTTGCAGCTAGT
TAATATTTTCATCTTTTGCTTATTTCTACAAGTCAGTGAAATAAATTTGATTTAGGAAGTGTGAGGATGTTCAAAG
GAAAGGGTAAAAGTGTTTCATGGGAAAAAGCTCTGTTTAGCACATGATTTTATTGTATTGCGTTATTAGCTGAT
TTTACTCATTTTATATTTGCAAAATAAATTTCTAATATTTATTGAAATTGCTTAATTTGCACACCCTGTACACAC
AGAAAATGGTATAAAATATGAGAACGAAGTTTAAATTTGTGACTCTGATTCATTATAGCAGAACTTTAAATTTCC
CAGCTTTTTGAAGATTTAAGCTACGCTATTAGTACTTCCCTTTGTCTGTGCCATAAGTGCTTGAAAACGTTAAGG
TTTTCTGTTTTGTTTTGTTTTTTAATATCAAAGAGTCGGTGTGAACCTTGGTTGGACCCCAAGTTCACAAGAT
TTTTAAGGTGATGAGAGCCTGCAGACATTCTGCCTAGATTTACTAGCGTGTGCCTTTTGCTGCTTCTCTTTGAT
TTCACAGAATATTCATTACAGAAGTCGCGTTTCTGTAGTGTGGTGGATTCCCACTGGGCTCTGGTCTTCCCTTGG
ATCCCGTCAGTGGTGTCTGCTCAGCGGCTTGCACGCAGACTTGCTAGGAAGAAATGCAGAGCCAGCCTGTGCTGCC
CACTTTCAGAGTTGAACCTTTAAGCCCTTGTGAGTGGGCTTACCAGCTACTGCAGAGGCATTTTGCAATTTGTC
TGTGTCAAGAAGTTACCTTCTCAAGCCAGTGAAATACAGACTTAATTTGTCATGACTGAACGAATTTGTTTATT
TCCCATTAGGTTTAGTGGAGCTACACATTAATATGTATCGCCTTAGAGCAAGAGCTGTGTTCCAGGAACCAGATC
ACGATTTTTAGCCATGGAACAATATATCCCATGGGAGAAGACCTTTCAGTGTGAACGTGTTCTATTTTTGTGTTAT
AATTTAACTTCGATTTCTCATAGTCTTTAAGTTGACATTTCTGCTTACTGCTACTGGATTTTTGCTGCAGAA
ATGTATCAGTGGCCACATTAAACATACCAGTTGGATCATGATAAGCAAAATGAAAGAAATAATGATTAAGGGAA
AATTAAGTGACTGTGTTACACTGCTTCTCCCATGCCAGAGAATAAACTCTTTCAAGCATCATCTTTGAAGAGTCG
TGTGGTGTGAATTGGTTTGTGTACATTAGAATGTATGCACACATCCATGGACACTCAGGATATAGTTGGCCTAAT
AATCGGGGCATGGGTAAAACCTTATGAAAATTTCTCATGCTGAATTGTAATTTCTCTTACCTGTAAAGTAAAAAT
TTAGATCAATTCATGTCTTTGTTAAGTACAGGGATTTAATATATTTTGAATATAATGGGTATGTTCTAAATTTG
AACTTTGAGAGGCAATACTGTTGGAATTATGTGGATTCTAACTCATTTTAAACAAGGTAGCCTGACCTGCATAAGA
TCACTTGAATGTTAGGTTTCATAGAACTATACTAATCTTCTCACAAAAGGTCTATAAAATACAGTCGTTGAAAAA
AATTTTGTATCAAAATGTTTGAAAAATTAGAAGCTTCTCCTTAACCTGTATTGATACTGACTTGAGTTATTTTCT
AAAATTAAGAGCCGTATACCTACCTGTAAAGTCTTTTACATATCATTTAAACTTTTGTGTTGATTATTACTGATT
TACAGCTTAGTTATTAATTTTTCTTTATAAGAATGCCGTGATGTGCATGCTTTTATGTTTTTTAGAAAAGGGTG
TGTTTGGATGAAAGTAAAAAATAAATCTTTCACTGTCTCT

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FIGURE 704

MRYLLPSVLLGTAPTYVLAWGVWRLLSAFLPARFYQALDDRLYCVYQSMVLFFFENYTGVOILLYGDLPKNKEN
IIYLANHQSTVDWIVADILAIRQNALGHVRYVLKEGLKWLPLYGCYFAQHGGIYVKRSKAFNEKEMRNKVQSYVD
AGTPMYLVIFPEGTRYNPEQTKVLSASQAFAAQRGLAVLKHVLTPIKATHVAFDCMKNYLDIYDVTVVYEGKD
DGGQRRESPTMTEFLCKECPKIHIDRIDKKDVEEQEHMRRWLHERFEIKDKMLIEFYESPDPERRKRFPGKS
VNSKLSIKKTLP SMLILSGLTAGMLMTDAGRKLYVNTWIYGTLLGCLWVTIKA

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FIGURE 705

AGCGGCGAGGGCTGGATCCTGGGCCAAATATATGCCAACAACGACAAGCTCTCCAAGAGGCTGAAGAAAGTGTGG
AAGCCACAGCTGTTTGAGCGAGAGTTCTACAGTGAGATCCTGGACAAGAAGTTCACAGTGACTGTGACCATGCGG
ACCCTGGACCTCATCGATGAGGCTTACGGGCTCGACTTTTACATCCTCAAGACCCCGAAGGAGGACCTGTGCTCC
AAGTTTGGGATGGAGCTGAAGCGAGGGATGCTGCTGCGGCTTGCCCGGCAGGACCCCGAGCTGCACCCCGAGGAC
CCCGAGCGGCGGGCAGCCATCTACGACAAGTACAAGGAATTTGCCATCCCAGAGGAGGAGGCAGAGTGGGTGGGC
CTCACGCTGGAGGAGGCCATTGAGAAGCAGAGACTTTTGGAGGAGAAGGACCCTGTACCCCTGTTCAAGATCTAT
GTGGCGGAGCTGATCCAGCAGCTGCAGCAGCAGGCACTGTCAGAGCCGGCGGTGGTGCAGAAGACAGCCAGTGGC
CAGTGACCACACAGCTCCTCCATGCCTGACCAACAGGCCCCAGCTTTCCCTGCCAGGCCCTTTGCACTGAGGACAC
AGATCCCCGGGGAGCTGTGAGGGCCACCGGTGGGCAGTGGGTGGATCCTGGTTTTCGTGTGCTGCCCCATGCACCTTC
CAGCCCGGGGCCAGCTTGGCAGGGATCCCCAGGAGGCCTGGGCCGCCAGAGGCTCCTCTCAGGCTGGGCCCCGA
CGTTTGCGGCAGTGTTCCCTTGTCCCGTGGGGCCGGGAGCGAGTAAAGTCTGGGCCAGGC

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FIGURE 706

MRTLDLIDEAYGLDFYILKTPKEDLCSKFGMELKRGMLRLRLARQDPQLHPEDPERRAAIYDKYKEFAIPEEEAEW
VGLTLEEAIKQRLLEEKDPVPLFKIYVAELIQQLQQQALSEPAVVQKTASGQ

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FIGURE 707

CCGCTTTGTTGCCTGAGGTGGGTGGCGGTGGAAGTTAAGGGAGTCAGGGGCTATCGCTCCTCGAGACTCGCAGTC
GCGGCCACTGCAGTCACTTCGCCAGTTAGCCCTTAGGGTAGGAGTCGCGCCGGCAGCAGCCATCAGCGGCGGCGT
GTACGGGGGAGATGAAGTTGGAGCCCTTGTTTTTGACATTGGATCCTATACTGTGAGAGCTGGTTATGCTGGTGA
GGACTGCCCAAGGTGGATTTTCTACAGCTATTGGTATGGTGGTAGAAAGAGATGACGGAAGCACATTAATGGA
AATAGATGGCGATAAAGGCAAACAAGGCGGTCCCACCTACTACATAGATACTAATGCTCTGCGTGTTCGAGGGA
GAATATGGAGGCCATTTACCTCTAAAAAATGGGATGGTTGAAGACTGGGATAGTTTCCAAGCTATTTTGGATCA
TACCTACAAAATGCATGTCAAATCAGAAGCCAGTCTCCATCCTGTCTCATGTGAGAGGCACCGTGAATACTAG
AGCAAAGAGAGAGAAAAGTACAGAGTTAATGTTTGAACACTACAACATCCCTGCCTTCTTCCTTTGCAAACTGC
AGTTTTGACAGCATTTGCTAATGGTCTTCTACTGGGCTGATTTTGGACAGTGGAGCCACTCATACCACTGCAAT
TCCAGTCCACGATGGCTATGTCTTCAACAAGGCATTGTGAAATCCCCTCTTGCTGGAGACTTTATTACTATGCA
GTGCAGAGAACTCTTCCAAGAAATGAATATTGAATTGGTTCCCTCCATATATGATTGCATCAAAAGAAGCTGTTTCG
TGAAGGATCTCCAGCAAAGTGGAAAAGAAAAGAGAAGTTGCCTCAGGTTACGAGGTCTTGGCACAATTATATGTG
TAATTGTGTTATCCAGGATTTTCAAGCTTCGGTACTTCAAGTGTGAGATTCACTTATGATGAACAAGTGGCTGC
ACAGATGCCAACTGTTTATTATGAATTCCTCAATGGCTACAATTGTGATTTTGGTGCAGAGCGGCTAAAGATTCC
AGAAGGATTATTTGACCCCTTCCAATGTAAAGGGGTATCAGGAAACACAATGTTAGGAGTCAGTCATGTTGTCAC
CACAAGTGTGGGATGTGTGATATTGATATCAGACCAGGTCTCTATGGCAGTGTAAATAGTGGCAGGAGGAAACAC
ACTAATACAGAGTTTACTGACAGGTTGAATAGAGAGCTGTCTCAGAAAACCTCCTCCAAGTATGCGGTTGAAATT
GATTGCAATAATACAACAGTGAACGGAGGTTTAGCTCATGGATTGGCGGCTCCATTCTAGCCTCTTTGGGTAC
CTTTCAACAGATGTGGATTTCCAAGCAAGAATATGAAGAAGGAGGGAAGCAGTGTGTAGAAAAGAAAATGCCCTTG
AGAAAGAGTTCCCAAGCTTCTACCTTCCCTTTTGTCACCTTACGTTTCATAGCTTTTAGTATACTCAGGAAAAGAA
GACCATCTTTTGTAGAAATGTTTATACATTTATGCATATTTCAATTTCCACTTAAATTTATTTAAAGCTTTAACTG
GCTCTATAAATTAAGTTTGTGCTTTCCTTGAAATGCACTTATTCTTATTACAAGCAITTTTATAATTTTGTATAAA
TGTCTATTTTCTCTAAATATTTGCTTTTCAGTAAATGCTTTCCAACCTCTGTTTAGTGTATTAATTACCAGTGA
TTGGTAGAACTGCTTTTATTGACTAGTAAAAGTTACTGCCTAGTCTTTTACCTTAGGCTTACAGAATTAAATAA
AAATTAGCCATTCCAGAAATATAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 708

MSGGVYGGDEVGALVFDIGSYTVRAGYAGEDCPKVDFTAIGMVVERDDGSTLMEIDGDKGKQGGPTYIDTNAL
RVPRENMEAISPLKNGMVEDWDSFQAILDHTYKMHVKSEASLHPVLMSEAPWNTRAKREKLTELMFEHYNIPAFF
LCKTAVLTAFANGRSTGLILDGATHHTTAIPVHDGYVLQQGIVKSPLAGDFITMQCRELFQEMNIELVPPYMIAS
KEAVREGSPANWKRKEKLPQVTRSWHNYMCNCVIQDFQASVLQVSDSTYDEQVAAQMPTVHYEFPNGYNCDFGAE
RLKIEGLFDPSNVKGLSGNTMLGVSHVVTTSVGMCDIDIRPGLYGSVIVAGGNTLIQSFTDRLNRELSQKTPPS
MRLKLIANNTTVERRFSSWIGGSILASLGTFFQMWISKQEYEEGGKQCVERKCP

[illegible]

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FIGURE 710

MKAVQADQERERQRRLEVEREAEKKREAKQRAKEAQERELRKREKAEKERRRKEYDALKAAREQEKKPKKEAN
QAPKSKSGSRPRKPPPRKHTRSWAVLKLLLLLLFGVAGGLVACRVTELQQQPLCTSVNTIYDNAVQGLRRHEIL
QWVLQTDSSQQ

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FIGURE 711

GGGACCCTGGTGACCAAAGTGGCTCCGGTCAGCGCCCCCTCCTAAAGTCAGCAGCGGGCCCTAGGCTGCCTGCTCCT
CAGATAGTCGCCCGTGAAAGCCCCCAACACCACGACAATCCAGTTTCCTGCTAATTTGCAGCTTCCTCCAGGAACC
GTTTTGATTAAAAGTAACAGTGGTCCGTTGATGTTGGTATCTCCTCAGCAAACCTGTAACAAGAGCCGAGACCACA
AGTAACATAACCTCAAGGCCAGCAGTACCAGCGAATCCTCAAACAGTCAAAATCTGTACAGTGCCGAACCTCTAGC
TCACAATTAATCAAGAAAGTGGCAGTGACACCTGTTAAAAAATTGGCACAAATAGGAACTACTGTGGTAACCACT
GTTCCGAAGCCTTCCTCAGTACAATCTGTGGCTGTGCCAACCAGTGTCTCACAGTTACTCCTGGAAAGCCATTG
AATACTGTAACACCCTGAAGCCTTCAAGTTTGGGAGCATCATCCACTCCTTCAAATGAGCCCAATCTTAAAGCA
GAGAACTCAGCAGCTGTTTCAGATTAATCTTTCTCCGACAATGCTAGAAAATGTGAAGAAATGCAAGAACTTCCTT
GCAATGTTAATAAACTAGCATGTAGTGGATCACAGTCCCCTGAAATGGGGCAAAATGTGAAGAACTGGTGGAA
CAACTTTTGGATGCAAAAATCGAAGCAGAAGAATTTACTAGGAACTGTATGTTGAACTCAAGTCTTCACCTCAG
CCTCACCTGGTTCCTTTTCTTAAGAAAAGCGTGGTTGCCTTACGACAACCTTCTGCCTAACTCCCAGAGCTTCATC
CAGCAATGTGTTTCAGCAGACTTCTAGTGACATGGTCATTGCTACCTGTACTACAACAGTAACAACCTTCTCCTGTG
GTGACAACCTACAGTGTCTCAAGCCAGTCTGAAAAGTCAATTATTGTTTCTGGAGCAACAGCACCAGAACTGTG
TCAGTGCAAACCTTTGAACCCACTTGTCTGGTCCAGTGGGAGCAAAAGCTGGAGTTGTGACACTTCATTCTGTGGGC
CCAACCTGCTGCAACAGGAGGAACAACAGCTGGAACCTGGTTTGCCTCAGACTTCAAAACCACTTGTGACATCTGTG
GCAACACAGTGACCACGGTCTCACTGCAACCTGAAAAGCCAGTTGTCTCTGGAACAGCAGTAACACTGTCCCTT
CCAGCAGTAACCTTTGGAGAACTTCAGGTGCAGCTATTTGTCTTCCATCTGTGAAACCTGTTGTTTCTTCTGC
TGGGACCACATCTGCAAGCCTGTATTGGGACTCCAGTTCAAATCAAACCTTGCCAGCCGGGCCCTGTCTTTCA
CAACCAGCTGGGATTCCAACAGGCAGTTCAAGCAAGCAACTATTCTCATTGTTTCACGTAGTTTCAGCAGCCTTCA
GGAGGCAATGAAAACAAGTGACCACAATTTACATTCTCTCAACATTGACCATTAGAAAATGTGGACAGAAGACG
ATGCCAGTGAACACCATAATACCTACTAGTCAGTTTCCTCCAGCTTCCATTCTAAAGCAAATTACTCTGCCTGGA
AATAAAATTTCTGTCACTTCAAGCATCTCCTACTCAGAAAAATAGAATAAAAGAGAATGTAACATCATGCTTCCGA
GATGAGGATGACATCAATGATGTGACTTCTATGGCAGGGGTCAACCTTAATGAAGAAAATGCCTGCATCTTAGCA
ACAAACTCTGAATTGGTTGGCACACTCATTCACTCATGTAAAGATGAACCATTTCTTTTTATTGGAGCTCTACAA
AAGAGAATCTTAGACATTGGTAAAAAGCATGACATTACAGAACTTAACCTCTGATGCTGTGAACTTGATCTCCCAA
GCAACACAGGAACGACTACGAGGCCCTTCTAGAAAAACTGACTGCAATTGCTCAGCATCGAATGACTACTTACAAG
GCAAGTGAAAATTACATCCTGTGTAGTGATACCAGGTACAGCTCAAATTTCTTGAAAAGCTGGATCAATTGGAG
AAGCAGAGAAAGGATTTGGAAGAAAGAGAAATGTTACTTAAGGCAGCCAAGAGTCGTTCTAATAAAGAAGATCCA
GAACAGCTGAGATTAAAGCAGAAAGCCAAAGAGTTACAGCAATTGGAACCTGCACAGATACAGCATAGAGACGCT
AATCTCACAGCTCTTGCAGCTATTGGACCAAGGAAGAAGAGACCCTAGAATCTGGAATTGAGGGCTTAAAGAC
AACCTTCTTGCTTCTGGGACATCCAGCCTGACAGCCACCAAACAGTTGCATCGTCCAAGAATCACGAGAATCTGC
CTCAGGGACTTGATATTTTGTATGGAACAGGAACGGGAGATGAAGTATTCTCGAGCTCTATACCTGGCCCTTCTG
AAGTGAACCACTCCACTCTTCCATCCACATCCTTGCTATTTACTGCCAAAGAAGACACAAAGCATTGTTGCACTGT
CCTGAAATTTCAATTTCTGGAAAATAACACCAACATGAAAGAGCATTGTTTACGATTAGAACCTTTATTAACCTT
ACCTAT

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FIGURE 712

GTLVTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLMLVSPQQTIVTRAETT
SNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPL
NTVTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPMGQNVKKLVE
QLLDAKIEAEETFTRKLYVELKSSPQPHLVPFLKKSVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSVP
VTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSV
ANTVTTVSLQPEKPVVSGTAVTSLPAVTFGETSGAAICLPVSKPVVSFCWDHICKPVIGTPVQIKLAQPGPVLS
QPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMVNTIIPTSQFPPASILKQITLPG
NKILSLQASPTQKNRIKENVTSCFRDEDDINDVTSMAGVNLNEENACILATNSELVGTLIQSKDEPFLFIGALQ
KRILDIGKKHDITELNSDAVNLISQATQERLRGLLEKLTATAQHRMTTYKASENYILCSDTRSOLKFLEKLDQLE
KQRKDLEEREMLLKAAKSRSNKEDPEQLRLKQKAKELQQLELAQIQHRDANLTALAAIGPRKKRPLESGIEGLKD
NLLASGTSSLTATKQLHRPRITRICLRDLIFCMEQEREMKYSRALYLALLK

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FIGURE 713

ATGGCGGCGGCGGCGGTGGTGGAGTTCCAGAGAGCCCAGTCTCTACTCAGCACCGACCGGGAGGCCTCCATCGAC
ATCCTCCACTCCATCGTGAAGCGTGACATTCAGGAAAACGATGAAGAGGCAGTGCAAGTCAAAGAGCAGAGCATC
CTGGAAC TGGGATCTCTCCTGGCAAAGACTGGACAAGCTGCAGAGCTTGGAGGACTCCTGAAGTATGTACGACCC
TTCTTGAATTCCATCAGCAAGGCTAAAGCAGCTCGCCTGGTCCGATCTCTTCTTGATCTGTTTCTTGATATGGAA
GCAGCTACAGGGCAGGAGGTGAGCTGTGTTTAGAGTCCATCGAATGGGCCAAGTCAGAGAAAAGAACTTTCTTA
CGCCAAGCTTTGGAGGCAAGACTGGTGTCTTTGTACTTTGATACCAAGAGGTACCAGGAAGCATTGCATTGGGT
TCTCAGCTGCTGCGGGAGTTGAAAAGATGGACGACAAAGCTCTTTTGGTGGAAGTACAGCTTTTAGAAAGCAAA
ACATACCATGCCCTGAGCAACCTGCCGAAAGCCCGAGCTGCCTTAACTTCTGCTCGAACCACAGCAAATGCCATC
TACTGCCCCCTAAATTGCAGGCCACCTTGGACATGCAGTCGGGTATTATCCATGCAGCAGAAGAGAAGGACTGG
AAAAC TCGTACTCATACTTCTATGAGGCATTTGAGGGTTATGACTCCATCGACAGCCCCAAGGCCATCACATCT
CTGAAGTACATGTTGCTGTGCAAAATCATGCTCAACACCCCAGAAGATGTCCAGGCTTTGGTGAGCGGGAAGCTT
GCAC TTCGGTATGCAGGGAGGCAGACAGAAGCATTAAATGCGTGGCTCAGGCTAGCAAGAACAGATCACTGGCA
GATTTTGAAAAGGCTCTGACAGATTACCGGGCAGAGCTCCGGGATGACCAATCATCAGCACACACTTGGCCAAG
TTGTATGATAACTTACTAGAACAGAATCTGATCCGAGTCATTGAGCCTTTTTCCAGAGTACAGATTGAACACATA
TCTAGTCTCATCAAAC TCTCCAAGGCCGACGTGGAAAGGAAATTATCACAGATGATTCTTGACAAGAAATTT CAT
GGGATTTTGACCAGGGGGAGGGTGTCTGATTATTTTCGATGAACCCCCAGTAGATAAAACTTACGAAGCTGCT
CTGGAACAATTCAGAACATGAGCAAAGTAGTGGATTCCCTCTACAACAAAGCCAAGAACTGACATAG

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FIGURE 714

MAAAVVEFQRAQSLLSTDREASIDILHSIVKRDIQENDEEAVQVKEQSILELGSLLAKTGQAAELGGLLKVVRP
FLNSISKAKAARLVRSLLDLFLDMEAATGQVELCLESIEWAKSEKRTFLRQALEARLVSLYFDTKRYQEALHLG
SOLLRELKKMDDKALLVEVQLLESKTYHALSNLPKARAALTSARTTANAIYCPPKLQATLDMQSGIIHAAEEKDW
KTAYSIFYEAFEGYDSIDSPKAITSLKYMLLCKIMLNTPEDVQALVSGKLALRYAGRQTEALKCVAQASKNRSIA
DFEKALTDYRAELRDDPIISTHLAKLYDNLLEQNLIIRVIEPFSRVQIEHISSLIKLSKADVERKLSQMILDKKFH
GILDQGEGLIIFDEPPVDKTYEAALETIQNMSKVVDSDLYNKAKKLT

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FIGURE 715

GAGATGGTGATTAAATCCGGGACTTTTAGCATATGGAACAGACCAAGAGGGATTGTTTCAGAGAGGGCATCTCAT
GTGCAGAAAAACAGGTTGTGAAGTCAAACGCAGCTCAGATTCTCACCAGCTGTGCGTATACCCTGACGAGTCCCC
TCACCATTCTGGGCCTTAGTCCCCCTCTGAAAAATGGGACATGGGCACCAGAGAGACTCCTGAGAGCTCCCTTAGT
GCTCTTAGAGGAGACAGGGGAGGTCTCCTTTATCTTTGACCCCTAACCCCTCAGACTTCAGAGGCGGGAAGTGC
AGCGATGATACAAATGGTGTGGTGGAAAGAATGCCGTTTTGGAGTCAGGACACCTGGGTTTGAATCCACTTGCAG
CCACTTGCAGGCTGCTTGACCTTGAACGTATCGTGTCTGATCGTTTCACCTTGGGATCTGTACCTGTGAAGTGGG
TGAAAGTTAAAGAGATAATAAAGTAACAGTCGTGAAAAA

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FIGURE 716

EMVIKSGTFSIWNRPRGIVSERASHVQKNRL

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FIGURE 717

GATCCGGAAGTCGGAGCCTAGCTGCGCGAGAGTTTCTGCTCGCTCAACCGAGTTGTCTGTTGCCCTCGCTTCTC
AGATCCCCGCCGGAAGTGAAGAGAGCAAGCAGATTTGAACCTATCTGCTTTCAAGCTGGTCATCATGATGAAACT
TAGACACAAAAATAAAAAGCCAGGTGAAGGTTCCAAGGGCCACAAGAAGATAAGTTGGCCCTACCTCAGCCTGC
AAAGCAAAATGGGAAGAAAGCAACCTCCAAAGTGCCCTCTGCACCTCATTGTTTACCCCCAATGATCATGCCAA
TCGAGAGGCTGAATTAAAGAAGAAGTGGGTTGAGGAGATGAGGGAGAAGCAGCAAGCCGCCGGGAGCAAGAAAG
ACAAAAACGCAGGACCATTGAGAGCTACTGTCAGGATGTCCTAAGACGCCAGGAGGAGTTTGAACATAAGGAGGA
AGTTTTGCAGGAATTAAATATGTTTCTCAGCTGGATGACGAGGCCACGAGGAAGGCTTATTACAAGGAGTTCCG
TAAGGTGGTGGAACTACTCTGATGTGATTCTGGAAGTCTGGATGCCAGAGACCCATTAGGCTGCCGCTGCTTCCA
AATGGAGGAGGCTGTCTGCGAGCACAAGGCAACAAGAAGCTGGTCTTGAACAAGATTGACCTGGTCCC
CAAGGAGGTTGTGGAGAAATGGCTGGATTACCTTCGGAATGAGTTGCCAACCGTGGCTTTCAAGGCCAGTACCCA
GCATCAGGTCAAAAACCTGAATCGTTGCAGTGTGCCAGTAGATCAGGCCCTCTGAGTCACTGCTGAAAAGCAAAGC
CTGCTTTGGAGCTGAAAACCTCATGAGGGTTCTGGGGAACATTGCGCCCTTGGTGAAGTGCACCCACATTCTG
TGTGGGTGTTGTGGGTCTTCCCAATGTTGGGAAGAGCAGCCTGATCAATAGCCTGAAGCGCAGCCGCGCATGCAG
CGTGGGAGCTGTTCTGGAATTACCAAATTCATGCAGGAGGTCTACCTGGACAAGTTCATCCGGCTCTTGGATGC
TCCAGGCATTGTCCAGGGCCCAACTCAGAGGTGGGCACCATCCTGCGTAACTGCGTCCACGTGCAGAAGCTGGC
AGACCTGTGACCCCACTGGAGACCATCCTGCAGCGCTGCAACCTGGAGGAGATTCCAACCTATTATGGCGTCTC
TGGGTTCAGACCACTGAGCACTTCTGACGGCAGTGGCCACCCTTGGGGAAGAAGAAGAAGGGAGGCTTATA
TAGTCAGGAACAGGCGGCCAAAGCTGTCTAGCTGACTGGGTGAGCGGGAAGATCAGCTTCTATATACCACCACC
AGCCACTCACACTCTGCCCACCCATCTCAGTGTCTGAGATCGTTAAGGAAATGACCGAGGTCTTTGACATCGAGGA
TACTGAGCAGGCCAATGAAGACACCATGGAATGCTTGGCCACCGGAGAATCTGATGAGCTGTTGGGTGACACGGA
CCCCTTGAAATGGAGATCAAGTTGCTCCATTCTCCGATGACGAAAATAGCAGATGCCATTGAAAATAAAACCAC
CGTGTATAAGATTGGAGATCTCACTGGGTATTGCACCAATCCAAACCGTCATCAGATGGGGTGGGCTAAACGCAA
TGTGGACCACCGCCCTAAGAGCAACAGTATGGTGGATGTCTGCTCAGTGGACCGCCGCTCAGTGTCTGCAGAGGAT
CATGGAGACGGACCCCTGCAACAGG3CCAGGCTCTGGCATCTGCCCTGAAAAATAAGAAGAAGATGCAGAAACG
TGCAGATAAAATCGCCAGCAAGCTGTCTGATTCCATGATGTCTGCTCTCGACCTCTCTGGCAATGCTGATGATGG
TGTTGGTGACTTAATCGACTGATCTCACTTCCCTTCCGCTCCAAGCACCAGTTCGGTGGTACGGGGGAATACCAG
TGAAATAGTTTGGTTCTCCCTGAAGCATCTGCATATTGAAAGAACGCTTTCCCACTGTGTGTCTTCTCCCCCTC
CTCCAGTAAAAACAGTCCCGGCTGGGTGCTGTGGCTCACGTCTGTAATCCAGCACTTTGGGAGGCCGAGGTGGG
CGGATCACCTGAGGTGGGAGTTTCGAGACCAGCCTGGCCAACATGGTGAGGCCCCGTCTCTACTAAAAATACAAA
AAAATTTAGCCGTGCTTGGTGGCACCTGTAATCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCCTGAACCT
GGGAGACTAAGGCAGGAGAATCGCCTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCCAGACGGCACCATTGCACT
CTAGCCTGGGCAACAACACGAACTCCGTCCC

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FIGURE 718

MMKLRHKNKKPGEGSKGHKKISWPYPQPAKQNGKKATSKVPSAPHFVHPNDHANREAELKKKWVEEMREKQQAAR
EQERQKRRTIESYQDVLRRQEEFEHKEEVLQELNMFQQLDDEATRKAYYKEFRKVVEYSDVILEVLDARDPLGC
RCFQMEEAVLRAQGNKKLVVLNKKIDLPKEVVEKWLDYLRNELPTVAFKASTQHQQVKNLNRCSVPVDQASESL
KSKACFGAENLMRVLGNYCRLGEVRTHIRVGTVGLPNVGKSSLINSLKRSRACSVGAVPGITKFMQEVYLDKFIR
LLDAPGIVPGPNSVGTILRNCVHVQKLADPVPVETILQRCNLEEISNYYGVSGFQTTEHFLTAVAHRLGKKKK
GGLYSQEQAQAKAVLADWVSGKISFYIPPPATHLPTHLSTAEIVKEMTEVFDIEDTEQANEDTMECLATGESDELL
GDTDPLEMEIKLLHSPMTKIADAIENKTTVYKIGDLTGCTNPNRHQMGWAKRNVDRPKSNSMVDVCSVDRRSV
LQRIMETDPLQQGQALASALKNKKKMQRADKIASKLSDSMMSALDLSGNADDGVGD

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FIGURE 719

GGGTGCTTTACTCCTTCTGTGCTTGGAGGCTTACCCAAGGAGATGGAGGGCAGGAGAGGCCGATGCCTA
GCGTGCTTGCTGCTTACAGGGGTGGTGTACAGGTCACCATTTATTATTAAATTTTACTTTTTTGATCCCTAC
CACATGCTCAACATGGTATTGAGTCCTCAAGAATA TAAAAAGAAAATACAACAGGAACAGTAGTCATTAAGTGT
TTGTTCTGGACTTTAATAAAAGTACAGAGGGTCTTGGAGTACAAAGGCAAAGACATTTAGCTGTGTATAGAATGG
GTGGGGGAATGTGTTCCATGGTTTGGCATTGAGTTCAGCAACATTCCTGAGAGAAATCAACTAGCCCCCTTATAG
AGAAGAGGAAANNNAGGAATTTCTTTTTTATAGTATTGGATAAAG
TTTGGTGTGTTTTACAGAGGAGAAGCAATGGGTCTTAGCTCTTTCTCTATTATGTTATCATCCTCCCTTTTTTGTA
CAATATGTTGTTTACCTGAAAGGAAGGTTTCTATTGTTGGTGTGGACCTGGACAAAGTCCAAGTCTGTGGAAC
TAAAACCTTGAAGGTCTGTATAGGACTCTGGACAATCTCACACCTTAGCTATTCCCAGGGAACCCAGGGGGC
AACTGACATTGCTCACAAGATGTTCTCCTGATGTAGCTTGAGATATAAAGGAAAGGCCTGCACAGGTGGCTGTTT
CTTGCTGTGTTATGTC

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FIGURE 720

VLYSFCAWRLTQLKGDGGQERPMPSPVPAAYRGGVTGHHYSLKFYFFDPLPHAQHGISSRI

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FIGURE 721

GAGACATACAGGACAGAGCATGGCTCGCCTACAGACTGCACTCCTGGTTGTCCTCGTCCTCCTTGCTGTGGCGCT
TCAAGCAACTGAGGCAGGCCCCCTACGGCGCCAACATGGAAGACAGCGTCTGCTGCCGTGATTACGTCCGTTACCG
TCTGCCCCCTGCGCGTGGTGAAACACTTCTACTGGACCTCAGACTCCTGCCGAGGCCTGGCGTGGTGTGCTAAC
CTTCAGGGATAAGGAGATCTGTGCCGATCCCAGAGTGCCCTGGGTGAAGATGATTCTCAATAAGCTGAGCCAATG
AAGAGCCTACTCTGATGACCGTGGCCTTGGCTCCTCCAGGAAGGCTCAGGAGCCCTACCTCCCTGCCATTATAGC
TGCTCCCCGCCAGAAGCCTGTGCCAACTCTCTGCATTCCCTGATCTCCATCCCTGTGGCTGTACCCCTTGGTCAC
CTCCGTGCTGTCACTGCCATCTCCCCCTGACCCCTCTAACCCATCCTCTGCCTCCCTCCCTGCAGTCAGAGGGT
CCTGTTCCCATCAGCGATTCCCTTGCTTAAACCCCTTCCATGACTCCCCACTGCCCTAAGCTGAGGTGAGTCTCCC
AAGCCTGGCATGTGGCCCTCTGGATCTGGGTTCCATCTCTGTCTCCAGCCTGCCACTTCCCTTCATGAATGTTG
GGTCTAGCTCCCTGTTCTCCAAACCCATACTACACATCCCACTTCTGGGTCTTTGGCTGGGATGTTGCTGACAC
TCAGAAAGTCCCACCACCTGCACATGTGTAGCCCCACCAGCCCTCCAAGGCATTGCTCGCCCAAGCAGCTGGTAA
TTCCATTTCAATGATTAGATGTCCCCTGGCCCTCTGTCCCCTCTTAATAACCCCTAGTCACAGTCTCCGCAGATT
TTGGGATTTGGGGGTTTTCTCCCCACCTCTCCACTAGTTGGACCAAGGTTTCTAGCTAAGTTACTCTAGTCTCC
AAGCCTCTAGCATAGAGCACTGCAGACAGGCCCTGGCTCAGAATCAGAGCCCAGAAAGTGGCTGCAGACAAAATC
AATAAACTAATGTCCCTCCCTCTCCCTGCCAAAAGGCAGTTACATATCAATACAGAGACTCAAGGTCACIAGA
AATGGGCCAGCTGGGTCAATGTGAAGCCCCAAATTGCCAGATTACCTTTCTTCCCCCACTCCCTTTTTTTTT
TTTTTTTTTTTGGAGATGGAGTTTCGCTCTTGTACCCACGCTGGAGTGCAATGGTGTGGTCTTGGCTTATTGAAG
CCTCTGCCTCCTGGGTTCAAGTGATTCTCTTGCCCTCAGCCTCCTGAGTAGCTGGGATTACAGGTTCTCTGCTACCA
CGCCCAGCTAATTTTTTGTATTTTTAGTAGAGACGAGGCTTACCATGTTGGCCAGGCTGGTCTCGAACTCCTGTC
CTCAGGTAATCCGCCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACAGTGCCTGGCCTCTTCC
CTCTCCCCCACTGCCCCCCCCCACTTTTTTTTTTTTTTTTTATGGCAGGGTCTCACTCTGTGCGCCAGGCTGGAGTGC
AGTGGCGTGATCTCGGCTCACTACAACCTCGACCTCCTGGGTCAAGTGATTCTCCACCCAGCCTCCCAAGTA
GCTGGGATTACAGGTGTGTGCCACTACGGCTGGCTAATTTTGTATTTTTAGTAGAGACAGGTTTACCATATTG
GCCAGGCTGGTCTTGAACCTCTGACCTCAAGTGATCCACCTTCCTTGTGCTCCCAAAGTGCTGAGATTACAGGCG
TGAGCTATCACACCCAGCCTCCCCCTTTTTTTCCTAATAGGAGACTCCTGTACCTTTCTTCGTTTTACCTATGTG
TCGTGTCTGCTTACATTTCTTCTCCCTCAGGCTTTTTTGGGTGGTCTCCAACCTCCAATACCCAGGCCTGG
CCTCTCAGAGTACCCCCCACTTCCACTTTCCCTGCCTCCTTCTTAAATAGCTGACAATCAAATTCATGCTATGG
TGTGAAAGACTACCTTTGACTTGGTATTATAAGCTGGAGTTATATATGTATTTGAAAACAGAGTAAATACTTAAG
AGGCCAAATAGATGAATGGAAGAATTTTAGGAACTGTGAGAGGGGGACAAGGTGAAGCTTTCTGGCCCTGGGAG
GAAGCTGGCTGTGGTAGCGTAGCGCTCTCTCTCTCTGTCTGTGGCAGGAGCCAAAGAGTAGGGTGTAATTGAGTG
AAGGAATCCTGGGTAGAGACCATTCTCAGGTGGTTGGGCCAGGCTAAAGACTGGGAGTTGGGTCTATCTATGCCT
TTCTGGCTGATTTTTGTAGAGACGGGTTTTGGCATGTATACCAGGCTGGTCTCAAACCTCCTGGGCTCAAGCGAT
CCTCCTGGCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAATCACTGCGCCTGGCTTCCTCTCCTCTTGAG
AAATATTCTTTTCATACAGCAAGTATGGGACAGCAGTGTCCAGGTAAAGGACATAAATGTTACAAGTGTCTGGT
CCTTTCTGAGGGAGGCTGGTGCCGCTCTGCAGGTAATTTGAACCTGTGGAATTGGAGGAGGCCATTCACTCCCT
GAACCCAGCCTGACAAATCACAGTGAGAATGTTACCTTATAGGCTTGCTGTGGGGCTCAGGTTGAAAGTGTGGG
GAGTGACACTGCCTAGGCATCCAGCTCAGTGTCTCATCCAGGGCCTGTGTCCCTCCCGAACCCAGGGTCAACCTGCC
TGCCACAGGCACTAGAAAGACGAATCTGCCTACTGCCCATGAACGGGGCCCTCAAGCGTCCCTGGGATCTCCTTCT
CCCTCCTGTCTGTCTTGCCCTCAGGACTGCTGGAAAATAAATCCTTTAAATAGTAAAAA

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FIGURE 722

MARLQTALLVVLVLLAVALQATEAGPYGANMEDSVCCR DYVRYRLPLRVVKH FYWTS DSCPRPGVLLTFRDKEI
CADPRVPWVKMILNKLSQ

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FIGURE 723

GGCAGGCGCGTGGCCGGGCGCGGCGCGATGAGTGGGGCCCGGGCGGCGCCCGGGGCGCGGGCAACGGCGCGGT
CCGGGGGCTGCGGGTGGACGGGCTGCCCCGCTGCCAAAGAGCTTGAGCGGGCTGCTGCACTCGGCGTCGGGCGG
CGGCGCGTCTGGGGGCTGGCGGCACCTGGAGCGGCTGTACGCGCAGAAGTCGCGCATCCAGGACGAGCTGAGCCG
CGGGGGCCCGGGCGGCGGCGGGGCCCCGGGCGGCAGCGCTGCCCGCCAAGCCTCCCAACCTGGACGCGCGTCTGGC
GCTGCTCCGCAAAGAGATGGTTGGTCTCCGCCAGCTGGACATGTCCTTGCTCTGCCAACTGTACAGCCTCTACGA
GTCGATTCAGGAGTACAAGGGGGCATGCCAGGCAGCCTCCAGCCAGACTGCACTTACGCTCTGGAGAACGGCTT
CTTCGATGAAGAGGAGGAATATTTCCAGGAGCAGAACTCCCTGCACGACAGGAGGGACCGAGGCCCTCCTCGGGA
CTTGCTCACTGCCTGTCTCCTCCCTCTCCAGCAGCGACTGGATTCTGGAGTCCATCTAGAAGGGTCTTGGGAGGGAT
GTGACTGTTGGGAAGCCCTTCCTACTGGACACGCTGTCATCATTTGCTGCTTCTCTTGCAAGAAAGCACCTCCGT
TGTGGACGGTCCTCGGGCACAGGGGATGAGCGCTACCAGTTTTCATTTGTAGGCAGGGAGTTCTCCGCGGATGCAT
GGTGGCAGTCTGCTTTGATGGCAGCAGTTATCTGCTTAGGTGACCTAGAGGTCCCTCAGCAGTATCCTCCACACCT
ATTTATTGAGGTGCACCTGCTGGGGATTATAATGAGAATATAACAAGAGGATCTCGGTGAAAGGCCTTAGTGGG
TGTTTTGTGTGAGGTGGCTTGTAGCTAGCTACTTCCCTTACAGATGGTAGAGTATTCGAATCCTCTTTGTGTTAGG
GTTCTTGCTTCAGTTTGGGATGTATTAACCACCATTTCACTGCTTCCCTTCCCTCAATATGCTCTGCAGCTTT
TCTTGCTGTTTAAACCTCTCGCCTCAGCTTTATTTATTTGTAAGCTGCATTACTAACTGCCCAGTGATTTCGGTGA
AAGCTTTTTACTGAAAAAGTTAACATTTCTAGTCATCCAATCAACTGGCTTTTTTCAACCAAAATTTTATATCA
TTCTTTGTCTATCAGATACGAGAGGAAGGAAGATAATACGAAGACATGTTGAATAGTAAAAAAAAAAAAAAAAA
A

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FIGURE 724

MSGARAAPGAAGNGAVRGLRVDGLPPLPKSLSGLLHSASGGGASGGWRHLERLYAQKSRIQDELSRGGPGGGGAR
AAALPAKPPNLDAALALLRKEMVGLRQLDMSLLCQLYSLYESIQEYKGACQAASSPDCTYALENGFFDEEEYFQ
EQNSLHRRDRGPPRDLSLPVSSLSSSDWILESI

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FIGURE 725

AAATGCAGAGAAGAATGGGCAAAGACCAAAGACCCAACTGCTGCCCTCAGAAAACCTACCTGTCAAAAGGTGTGTG
GAAGGGCAGCTGCTTCGAGGACTTTCAAATATGGAAATGAAGAATATAGTCTCTGCATTGGCATAATACCCAGA
AATAATCGCTTAATGTATATTCATAGCTACCAAAGCTATGTGTGGAATAACATGGTAAGCAAGAGGATAGAAGAC
TATGGACTAAAACCTGTTCCAGGGGACCTCGTTCTCAAAGGAGCCACAGCCACCTATATTGAGGAAGATGATGTT
AATAATTACTCTATCCATGATGTGGTAATGCCCTTGCCTGGTTTCGATGTTATCTACCCAAAGCATAAAATTCAA
GAAGCCTACAGGGAAATGCTCACAGCTGACAATCTTGATATTGACAACATGAGACACAAAATTCGAGATTATTCC
TTGTGAGGGGCTACCGAAAGATCATTATTCGTCTCAGAATGTTAGCTGGGAAGTCGTTGCATATGATGATCCC
AAAATTCACCTTTTCAACACAGATGTGGACAACCTAGAAGGGAAGACACCACCAGTTTTTGTCTCTGAAGGCAAA
TACAGGGCTCTGAAAATGGATTTTTCTCTACCCCTTCTACTTACGCCACCATGGCCATTTCGAGAAGTGCTAAAA
ATGGATACCAGTATCAAGAACCAGACGCAGCTGAATACAACCTGGCTTCGCTGAGCAGTACCTTGTCCACAGATT
AGAAAACGTACACAAGTGTTTGTCTTCTGGCTCCCTGTGCATTTTTGTCTTAGTTTCAGACTCATATATGGATTTT
AAATCTTTGTAATAAAAAATTATTTGTATTTTTAAGTTTTTATTAGCTTAAAGAAATAATTTGCAATATTTGTACA
TGTACACAAATCCTGAGGTTCTTAATTTTAGCTCAGAATATAAATTAGTCAAAATACACTTCAGGTGCTTAAATC
AGAGTAAAATGTCAGCTTTACAATAATAAAAAAGGACTTTGGTTTAAAGTAGCAGGTTTAGGTTTTGCTACATT
CTCAAAGACAGCAGGAGTATTTGACACATCTGTGATGGAGTATACAACAATGCATTTTAAAGAGCAAATGCAACA
AAACAAATCTGGACTATGGATAAATAATTTGAGAGCTGCCACCCACAAATATAAATACAGTACTCATGCTGACTG
AAATAATAAGACATCTACAAATTTATAACAAAAAGTGATTGTCATTATCCTGCTTATGTACTAGATTGAGGCAA
GCATTATAGACTTTTTGGTTGCGGTGGCTTTTGCATTTATATTATCAATGCCTTGCAGGAACGTTGCATTGATAG
GCCCATTTTATTTTTTTTATTTTTTTTTTCGAGACAGGATCTCACTCTGTAGCACAGGCTGGATTGCAGTGCAATC
CTGCAATTCTCAATCTTGCACTGCAGCCTCGACCTCCCAGGCTCCAGTGACTCTCCACCTCAGCCTCCTAAGTA
GCTGGGAGTACAGGCGCGCACCACCGCCTAGCTGATTTTTGTATTTTTTGTAGAGACGGGGTTTGGCCATG
TTGCCGAGGCTAACTCCTGGGATTACAGGCATGAGCTGTGCTGGCCGGGTTTTTTTTTCTTGATGTAAACGTGTA
CAGCTGTTTTATTAGTTAAGGTCTAATTTTTACTCTAGGTGCCTTTTATGTTTCAAGACTCTTCCACTGGACTGG
TATTTGCTCAAAAATAAATAATGGTAGAGAAGAAAACCTATAAAAATGGACAAGGCTTTCTTCTATCAGTAGCGTT
TACCCTTTGTACCAGTGGCTTTGGTATTTCCATGTCTGGCATTGCATAAACTTCTCTGGTGTGAAAGGATAAAT
ATGCCTTTCTAAAGTTGTATATCAAAATTGTATCAATTTTTATTTTCTATGATTCTAGAAACAAATGTAATAAA
TATTTTTAAATCTCCTTTCTACTGGTTATGTAAATAAATCAAATAAATATATCAAAAAAAAAAAAAAAAAA

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FIGURE 726

MKNIVSAFGIIPRNNRLMYIHSYQSYVWNNMVSKRIEDYGLKPVPGDLVLKGATATYIEEDDVNNYSIHDVVMPL
PGFDVIYPKHKIQEAYREMLTADNLDIDNMRHKIRDYSLSGAYRKIIIRPQNVSWEVVAYDDPKIPLFNTDVDNL
EGKTPPVFASEGKYRALKMDFSLPPSTYATMAIREVLKMDTSIKNQTQLNTTWLR

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FIGURE 727

ATGGCAGTGACAACTCGTTTGACATGGTTGCACGAAAAGATCCTGCAAATCATTTTGGAGGGAAGCGGCTTAGC
CTTCTCTATAAGGGTAGTGTCCATGGATTCCGTAATGGAGTTTTGCTTGACAGATGTTGTAATCAAGGGCCTACT
CTAACAGTGATTTATAGTGAAGATCATATTATTGGAGCATATGCAGAAGAGAGTTACCAGGAAGGAAAGTATGCT
TCCATCATCCTTTTTGCACTTCAAGATACTAAAATTTGAGAATGGAACTAGGACTATGTACACCAGAAACACTG
TTTTGTTGTGATGTTACAAAATATAACTCCCCAACTAATTTCCAGATAGATGGAAGAAATAGAAAAGTGATTATG
GACTTAAAGACAATGGAAAATCTTGGACTTGCTCAAAATTGTACTATCTCTATTTCAGGATTATGAAGTTTTTCGA
TGCGAAGATTCACTGGATGAAAGAAAGATAAAAGGGGTCATTGAGCTCAGGAAGAGCTTACTGTCTGCCTTGAGA
ACTTATGAACCATATGGATCCCTGGTTCAACAAATACGAATTCTCCTCCTGGGTCCAATTGGAGCTCCCAAGTCC
AGCTTTTTCAACTCAGTGAGGTCTGTTTTCCAAGGGCATGTAACGCATCAGGCTTTGGTGGGCACTAATACAAC
GGGATATCTGAGAAGTATAGGACATACTCTATTAGAGACGGGAAAGATGGCAAATACCTGCCGTTTATTCTGTGT
GACTCACTGGGGCTGAGTGAGAAAGAAGCGGCCTGTGCAGGGATGACATATTCTATATCTTGAACGGTAACATT
CGTGATAGATACCAGTTTAATCCCATGGAATCAATCAAATTAAATCATCATGACTACATTGATTCCCCATCGCTG
AAGGACAGAATTCATTGTGTGGCATTGTATTTGATGCCAGCTCTATTCAATACTTCTCCTCTCAGATGATAGTA
AAGATCAAAGAATTCAAAGGGAGTTGGTAAACGCTGGTGTGGTACATGTGGCTTTGCTCACTCATGTGGATAGC
ATGGATTTGATTACAAAAGGTGACCTTATAGAAATAGAGAGATGTGAGCCTGTGAGGTCCAAGCTAGAGGAAGTC
CAAAGAAAAC TTGGATTTGCTCTTTCTGACATCTCGGTGGTTAGCAATTATTCCTCTGAGTGGGAGCTGGACCCT
GTAAAGGATGTTCTAATTCTTTCTGCTCTGAGACGAATGCTATGGGCTGCAGATGACTTCTTAGAGGATTGCTT
TTTGAGCAAATAGGGAATCTAAGGGAGGAAATTATCAACTGTGCACAAGGAAAAAAATAG

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FIGURE 728

MAVTTRLTLWLHEKILQNHFGGKRLSLLYKGSVHGF RNVLLDRCCNQGPLTLTVIYSEDHIIIGAYAEESYQEGKYA
SIILFALQDTKISEWKLGLCTPETLFCCDVTKYNSPTNFQIDGRNRKVIMDLKTMENLGLAQNCTISIQDYEVFR
CEDSLDERKIKGVIELRKSLLSALRTYEPYGSILVQQIRILLGPIGAPKSSFFNSVRSVFQGHVTHQALVGTNTT
GISEKYRTYSIRDGKDGKYLFFILCDSLGLSEKEGGLCRDDIFYILNGNIRDYQFNPMESIKLNHHDYIDSPSL
KDRIHCVAFVFDASSIQYFSSQMIVKIKRIQRELVNAGVVHVALLTHVDSMDLITKGDLEIERCEPVRSKLEEV
QRKLGFALSDISVVSNYSSSEWELDPVKDVLILSALRRMLWAADDLFLEDLPFEQIGNLREEIINCAQGKK

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FIGURE 729

GCAGACGCTGCCGTGGAATCCTTGACTCTAGTTCTCTGAGTCGATTGTGATCATGGCTGCTGAGTCTGATGTTCT
GCATTTCCAGTTTGAACAGCAAGGAGATGTGGTCTTGCAGAAAATGAATCTTTTGAGACAGCAGAATTTATTTTG
TGATGTATCAATTTACATTAATGACACTGAGTTCAGGGGCGACAAGGTGATTTTGGCTGCTTGCTCCACTTTTAT
GAGAGATCAGTTTTTACTCACACAGTCAAAACATGTCAGAATCACCATCTTACAGAGTGCAGAAGTTGGCAGAAA
ATTGTTACTGTCTTGCTATACTGGAGCACTTGAAGTTAAAAGGAAAGAGCTTTTGAAATACCTGACTGCTGCCAG
TTACCTTCAGATGGTTCACATTGTGGAAGTGCACAGAAGCTTTGTCAAAGTATCTGGAAATGATCTTTCTAT
GAAAAACAACAACCAACACACTGACCTGTGTCTGAGTCTTCTGATCCTGATGTTAAGAATGAAGTGAATAATTCTGA
TAAAGACTGTGAGATAATTGAAATTTTCAAGATAGTCTGTAAACATAGATTTCCATGTTAAAGAAGAGGAAAAG
CAATGCTTTCAGTCTACAGTAGAGAGTCTGACATCAGAGAGAAAGGAAATGAAGTCACCAGAGCTGTCTACAGT
AGACATAGGTTTTAAAGACAATGAAATTTGTATCCTTCATGTAGAATCCATCAGTACAGCTGGTGTGAAAATGG
GCAGTTTTTACAGCCCTTGACCTCTTCAAAGCAAGCATGATTTCTCTGAAACACAGCATTTCATTGATCAATTC
TACAGTTGAGAGCAGAGTGGCTGAAGTTCCTGGGAATCAAGATCAGGGCTTATTTTGTGAGAATACTGAAGGAAG
TTATGGTACAGTGAGTGAGATTGAGAATCTGGAGGAAGGTTATTCACTGAGGCACCAGTGCCCCAGGTGTCTCTCG
AGGCTTTCTTCATGTTGAAACTATCTGCGCCACCTTAAATGCATAAACTATTCTTATGCTTACAGTGCGGAAA
AACATTTACACAGAAGAAAAATCTCAACCGACACATCCGAGGACACATGGGCATACGGCCCTTTCAGTGTACTGT
GTGCTTGAAGACATTTACTGCCAAAAGCACACTTCAGGACCACTTGAACATACACAGTGGGGATCGGCCATACAA
ATGCCACTGTTGTGATATGGATTTCAAGCACAAAGTCTGCTCTCAAAAAGCACTTAACCTCTGTCCATGGCAGAAG
CAGTGGTGAAAACTATCTAGGCCTGATCTCAAAAGGCAAGTCTACTATAATTATAATCACAGACTGTATATAT
AAMGTTTGTATTATTCTATTACGCAAGTCTTCTGTAGAGATGCAGCATTGTGAATATTTTATCCCCCAATCTT
TGTTTCTTATATTTTGTGCGCTTACACATAATCATTTCTTCTGAACTTCTAACAGTTCCAAAGTTATGGGAGGCA
CAGTAAAGCTGATGGGATTCTGTCTCATCTCATACCTTACATATAAGTCTCAGTAGTATCCCTAGAGAAATAGTG
TTCCTCTCTTATATATTCTTGATTCTAGTGACAAAGGATCCAGCAGTATTTGCAGATTCCGATTGGAGTCTCTA
GGTAATTGATTTAAGTATAAAATCCAATCATATAAAACTTTAATGAATTAGGATAACAAGAAGAGAAAAATAAAG
GTAAAAACACTATTACCTGTTTCTAGTCACTTTAGAACAGATGGCACTAAAAAAATTTTTTTTTTAACTTTTTACC
AGCTGTTCTTGATTCCAACTAAACACCAAGATACTTTTCATTTTAAATGTATAAAGTAACAATTGAGATTCA
CTTGGAATAGCAGAATTTTTTATACAGGGTTAATAATCCTTAAATACTTTTTATTTCCATGCCTTATTAGTAT
ACATACTTAAGAAATGGTTCATTGGGCCCCGAGTTTCTGATTTTATTTAATAACAATCGGATTTAATAATTTGTG
GCCAGTAAATTATACCATTGGCATGAAGCTGTGAAAAATGAGAAATCTACCTTTACCAGGGATATCTGTCTA
CTGTTTTTAAAGTTCTCTCTATTTTATTTTTTATTTAATCATGAAGTAAATTTGAAATTTCTTCTTGGTGTATAG
TTCTGTGAATTTTAAACAGAAAGATTTGTGCACCACTACTGCAGTCGGTACAGAACAGTTCCTTCACTCCCAATAG
CTCTCTTAAGCTGTCCCTTTGTAGTCAGCTCCTTCTAGCTCTAATCCTGGCAACAGTTCCTCGTCACTATTATTT
TGCCTTTTCTGGACTGTCTATATAACAGAACTTTATAGTACGTTCCCTCTTGAAATGCTTTTTTACCAGCATAA
TGACTTTGAGGTTTCATCCATGTCAATTTTAAATTTTGAATTGGCAATATATATTCTAGCTGTTACTAGATGAGCAA
TTTTAAAAAGGTGTAGCTATTAGTGTGTATTTTTTCAATTTACATTAATGTAATTTCCATTCACTATGTGTTGATA
AAAATCTTAACCATCCCTAGAGTTTTATATTTCCAAAAATATGCCAAAAGGAAAACATGACTGTATGATTATTT
TAGCGAGAGTCATATTTGAGATGGTGTCTGAGCCATAGTTCCTAACAATCTCCGTCTACATATAACACAAAAC
TTTATAAATTATTTTAAACAAAGATTAAATATACTGCAGGGCAAATAATATTCTCTAAAACACAGGAAGTCTTT
TCGTAAAGAAGACTGACTAGATGCATCTTTCTTTGAAGCTGTTCTAGTCTCCTCTAGTTAACTTAGCTTTATGT
AGAATYTCTACTGTATTTAATTTTATTTGAAGCCCTTCTGTATTTTAAATGTAATATACTTTGTACCATTTATA
AAAATTGTGTGATGAATGAATCACATGTTGTTGTATAAGTGTAACTTTTTTGTGCAATTTTGTGGGAAAGA
CATCTCCACTGAATTTTAACTTTTCCCTGAGACTTTCAAGAATGCAGGTCTCGTTTGATGAAAAACCGACTTCA
TAACCYAATGTTACTAGTTAGCGACATTGTGCTGAATTCCTTGAACTTTTTAACTTTATATGTAAATAACTT
TGATCTTGGTCATTTGAAAGATCATTTCCAGGTCTAAAATCCATGATTTTGTATTTAATTCTYCCTGAGAACAG
AAGAGGGGAAAGCAAGAGAGGACGGTTTTTGTGCTTTATGAACCTTTGTTACTTAAGTACTCCATTGGAGACATAA
TTTTTCTAATTAGTGGATCTTTTCCACTGGAAAGTGTGATAGCTCATTGCTAATTTTTTCAATTCATAGTTCATTG
CTTCCATTTGACCTAAGATTGGCCATTTGTTGGTGTGAAATATTTTTCTTTTCAGAAATAGTTTACTAGTGATTG
AAGTACTTTTTCTTATTTTTGCTTCTATTATAAAATGGCGTGGGG

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FIGURE 730

MAESDVLHFQFEQQGDVVLQKMNLLRQQNLFCDVSIYINDTEFQGHKVILAACSTFMRDQFLLTQSKHVRIITL
QSAEVGRKLLLSCTGTGALEVKRKELLKYLTAAASYLQMVHIVEKCTEALSKYLEIDLSMKNNNQHTDLCQSSDPDV
KNEDENSDKDCEIIEISEDSPVNIDFHVKEEESNALQSTVESLTSEKEMKSPELSTVDIGFKDNEICILHVESI
STAGVENGGQFSQPCTSSKASMYFSETQHSLINSTVESRVAEVPNGDQGLFCENTECSYGTVSEIQNLEEGYSLR
HQCPRCPRGFLHVENYLRHLKMHKLFLCLQCGKTFQKKNLNRHIRGHMGIRPFQCTVCLKTFTAKSTLQDHLNI
HSGDRPYKCHCCDMDFKHKSALKKHLTSVHGRSSGEKLSRPDLKRQSL

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FIGURE 731

ATGGCGGTAGCGGCGGCGGCGGCGGCGGCTGGGCGGCTGGCGCGGAGGCGGCGGCGGCGCAGCGGAGCGGGCTG
CTGGAAGTTTTGGTGCGGGATCGCTGGCACAAAGTTCTGGTGAAGTTGAGCGAGGACGCCCTGGTTCTGAGCAGC
GAGGAGGGCGCTGCGGCGTACAACGGCATCGGGACCGCCACCAATGGCTCGTTCTGCAGGGGCGCCGGGGCTGGG
CACCCGGGCGCGGGCGGCGCGCAGCCCCGGACTCGCCCGCGGGGTCCGCACCGCTTTACCGACCTGCCCCGAG
CAGGTGCCCCGAGTCCATCTCGAACCAGAAGCGTGGCGTGAAGGTGCTGAAGCAGGAGCTGGGCGGGCTGGGGATC
AGCATCAAGGGGGCAAGGAGAACAAGATGCCCATCCTCATCAGCAAGATCTTCAAGGGGCTGGCGGCGGACCAG
ACCCAAGCCCTGTACGTGGGCGACGCCATCCTGTCTGGTGAACGGAGCCGACCTGCGGGACGCCACCCACGACGAG
GCGGTGCAGGCGTTGAAGCGCGCGGGCAAGGAAGTGTCTGTTGAAGTGAAGTACATGCGAGAAGCCACGCCCTAT
GTGAAGAAAGGATCCCCAGTATCCGAGATTGGGTGGGAAACACCTCCGCCTGAATCCCCTCGGTTAGGGGGCAGC
ACCTCAGACCCCCGTCATCGCAGTCCTTCTCCTTCCACAGAGACCGGAAAAGCATCCCCCTCAAATGTGCTAC
GTCACTCGGAGTATGGCCTTGGCCGACCCTGAGAACAGGCAGCTTGAATCCACTCTCCAGATGCTAAGCACACG
GTGATCCTAAGGAGCAAGGACTCAGCCACGGCCCAGGCATGGTTTCAGTGCCATCCATTCCAACGTTAATGACCTG
CTGACCCGAGTGATTGCTGAGGTCAGAGAGCAGCTGGGAAAACAGGCATTGCTGGGAGCCGAGAGATTAGGCAT
CTTGGCTGGCTTGAGAAAAGGTGCCAGGGGAGAGCAAGAAACAGTGAAACCAGCCCTGGTTGTGCTGACTGAG
AAAGACCTTTTAATCTATGACAGCATGCCACGGAGGAAGGAAGCCTGGTTCAGCCCAGTTACACATACCCTCTT
CTTGCCACCAGGCTGGTCCATTCAGGTCCAGGAAAGGGATCACCCAGGCTGGTGTGGATCTGTCTTTGCAACG
CGAACTGGTACCAGGCAAGGGATTGAAACACATCTCTTCAGAGCAGAGACCAGCAGGGACCTCTCCACTGGACA
AGGAGCATAGTACAGGGTTGCCACAATTCTGCTGAACTCATTGCTGAAATCAGCACTGCTTGACCTACAAAAAC
CAGGAGTGCCGTTTGACCATACATTATGAGAATGGATTTTCTATTACCACTGAACCACAGGAGGGTGCCTTTCCC
AAGACCATCATACAGTCTCCTTATGAAAAGCTCAAAATGTCTTCAGATGATGGAATCAGGATGCTGTATTAGAT
TTTGGAGGCAAAGATGGAGAGATTCAACTGGACCTTCATTCTGCCCAAGCCAATTGTTTTATCATTATTCC
TTCTGTCTAGCTAAGATTACAAGACTGGGCTTGGTGGCCTGA

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FIGURE 732

MAVAAAAAAGPAGAGGGRAQRSGLLEVLVRDRWHKVLVNLS DALVLSSEEGAAAYNGIGTATNGSF CRGAGAG
HPGAGGAQPPDSPAGVRTAFTDLPEQVPESISNQKRGVKVLKQELGGLGISIKGGKENKMPILISKIFKGLAADQ
TQALYVGDAILSVNGADLRDATHDEAVQALKRAGKEVLLLEV KYMREATPYVKKGSPVSEIGWETPPPE SPRLGGS
TSDPPSSQSFSFHRDRKSIPLKMCYVTRSMALADPENRQLEIHSPDAKHTVILRSKDSATAQAWFSAIHSNVNDL
LTRVIAEVREQLGKTGIAGSREIRHLGWLAEKVPGESKKQWKPALVVLTEKDLLIYDSMPRRKEAWFSPVHTYPL
LATRLVHSGPGKGSPQAGVDLSFATRTGTROGIETHLFRAETSRDLSHWTRSIVQGCHNSAELIAEISTACTYKN
QECRLTIHYENGFSITTEPQEGAFPKTIIQSPYEKCLKMSSDDGIRMLYLDFGGKDGEIQDLHLHSCPPIVFIHS
FLSAKITRLGLVA

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FIGURE 733

GTTTCATAATACAGCATGGTCTGGTAGTTTGCAAAATGGTGTGCTTTTGGGGAGATACACTAGCAATTTTTTTAA
AAAATGGAACAGTGTGATAGGAAGCCTGCTGGATGATTTCTTAAATATTCTAAATGTAAGTCAAATATGTTTTA
ATAACAAAGACTTAAATGGCTTTTCTCCCTAGAGACTGAAACTAGTATTCATTGTGTTTCAGAACTTAATTGGGCT
TGAACAGAGATTTAAATCTAATAACAAGTTAATAAATGTGTATGTTTTGTGTGGGTTTGGTAGTGATCTGTGG
TTCTATAGGGTTTAAATAGGAATTGCTTTTGATTGTGTTCTGGCTTTAGAAATGTGAGGCAAATTTTACATTCTTGG
TTCTATTAAGATTTTCTTAGGCATGCTAACATGCCAACAAAAGCCATGTAAGTATTGTATAAAAAGATTCACAT
TGTTAATTTAGCCATTTTGAAATTCAGATGAGTGAGCAAGTTGATAATGGCCTCATCTCTGACCTGAGAAAAAAC
AACTTTGACCCCTGTCTTAAATGCTTTAACCTTGAAGTTGCTTGAGACTTAAGAGGTCATGTTGCTTTAGGTT
TAATAAATAGCCTTAACTATTTGGAGGGGAAAAAAATGGGTCCACTTTTTTTTTTTTTTGGCGTTTGCATGTACAA
CTTTCTATTTTTAGCCTATATTTGGAAGAAAGCACTTAACATTTTAGGAATTCTTTTAAAGCTGCTTGCAAAG
TGTTGGTGATTTTACTGAAAACTTTTGAGATCTTCATTTTACAGGCAGACCTGTCTAACTACAAGCCAGACTTGG
GTTTTCTCCTGTAGTTTGAAGACACACTGACTCCTGACAAAATGCAGCCTGCAACTTCCTGGAGAACAACCTCAGT
GTCACATTAAAGTTTATTATGTATTTAATGATACACTGTTTAATTGACAGTTTTGCATAGTTTGTCTAACTTTAG
AGAATTAAGAGCCTCTCAACTGAGCAGTAAAGGTAAGGAGAGCTCAATCTGCACAGAGCCAGTTTTTGTGTTTG
ATGGAAATAAGATCATCATGCCCACTTGAGACTTCAGATTATTCTTTAGCTTAGTGTTGTATGAGTTACATCTT
ATTAAAGTCGAAATTAATGTAGTTTTCTGCCTTGATAACATTTTATATGTGGTATTAGTTTTAAAGGGTCATTAG
GAAAATGCACATATTCATGAATTTTAAAGCCCATAGAAAAGTTGAAGAATGCTTAATTTTCTTATCCAGTAATG
TAAACACAGAGACAGAACATTGAGATGTGCCTAGTTCTGTATTTACAGTTTGGTCTGGCTGTTTGAGTTCTAGCG
CATTTAATGTTAATAAATAAAATACTGAATTTTAAAGCTGTTAAGAAATTGTCCAGAACGAGAATATTGAAATAA
AACTTCAAGGTTATTATCGCAGTTTTTATGGCGTTTTTGTGTTTGTCACTACAG 3GTCTAAAGGTTACTTATT
AATTAATTGGGGAAGTGGAGACAAGGACCAAAGTTTATCTGGATTTTCTTATTTAATCTTCATTACCTGTGAAAT
ATGTAATTTGTATTCTTACTTTACATATGAGATCAGAAGTTCATTTTCAAGCAGANTGGAAAGGTGGTAAATGGAC
TCTGAATTTAAATATGTCAGTATTTTAAAGGTTATCTTCTGCCTAGTATTTTATGGAATCTGACAAGTTCTCA
GATCACACTTGTTTCCTTAAATCTTGGTAAGTCTGAAGCATTCTTCATTTTGTGTTTATATTATACACGTTAGTAAG
GTGGGAGTTCTTTTGTTTTTGTGNTTTTGGCCAGTTGATAACATGAAAGTTTAAAGAGAGGAGGCC

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FIGURE 734

FHNTAWSGSLQNGVLLGRYTSNFFKKWNSVIGSLLDDFLNILKCKSNMF

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FIGURE 735

GTGCGGTTGGGAACGCGGAGCGGACGGATTGCGATTCAACGGGGTTCCGGACCGCGCTGCGCT**ATGG**AGCAGGTCA
ATGAGCTGAAGGAGAAAGGCAACAAGGCCCTGAGCGTGGGTAACATCGATGATGCCTTACAGTGCTACTCCGAAG
CTATTAAGCTGGATCCCCACAACCACGTGCTGTACAGCAACCGTTCTGCTGCCATGCCAAGAAAGGAGACTACC
AGAAGCCTTATGAGGATGGCTGCAAGACTGTGCGACCTAAAGCCTGACTGGGGCAAGGGCTATTACGAAAAGCAG
CAGCTCTAGAGTTCTTAAACCGCTTTGAAGAAGCCAAGCGAACCTATGAGGAGGGCTTAAACACAGAGGCAAATA
ACCCTCAACTGAAAGAGGGTTTACAGAATATGGAGGCCAGGTTGGCAGAGAGAAAATTCATGAACCCTTTCAACA
TGCCTAATCTGTATCAGAAGTTGGAGAGTGATCCAGGACAAGGACACTACTCAGTGATCCTACCTACCGGGAGC
TGATAGAGCAGCTACGAAACAAGCCTTCTGACCTGGGCACGAACTACAAGATCCCCGGATCATGACCACTCTCA
GCGTCTCTTGGGGTCGATCTGGGCAGTATGGATGAGGAGGAAGAGATTGCAACACCTCCACCACCACCCCTC
CCAAAAAGGAGACCAAGCCAGAGCCAATGGAAGAAGATCTTCCAGAGAATAAGAAGCAGGCACTGAAAGAAAAAG
AGCTGGGGAACGATGCCTACAAGAAGAAAGACTTTGACACAGCCTTGAAGCATTACGACAAAGCCAAGGAGCTGG
ACCCCACTAACATGACTTACATTACCAATCAAGCAGCGGTATACTTTGAAAAGGGCGACTACAATAAGTGCCGGG
AGCTTTGTGAGAAGGCCATTGAAGTGGGGAGAGAAAACCGAGAAGACTATCGACAGATTGCCAAAGCATATGCTC
GAATTGGCAACTCCTACTTCAAAGAAGAAAAGTACAAGGATGCCATCCATTTCTATAACAAGTCTCTGGCAGAGC
ACCGAACCCAGATGTGCTCAAGAAATGCCAGCAGGCAGAGAAAATCCTGAAGGAGCAAGAGCGGGCTGGCTACA
TAAACCCCGACCTGGCTTTGGAGGAGAAGAACAAAGGCAACGAGTGTTTTTCAGAAAGGGGACTATCCCCAGGCCA
TGAAGCATTATACAGAAGCCATCAAAAGGAACCCGAAAGATGCCAAATTATACAGCAATCGAGCTGCCTGCTACA
CCAAACTCCTGGAGTTCCAGCTGGCACTCAAGGACTGTGAGGAATGTATCCAGCTGGAGCCGACCTTCATCAAGG
GTTATACACGGAAAGCCGCTGCGCTGGAAGCGATGAAGGACTACACCAAGCCATGGATGTGTACCAGAAGGCGC
TAGACCTGGACTCCAGCTGTAAGGAGGCGGCAGACGGCTACCAGCGCTGTATGATGGCGCAGTACAACCGGCACG
ACAGCCCCGAAGATGTGAAGCGACGAGCCATGGCCGACCCTGAGGTGCAGCAGATCATGAGTGACCCAGCCATGC
GCCTTATCCTGGAACAGATGCAGAAGGACCCCAAGGCACTCAGCGAACACTTAAAGAATCCTGTAATAGCACAGA
AGATCCAGAAGCTGATGGATGTGGGTCTGATTGCAATTCGG**TGAT**GACTTGTTTCATCCCCCTTCCCTTCGCCCT
CATGTGGAAAGAGGAGCTGGGACCGCGGCGAGCAGCACGGAGCGGAAGGGAGAGCAGGGGAGAGAAGGCCTCATC
TCICTATATTTATACATAACCCCGGGGAAGACACAGAGACTCGTACCTGCGCTGTTTGTGCCGCCGCTGCCTCTG
GGCCCTCCCAGCACACGCATGGTCTCTTACCCTGCCCTCGAGTTCCATGTCTCTTTCCCTTGCCCCTAGTTGC
TGTCTCGGCTGCTCTCCCATAGTTGGTTTTTTTTTTATTTGGGGCAGTGGGCATGTTATGGGGAGGGGAGGGGGT
TCTTCCAGCCTCAGGTCCCAGCTGTCTCACGTTGTTATTCTGCGTCCCCTTCTCCAATAAAACAAGCCAGTTGG
GCGTGTTTATAAC

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FIGURE 736

MEQVNELKEKGNKALSVGNIDDAQCYSIAIKLDPHNHVLVSNRSAAYAKKGDYQKAYEDGCKTVDLKPDWGKGY
SRKAAALEFLNRFEEAKRTYEEGLKHEANNPQLKEGLQNMEARLAERKFMNPFNMPNLYQKLESDPRTRTLSDP
TYRELIEQLRNKPSDLGTKLQDPRIMTTLSVLLGVDLGSMDEEEEIATPPPPPPPKKETKPEPMEEDLPENKKQA
LKEKELGNDAYKKKDFDTALKHYDKAKELDPTNMTYITNQAAVYFEKGDYNKCRELCEKAIEVGRENREDYRQIA
KAYARIGNSYFKEEKYKDAIHFNKSLAEHRTPDVLKCKQQAEEKILKEQERLAYINPDLALEEKNGNECFQKGD
YPQAMKHYTEAIKRNPKDAKLYSNRAACYTKLLEFQLALKDCEECIQLEPTFIKGYTRKAAALEAMKDYTKAMDV
YQKALDLDSSCKEAADGYQRCMMAQYNRHDSPEDVKRRAMADPEVQQIMSDPAMRLILEQMOKDPQALSEHLKNP
VIAQKIQKLMDVGLIAIR

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FIGURE 737A

GCGCGCCCCGGGCGCGGGGCGGCGGCAGCGCGGCGCGCGGGGAGGCGGGGAGGCGGGGGCCCCGGCCGGACGCC
CCTGCGCCCCCTCCCCGCGCCCCGGCGAGGGCGGAGCGCGCTGGCCCTGCAGCCTCCGGCCCCCCCCGGCCCCG
CCGCTCCCCCGGGACGTGGGACGCGGGCGCAGGCGGGGTCCGCGCGCGGGCGGGCGGGGGACGGGCGGAGTCAA
AAGTCTATTGAAAAAGCAGAGAGAGAATGCCTCGGTGTGTAAGTGGAGTGATGAGGACCTGATCTCTGGGCCGTG
TGGGAACACTGGCTGCCATTTTCATCACAGTCAACCTGGACTCACAGAATTTCAAGAGCTTGTCGGTTGGGTCAAG
AATGAACCTACGCATGACGGCGTGCTGATCCTGGGTTTCTAGTCATCCTTTTTAAGCTGCAAAGAAGCATTGCA
GACGTTGTCTCATGGGTACCGCTTGCCAACTTTGGAGGATGTGAAGCCGGTAGAGAAATAAAGCATCGCCCCCTCT
GCGCGCCCCCTCCCCGTCTGCTAGAAATGTTTCTCATGAACGCTTCTCCAGTGGTTGCTCTCCAGTCCAAATGGGAG
GCCTTTGGCCCCGCCAGGGAGCTGTAGGTTCCCCAGGTGCTTCTCGGAGGCTGACGAGGGCGTGAGAGCGCGTCTG
GTGAGCGCCCCGGGTGCAGATGCTTATCAGCACTCTGCAGCGCGACGGGGCTGCTCGGGGCACCAGCGATGAGCGC
GCCGCACAGAGGGGCCACAGGGCAGAGGGATGCCACGACGCCAGGCCGGCTGCCAAGCCCACCGTGCACAAGGAG
CCACCCGCGTTGGCTGTCTGTGGTCTCGTTGCTGACTTTGACCCCATGGGGGAGGAGGAAACTACAGACTTTGGC
CGTTGGTGCTAGATTACAGACAGTGATGATTCCTGGACAGGGACATTGAGGAGGCCATCCAGGAGTACCTGAAG
GCAAAGAGTGGAGCCGCACAGCCCGGGGCCGGCGGGGCCAGCCAGGTGCAGCCAGCCTTCCAGGGCCGCAGGC
GGAGGCAGTAGATGTAAGCCGGAACCGGCTCACGGCAGTGCCCCGACTGCCCTGTGTCCCCAAAACCTTGACCT
GGATCAGGTGGTGGCCCCGGCAGCCAGGTGGGATCCAGCAAGGACCAGGGCTCCGCTCCCCGGTCAGTGTGAGC
AGCGATGACTCCTTCGAGCAGAGCATCAGGGCGGAAATAGAACAGTTTCTGAATGAGAAGAGACAGCATGAGACC
CAAAATGTGATGGGTGAGTGGAGAAGAAACCAGACACAAATGAAAATTCCGCCAAGTCACTCTTGAAATCCCAC
CAAGAGCCGCTACAAAGGTGGTGCATCGGCAGGGCCTGCTGGGCGTCCAGAAGGAGTTTGCTTCCGCAAACT
CCCCGGTTAGCGAAGATGAACGTCCAGCCCAGAAGCCTCAGGTCCAAGGTACAACCACGCAGGAGAACGAGGGC
AGCACGAAGCCGGCAACCCCTGCCGCCCTTCAGAAGCAGCACAGAATAAAGGTGGGATCAAAAGGAGCGCCAGC
GCTGCAAGGAGGGGAAAGCGAGTCATGAGTGCGGCACAGGCGTCCGAGGCGTCCGACTCCAGCAGCGACGATGGC
ATTGAGGAGGCCATCCAGCTGTACCAGCTGCAGAAAACACGCAAGGAGGCCGACGGGGACCTGCCCCAGAGGGTC
CAACTCCGAGAGGAGAGAGCGCCTGACCCTCCCGCACACAGCACAAAGCAGTGCCACAAAAAGTGCTTGGCCGAG
ACCCACAGGAAAAACCCAGCAAGAAGAAGCTAGTGGCCACCAAGACCATGGACCCTGGTCCAGGGGGCCTGGAC
ACTGACCATGCCCCAAGCTCCTGAAGGAAACCAAGCTCCACCTCCAGCGAGCCCTGCTTCCAGGAGTGAGTTT
GTGGAACGGTCTCTGTCCGGGCGGACACATCTGCTGAGCTGATGTGTGCAGAAGCAATCCTGGACATCTCCAAG
ACGATCCTGCCGGCCCCGTAGAGGGCAGTGACGGTCCCTGTCCGCAAGCCACTTCTACTCCCCGAACGTG
CCTTCCCGCTCTGACGGCGACAGTAGCTCCGTGGACAGCGATGACAGCATCGAGCAGGAAATCCGGACATTTTTG
GCCCTAAAGGCGCAGTCAGGGAGTTTGCTGGCCAGAGGTGAGAGCTGCCCCGAGGCTGCCAGGGTCCACTTTTG
CCGCTTGGCTCAACAGCCAGACCGGGCGGCCACAAGACCCCTCTCTCTAAAACACCAGACCCACTGCTGGGCTGC
AAAAGGAAGCGTAGAGGTGGTGGCCATGTGAGGCCATCCACGCCCAAGAAAATGCAGGAGGTGGTGAAAGACGGT
AGCCAGGATGCCGACCACAGCCAGGGGAGAGCTGAGCCCGGCCATGAGAGGCGAGACCTGCCATCCAGGGCAAA
GCCAGTGAGGCCCTGGGAGGGGAGGGCACCGCCAGGGGCCCTGGCGACACTCGCATGTACAGGGCCAGGGTAAG
ACAGACGAGGCAAGGCGCTAGACGAGAAAGAGAGCTCTGAAGACAAAAGCAGCTCCCTGGACAGTGACGAGGAC
CTGGACACAGCCATCAAGGACTTGTTAAGGTCCAAGCGAAAGCTCAAGAAGAGGTGCAGGGAGCCAGGGCTGCG
TGCAGGAAGAAGGTGAGTTCAGCACAGCCCAGACGCACCTTCTTGGAGCAGCTGGGCGGGCTCCGGAGAGACTGG
AAAGACAGGGGCCCGCCAGTGCTGAAGAGCTGCCTCTCCAAGTCCAAGAGAGACAGTGCGGAGGGTCTGGGAAG
AAACCCCCAGTGCTTTTGGCAGCACGGCAGAGAGGATGAGGCAGGAGGGTGCCGCGAGCCAGGACGCGGCCCTG
GCCTTCCGGGTGAGGAGACCCGCTCCGCTCTGCCTCCGAAGGGAATCCATTCCCAGGGAGTCCAGGGCCCA
GCTCCAGCCCCGGCTCCCTGTCTGATGACAGCAGTTCAAGTGACAGCGACAGCATCGAACTGGAGATTAGG
AAGTTTTTGGCGGAAAAGGCCAAGGAGTCAGTGAGCAGTTCAAGTTCAGGCAGAGGGCCCCACCGCTCTTGGG
ACAGGGGGCCAGCCAGGCCAGAGGTGCTGTGCAGGAAGGAGCCGCCCCACCGCTGGCGTGTGCACACGCAGC
CAGAGGGCCAGGGGGGTCCACATCTGGCCGAAGGGCTTCGAGGCACAGAGAGCGCAGGAGCACAGGGCACAGCT
GGTCTGTTACGCCAGGGCGGGAAGGGGCTCCCTGCTGCTCCTGCCCCAGGGGATCCGGTGGCGCCAGGAGCACC
AGCGGCGGTGTCTCCGCCAAGGGGCTCTCAGTGAGCAGGAGAAATGTTTACGTTACAAAGACCAGAGCCCACGA
GGGGCTGAGCCTGCTGCCAAAAGTGCTTTTGGTCAGCTGCCAGCTGTGCCACAGCGGGCACCGAGGCAGGAGGC
GCCAGAGGAACCTTTCACATGGGCTGCGGGAGCCCCGAGCTTCTGACCCCCAGCCCCGGGAGCGGAGAGGGACGCT

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FIGURE 737B

GGAGCCCAGGCCGACCGCACACCGCCCTGGAGCGACTTCGCCCACCAGAGTCGGCTGCCCAGCCCGTGGGTGCTG
CGCTCCGAAGGCAGAGATGCAGTGTGGAGGGGGGGCGTCGGGAGCGAGAGACAAGGGGTCCGAGGGCCCCGCC
CGGGGCCTGCCAGCCTGCCCTTGCGGGCTTCTCGCGCTGCTGTCCACCCAGCTCTTCCACTTTGGAAAGGGT
GTCTCCTGGGGGGGCAGGCAGGCTGGCCTCTTCAGCCCCACCTGGGGCTGCCTCTGCAGGGCCCCCTCCTTCTCG
GCCTTCAGGGAGGCCCAGGCCGGACCCAGCCCTGTCTTTGGAAGCCCACACTTGCTGGCAAAGAAGGACGGCGGC
CCCTGGCCAACCAGGAAGGCACAGGCAGGGCTGAGTTTGCATGACAGGAGGAGCTCGGGCTCGGAGGAAAGCATT
TTAGACCTGAGGTATCGACGAAGGGTCAACAGGGATGACCAGGAGCAGGACGCCTTGGGCAGTGACGCCAGTGAC
TTCAGCGACACCTCCACGGAGGACAGTGGCGGCAGCTCAGTAGTGAAGGTCTAAGCCCTCGAGCTGTGGGTTTCGC
GTCCTGGGTTGCGTGCATTCGTGGAAAGCGGCGTAGCCGTGCGTGTGTGTGATGGTTCCGTGGCTGCAAGGAAGG
GAAACAGTCTATTATACATAGCCCTGTATATATGTACACCAACATGAACTTTTATTTAACAGACGTGTCCTGGT
AAATATGATTTTTGTAGCTTTTTGTAAATTATTTAAAGTGATGTAAAGATATTTTGGAAAATACTGTTGTTCA
ATTTTGTAGGGTGTTCCTAACTGCAGTTTTCTGTGTTCTGCATACAAGTCTTAGCTTAGGAAACATTTGGTTCTT
ACCATCACAGCCAGGTTCACAGAGGCTCTGATGCTTTTTGGTTGATTGCTGGTGAGAATGGCCGGCGGTGGCTGC
AGTGGTAGCCTGAGGAAGGCCAAGCTGCCCTCCCTGGGAATCACTCAGATGCCCCAAGATGTCCGTTGGGAAGCT
CCCAGGACAGCACTTTTTATACAGAGGACACCGCCTCGGCCCCACGTCCTTAGAGGCCAGAGCACATCTGAAAAC
TGCAATCACAGCCGTCCGCTGGAAAAACGTTTCGAAGCACAGTGGCCAGCGAGCGAGCACGTGGCTACTCCCTGT
TGCATGTCAAATCCACACAGATGTCAGCGGCAGCTGCTCGGCAGCCCAGCCCTGGGCCTGGGTGGGTTCAITGCC
AATCTTGTTTCGATCACTAGATGATTCTAACATCGAAATAAACCTCTTTTTATATGGC

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FIGURE 738

MFLMNASPVVALQSKWEAFGPPGSCRFPRCFSEADEGVESASVSARVQMLISTLQORDGAARGTSDERAAQRGHRA
EGCHDARPAAKPTVHKEPPALAVCGLVADFDPMGEEETTDGFLVLDSDDSVDRDIEEAIQEYLKAKSGAAQP
GAGGAQPGAAQPSRAAGGSRCKPEPAHGSAPTALCPPKLVPGSGGGPGSQVGSSKDQGSASPVSVSSDDSFQES
IRAEIEQFLNEKRQHETQKCDGSVEKKPDNENSASLLKSHQEPPTKVVHRQGLLGVOKEFAFRKPPRLAKMNV
QPRSLRSKVTTTQENEGSTKPATPCRPSEAAQNKGKIKRSASAAARRGKRVMSAAQASEASDSSSDDGIEEAIQLY
QLQKTRKEADGDLQORVQLREERAPDPPAHSTSSATKSALPETHRKTPSKKKLVATKTMDPGPGGLDTHAPKLL
KETKAPPPASPARSEFVERSSCRADTSAELMCAEAILDISKTILPAPVEGSDGSLASPLFYSPNVPSRSDGDS
SSVSDSDSIEQEIRTFLLAKAQSGSLLARGESCPQAAQGPLLPPGLNSQTGGHKTPLSKTPDPLLGCRRKRRGGG
HVRPSTPKKMQEVVKDGSQDADHSQGRAEPGHERRDLPIQKASEALGGEGTARGPGDTRMSQGGKTDDEARRLD
EKESSEDKSSSLDSDDEDLDTAIKDLLRSKRKLKKRCREPRACRKKVRFSTAQTHFLEQLGGLRRDWKDRGPPVL
KSCLSKSKRDSGEGPGKKPPSVFGSTAERMROEGAASQDAALAFRVRRPASASASEGNFFPRESQGPAPSPGSL
DDSSSVSDSDSIELEIRKFLAEKAKESVSSSEVQAEGPTALGTGGPARPEVLCRKEPAPPPGVCTRSQRARGVPH
LAEGLRGTESAGAQTAGLFSQGGKGLPAAPARGDPVPPRSTSGGVSAKGLSVSRRNVYVHKDQSPRGAEPAAKS
AFGQLPSCATAGTEAGGARGTFHMGCGSPSFLTPSPGAERDAGAQADRTPPWSDFAHQSRLESPWVLRSEGRDAV
WRGGVGSERDKGSEGPARGLPSPPLAGFSPLLSTQLFHFHFGKGVSWGGRQAGLFSPLGLPLQGPSFSAFREAAQAG
PSPVFGSPHLLAKKDGGPWPTRKAQAGLSLHRRSSGSEESILDLRYRRRVNRDDQEQDALGSDASDFSdTSTED
SGGSSVVKV

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FIGURE 739

ATTTTGA CTGGCAAATGTGGCAGATTTCAGGGATGCAGGTGGATCCTTAACTGAGGTCAAGGTGGAAGAGGAAG
AAAGGGATCCGCAGAGTCCTGAATTTGAAATTGAGGAGGAGGAAGAAATGTTGTCATCCGTCATACCAGATTCCA
GGAGAGAAAATGAACTTCCCGATTTCCTCCACATTGATGAGTTTTTTACCCCTTAACTCAACACCATCTAGATCTG
CATATGATGAGCCTCATTGCTCGTAAATATTGAGAAACAGAACTAGAGTTGGAAAAACGACGACTGGATATCG
AGGCCGAAAGGCTGCAGGTAGAAAAGGAACGCCTACAAATCGAGAAAGAGAGGCTGCGGCATTTAGACATGGAAC
ATGAGCGGCTTCAGCTAGAGAAGGAGCGGCTGCAGATTGAAAGAGAAAAAGTTGAGGTTACAGATAGTCAATTCAG
AGAAACCGTCCTTGAAAAATGAACTTGGTCAAGGAGAAAAATCCATGCTTCAACCACAGGACATAGAAACAGAGA
AGTTAAACTTTGAGCGAGAACGCTTGCAACTGGAAAAGGATAGGCTGCAGTTTTTGAAGTTTGAATCTGAGAAGC
TGCAGATTGAAAAGGAACGCTTACAGGTAGAGAAAGACAGACTTCGAATTCAGAAAGAAGGACACTTGCAGTGAT
TTTTCCAGGCTTCCATTTAGCAAATGTTTGAAAAC TCTAGATTTTTCTCATATCAGGTGATATAATGATGGTTGC
TGGATTAGCTGTGGTTTTCTTGTCTAATGTCAAGTGTTCAGTAGGAAAAAGTTATATGTGGATAACTGTATGCCTAA
GTAGTATATAAAAGCTGTGCCCTAGCGTAAACAGTATAGCAGAACTTACTGTGCTGGACTCTTTACCTTATAAT
ATTACATAGAGTCTTGTATTGTCTGTGTACCCAGAGTTTACAATTATGTCCATATAAAATTCTAGCCCAGAAGTT
CTCATCTGGGGTAGATTTTGGCCTTCAGAAGACCAATTTGGTGATGTCTGGAGACATGTTGGGTTGTCAAACCTG
GGGTGGGGAAAAGGTTGCTACTGTGCAATGCATACCTCCTCAACACCCCCCACACTCAGTAAAGAATTTTCCAA
CCCAAATATCATTAGTCCTGAGGTTGAGAAACCTGTCTAGCCTAACTGTATACCTCTATAGCTATGTTTTAT
AGTTTTAGAATATTAACCTCAGATATTTATGTGGGTAGGTACTTAAATGGCCAAAAAAGTTTAACTATGAAATG
TTACTGTGTAGTATATTGAATATAGGAAGTGATGAAGATTATAGGTATTTTATTCCCATGTTTCCATCTATAAAT
AGCCTTCTCAGATTTCAGAAAACAATACAGAGAACATCAGAAATTTTCTAAAATGGGTCACCTTTGAAAAGAATTCT
TTTTCTCACTATTAATGCTTTAGAAGCAAGACGCAATTTTAAAGCTTTAGTTCCTTTTCTTTCAGTCATTGTCTT
AGTTTGGGTACAAAAATGTCATTTAGTAATGTACTGAAATCTTATAAGTGAATAGTTGAAGCTAGTAAAAATGA
TACCAGTATAAAAAATGGTACTTGTAGTCCATGAGCTTGAACCCAATGACTGATTGTTTGACTTTTAAATAAGTA
ATAGCAGCCATTTGGGAGTAGGGGGTAGGTGGGGAAGATGTACTCCGTATCAAATAATAATGATGTGAAATAAT
GATAGTAGGTATGTATTATGGATTGGAGAAGCACTTATTACACTATCTAACCTAATATGTAGAACAATTCCTGAG
AGTTGTATCTGTCGTTATTTCTGAATGTGAAGCTCAGAGAAGTGACACAGAGTAAATGGCTGATCTTCTATATTG
TAGTATATTTGTCCTTCCCTCTTCCCTGAGGAACAAAGCACGTATCTTTAGTCTCTTTGATATTTATTCTGAGA
CCAAGGGCTTGCTTGACCTGATGATTTTCTTTCAGCTCTCTGAAGGTGCTTTTTCCACAATCCAAGTGATTCTGA
TACACACTAAAGTTGAGAATCACTGCACTAGATCACTTTGTGTTTTCTGATTTTCAAGGTTGATACGTAGCTTTA
ATACAGCTCCTCTGTTGACAGTTATTACTTTAATTTGCAATTTGTTCCTTGTAAGAATGGCTGGAACTGTGTGT
TGACATTTGAGGATGGGTATGCAAGGAAAAAATATACTTCTGTTTACTTACTCTGACTTTGAAATAGTGTATT
TTCTATATCTGAAATAAATGCTTCTACCATAGAAAT

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FIGURE 740

MLSSVIPDSRRENELPDFPHIDEFFTLNSTPSRSAYDEPHLLVNIKQKLELEKRRLDIEAERLQVEKERLQIEK
ERLRHLDMEHERLQLEKERLQIEREKLRLQIVNSEKPSLENELGQGEKSMLQPQDIETEKCLKLERERLQLEKDRL
QFLKFESEKLQIEKERLQVEKDRLRIQKEGHLQ

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FIGURE 741

TGCGGGCGCGAGGTTCCCAGCAGGATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCCAGC
CCGCCCCGGGGCAGGATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTCGGTGTTTCATGATCCTGC
TGATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGACACGTCCTTCTCTAGGCCGCACACGG
GGCCGCCGCTGCCCCAGCCCCGGGCCGGACAGGGACAGGGAGCTCACGGCCGACTCCGATGTGACGAGTTTCTGG
ACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGACCTTCCCAGAAAGGAGACGGAGCAGCCGCCTGCGCCGGGGA
GCATGGAGGAGAGCGTGAGAGGCTACGACTGGTCCCCGCGCGACGCCCCGGCGCAGCCCAGACCAGGGCCGGCAGC
AGGCGGAGCGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACCTCCAGCCTGGCCTTCCCCACCAAGGAGCGCGCAT
TCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGGCCATCTACTGCTACGTGC
CCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTGAGCGGAAGCCTGCTGCACCGCGGTGCGCCCT
ACCGCGACCCGCTGCGCATCCCGCGCGAGCACGTGCACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGC
GCCGCTACGGGAAGCTCTCCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCTTCTCGTGCGCG
ACCCCTTCTGTCGCTGATCTCCGCCTTCCGCAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCGCAAGTTCTG
CCGTGCCCCATGCTGCGGCTGTACGCCAACCACACCAGCCTGCCCGCCTCGGCGCGCGAGGCCTTCCGCGCTGGCC
TCAAGGTGTCCTTCGCCAACTTTCATCCAGTACCTGCTGGACCCGCACACGGAGAAGCTGGCGCCCTTCAACGAGC
ACTGGCGGCAGGTGTACCGCCTCTGCCACCCGTCAGATCGACTACGACTTCGTGGGGAAGCTGGAGACTCTGG
ACGAGGACGCCGCGCAGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACA
GGACCGCCAGCAGCTGGGAGGAGGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCTGTATAAACTCT
ACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCAGAACTCCTCCGAGACTGAAAGCTTTCGCGTTGCT
TTTTCTCGCGTGCCTGGAACCTGACGCACGCGCACTCCAGTTTTTTATGACCTACGATTTTGCAATCTGGGCTT
CTTGTTCACTCCACTGCCTCTATCCATTGAGTACTGTATCGATATTGTTTTTTAAGATTAATATATTTTCAAGGTAT
TTAATACGAAAAAAAAAAAAAAAAAAAAA

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FIGURE 742

MTKARLFRLWLVLGSVFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRELTADSDVDEFIDKFLS
AGVKQSDLPRKETEQPPAPGSMEE SVRGYDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFTP KERAFFDDIP
NSEL SHLIVDDRHGAIYCYVPKVACTNWKRMIVLSGSL LHRGAPYRDPLRIPREHVHNASAH LTFNKFWRRYGK
LSRHLMKVKLKKYTKFLFVRDPFVRLISAFRSKFELENEEFYRKFAVPMRLRYANHTSLPASAREAFRAGLKVSF
ANFIQYLLDPHTEKLAPFNEHWROVYRLCHPCQIDYDFVGKLETLD EDAQLLQLLQVDRQLRFPPSYRNRTASS
WEEDWFAKIPLAWRQQLYKLYEADFVLF GYPKPENLLRD